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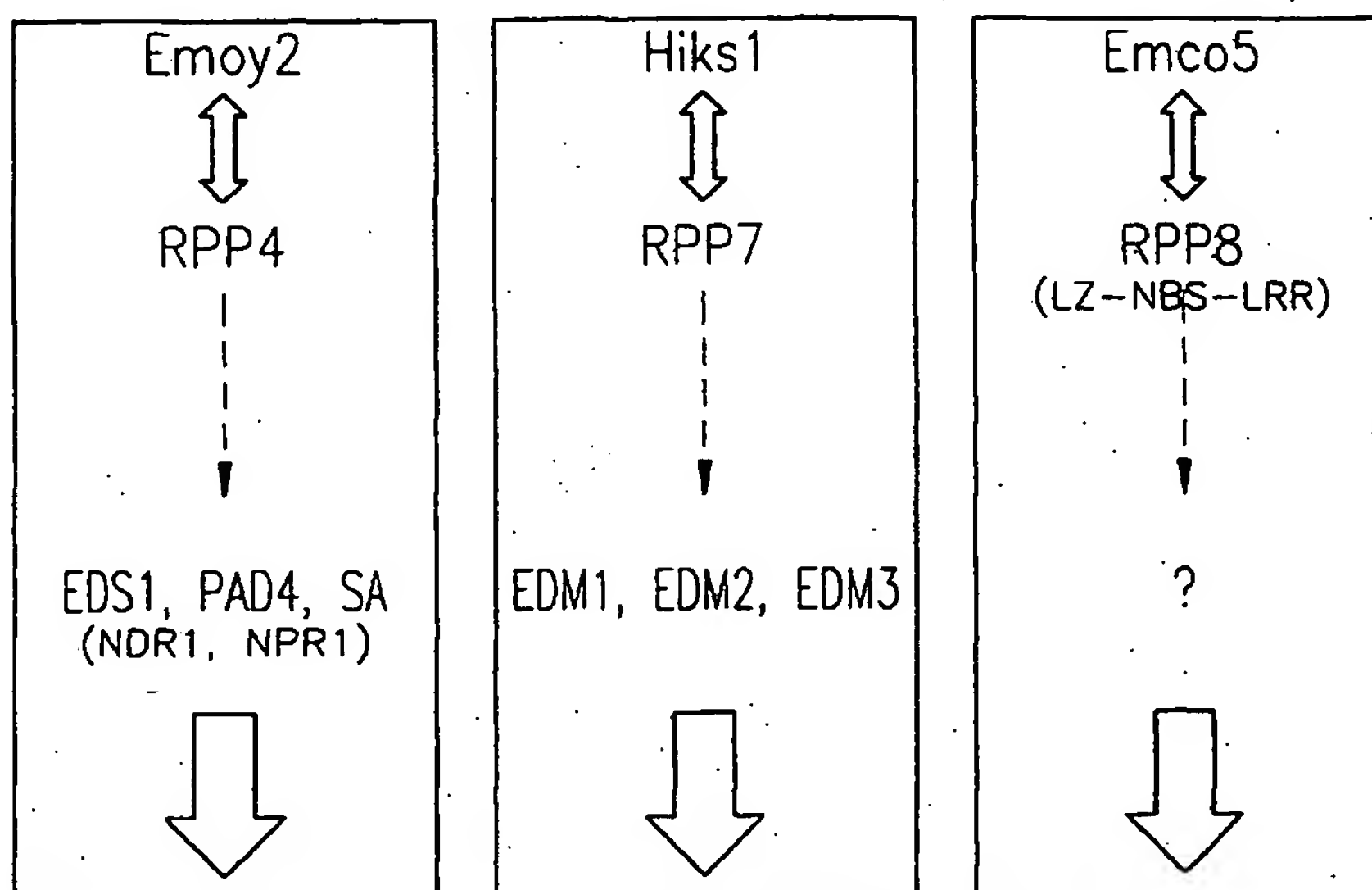
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(54) Title: PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION

RPP-DEPENDENT DEFENSE PATHWAYS



R E S I S T A N C E

(57) Abstract: Methods to identify genes, the expression of which is altered in response to pathogen infection, are provided, as well as the genes identified thereby.

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PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION

5

Cross-Reference to Related Applications

This application is a continuation-in-part application of U.S. application Serial No. 60/232,778, filed on September 15, 2000, and of U.S. application Serial No. 60/300,183, filed on June 22, 2001, the disclosures of which are
10 incorporated by reference herein.

Field of the Invention

The present invention generally relates to the field of plant molecular biology, and more specifically to the regulation of gene expression in plants in response to stress, e.g., to pathogen exposure.

15

Background of the Invention

Plants are capable of activating a large array of defense mechanisms in response to pathogen attack. A crucial factor determining the success of these mechanisms is the speed of their activation. Consequently, there is considerable
20 interest in understanding how plants recognize pathogen attack and control expression of defense mechanisms.

Some potential pathogens trigger a very rapid resistance response called gene-for-gene resistance. This occurs when the pathogen carries an avirulence (*avr*) gene that triggers specific recognition by a corresponding host resistance (*R*) gene. *R* gene specificity is generally quite narrow, in most cases only
25 pathogens carrying a particular *avr* gene are recognized. Recognition is thought to be mediated by ligand-receptor binding. *R* genes have been studied extensively in recent years. For a review of *R* genes, see Ellis et al. (1998); Jones et al. (1997); and Ronald (1998).

30 One of the defense mechanisms triggered by gene-for-gene resistance is programmed cell death at the infection site. This is called the hypersensitive response, or HR. Pathogens that induce the HR, or cause cell death by other means, activate a systemic resistance response called systemic acquired resistance (SAR). During SAR, levels of salicylic acid (SA) rise throughout the
35 plant, defense genes such as pathogenesis related (PR) genes are expressed, and the plant becomes more resistant to pathogen attack. SA is a crucial component

of this response. Plants that cannot accumulate SA due to the presence of a transgene that encodes an SA-degrading enzyme (*nahG*), develop a HR in response to challenge by avirulent pathogens, but do not exhibit systemic expression of defense genes and do not develop resistance to subsequent pathogen attack (Ryals et al., 1996). The nature of the systemic signal that triggers SAR is a subject of debate (Shulaev et al., 1995; Vernooji et al., 1994). SA clearly moves from the site of the HR to other parts of the plant, but if this is the signal, it must be effective at extremely low concentration (Willits et al., 1998).

SAR is quite similar to some reactions that occur locally in response to attack by virulent (those that cause disease) or avirulent (those that trigger gene-for-gene resistance) pathogens. In general, activation of defense gene expression occurs more slowly in response to virulent pathogens than in response to avirulent pathogens. Some pathogens trigger expression of defense genes through a different signaling pathway that requires components of the jasmonic acid (JA) and ethylene signaling pathways (Creelman et al., 1997).

One approach to understanding the signal transduction networks that control defense mechanisms is to use genetic methods to identify signaling components and determine their roles within the network. Considerable progress has been made using this approach in *Arabidopsis*-pathogen model systems.

R gene signal transduction

Genes such as *NDR1* and *EDS1*, as well as *DND1* and the lesion-mimic genes, likely act in signal transduction pathways downstream from *R-avr* recognition. *NDR1* and *EDS1* are required for gene-for-gene mediated resistance to avirulent strains of the bacterial pathogen *Pseudomonas syringae* and the oomycete pathogen *Peronospora parasitica*. Curiously, *ndr1* mutants are susceptible to one set of avirulent pathogens, whereas *eds1* mutants are susceptible to a non-overlapping set (Aarts et al., 1998). The five cloned *R* genes that require *EDS1* all belong to the subset of the nucleotide binding site-leucine rich repeat (NBS-LRR) class of *R* genes that contain sequences similar to the cytoplasmic domains of *Drosophila* Toll and mammalian interleukin 1 transmembrane receptors (TIR-NBS-LRR). The two genes that require *NDR1* belong to the leucine-zipper (LZ-NBS-LRR) subclass of NBS-LRR genes. There is another LZ-NBS-LRR gene, *RPP8*, that does not require *EDS1* or *NDR1*, so

the correlation between *R* gene structure and requirement for *EDS1* or *NDR1* is not perfect. Nevertheless, these results show that *R* genes differ in their requirements for downstream factors and that these differences are correlated with *R* gene structural type.

5 *NDR1* encodes a protein with two predicted transmembrane domains (Century et al. 1997). RPM1, which requires *NDR1* to mediate resistance, is membrane-associated, despite the fact that its primary sequence does not include any likely membrane-integral stretches (Boyes et al., 1998). It is possible that part of the function of *NDR1* is to hold *R* proteins close to the membrane. *EDS1*
10 encodes a protein with blocks of homology to triacyl glycerol lipases (Falk et al., 1999). The significance of this homology is not known, but it is tempting to speculate that *EDS1* is involved in synthesis or degradation of a signal molecule. *EDS1* expression is inducible by SA and pathogen infection, suggesting that *EDS1* may be involved in signal amplification (Falk et al., 1999).

15 It has been extremely difficult to isolate mutations in genes other than the *R* genes that are required for gene-for-gene resistance. A selection procedure was devised (McNellis et al., 1998) on the basis of precisely controlled inducible expression of the *avr* gene *avrRpt2* in plants carrying the corresponding resistance gene *RPS2*. Expression of *avrRpt2* in this background is lethal, as it
20 triggers a systemic HR. It is now possible to select for mutants with subtle defects in gene-for-gene signaling by requiring growth on a concentration of inducer slightly higher than the lethal dose.

Putative plant receptor proteins encoded by *RPP* genes (recognition of *P. parasitica*) mediate specific recognition of *Peronospora* isolates and trigger
25 defense reactions. Recently, McDowell et al. (2000) reported that two members of this class, *RPP7* and *RPP8* (the latter of which encodes a LZ-NBS-LRR type R protein) were not significantly suppressed by mutations in either *EDS1* or *NDR1*, and that *RPP7* resistance was also not compromised by mutations in *EIN2*, *JAR1* or *COI1*, which affect ethylene or jasmonic acid signaling, or in
30 *coi1/npr1* or *coi1/NahG* backgrounds. The authors suggested that *RPP7* initiates resistance through a novel signaling pathway that is independent of salicylic acid accumulation or jasmonic acid response components.

SA-dependent signaling

SA levels increase locally in response to pathogen attack, and systemically in response to the SAR-inducing signal. SA is necessary and sufficient for activation of PR gene expression and enhanced disease resistance.

- 5 Physiological analyses and characterization of certain lesion-mimic mutants strongly suggest that there is a positive autoregulatory loop affecting SA concentrations (Shirasu et al., 1997; Hunt et al., 1997; Weymann et al., 1995). Several mutants with defects in SA signaling have been characterized. These include *npr1*, in which expression of PR genes in response to SA is blocked;
- 10 *cpr1*, *cpr5*, and *cpr6*, which constitutively express PR genes; the *npr1* suppressor *ssil*; *pad4*, which has a defect in SA accumulation; and *eds5*, which has a defect in PR1 expression.

- Expression of the defense genes PR1, BG2, and PR5 in response to SA treatment requires a gene called NPR1 or NIM1. Mutations in *npr1* abolish
- 15 SAR, and cause enhanced susceptibility to infection by various pathogens (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 1997). NPR1 appears to be a positive regulator of PR gene expression that acts downstream from SA. NPR1 encodes a novel protein that contains ankyrin repeats (which are often involved in protein-protein interactions (Cao et al.,
- 20 1997; Ryals et al., 1997), and that is localized to the nucleus in the presence of SA (Dong et al., 1998). Consequently, it is unlikely that NPR1 acts as a transcription factor to directly control PR gene expression, but its nuclear localization suggests that it may interact with such transcription factors.

- PAD4 appears to act upstream from SA. In *pad4* plants infected with a
- 25 virulent *P. syringae* strain, SA levels, synthesis of the antimicrobial compound camalexin, and PR1 expression are all reduced (Zhou et al., 1998). SA is necessary, but not sufficient, for activation of camalexin synthesis (Zhou et al., 1998; Zhao et al., 1996). The camalexin defect in *pad4* plants is reversible by exogenous SA (Zhou et al., 1998). Mutations in *pad4* do not affect SA levels,
- 30 camalexin synthesis, or PR1 when plants are infected with an avirulent *P. syringae* strain (Zhou et al., 1998). Taken together, these results suggest that PAD4 is required for signal amplification to activate the SA pathway in response to pathogens that do not elicit a strong defense response (Zhou et al., 1998).

JA-dependent signaling

JA signaling affects diverse processes including fruit ripening, pollen development, root growth, and response to wounding (Creelman et al., 1997). The *jar1* and *coil* mutants fail to respond to JA (Feys et al., 1994; Staswick et al., 1992). *COII* has been cloned, and found to encode protein containing leucine-rich repeats and a degenerate F-box motif (Xie et al., 1998). These features are characteristic of proteins that function in complexes that ubiquitinate protein targeted for degradation.

In the past few years it has become apparent that JA plays an important role in regulation of pathogen defenses. For example, the induction of the defensin gene *PDF1.2* after inoculation of *Arabidopsis* with the avirulent pathogen *Alternaria brassicicola* does not require SA or NPR1, but does require ethylene and JA signaling (Penninck et al., 1996).

SA signaling and JA signaling pathways are interconnected in complicated ways. Studies in other systems have shown that SA signaling and JA signaling are mutually inhibitory (Creelman et al., 1997; Harms et al., 1998). However, synthesis of camalexin in response to *P. syringae* infection is blocked in *nahG* (Zhou et al., 1998; Zhao et al., 1996) and *coil* (Glazebrook, 1999) plants, strongly suggesting that camalexin synthesis requires both SA and JA signaling.

Induced systemic resistance (ISR)

Some rhizosphere-associated bacteria promote disease resistance (van Loon et al., 1998). This phenomenon, called ISR, has been studied using *Pseudomonas fluorescens* strain WCS417r to colonize *Arabidopsis* roots (Pieterse et al., 1996). Colonized plants are more resistant to infection by the fungal pathogen *Fusarium oxysporum* f sp *raphani* and *P. syringae* (Pieterse et al., 1996). ISR occurs in *nahG* plants, indicating that it is not a SA-dependent phenomenon (Pieterse et al., 1996). Rather, ISR appears to be JA- and ethylene-dependent. The observation that ethylene can induce ISR in *jar1* mutants led to the hypothesis that ISR requires a JA signal followed by an ethylene signal (Pieterse et al., 1998). No changes in gene expression associated with ISR have been detected (Pieterse et al., 1998), suggesting that it is different from activation of *PDF1.2* expression by *A. brassicicola*.

Curiously, ISR requires *NPR1* (Pieterse et al., 1996). This was unexpected in light of the fact that *NPR1* was previously known to be involved only in SA-dependent processes and ISR is SA-independent. If the SA-dependent signal is received, *NPR1* mediates a resistance response characterized by *PR1* expression, whereas if the ISR signal is received, *NPR1* mediates a different resistance response. It is difficult to imagine how this could occur, unless *NPR1* is interacting with different 'adapter' molecules to mediate the different signals. The ankyrin repeats found in *NPR1* could function in protein-protein interactions between *NPR1* and adapter proteins. Identification of proteins that interact with *NPR1*, and characterization of plants with loss-of-function mutations affecting those proteins, would be very helpful for understanding how *NPR1* acts in each pathway. It would also be worthwhile to determine if the *ssi1* or *cpr6* mutations suppress the ISR defect of *npr1* mutants.

Relevance to disease resistance

Characterization of the effects of various mutations on resistance to different pathogens has revealed that there is considerable variation in the extent to which pathogens are affected by defense mechanisms. SAR is known to confer resistance to a wide array of pathogens, including bacteria, fungi, oomycetes, and viruses. JA signaling is important for limiting the growth of certain fungal pathogens. In *Arabidopsis*, the SA pathway mutants *npr1* and *pad4* show enhanced susceptibility to *P. syringae* and *P. parasitica* (Cao et al., 1994; Delaney et al., 1995; Shah et al., 1997; Zhou et al., 1998; Glazebrook et al., 1997).

Overexpression of rate-limiting defense response regulators may cause the signaling network to respond faster or more strongly to pathogen attack, thereby improving resistance. For example, overexpression of *NPR1* caused increased resistance to *P. syringae* and *P. parasitica* in a dosage dependent manner (Cao et al., 1998). Moreover, *NPR1*-overexpression had no obvious deleterious effects on plant growth, in contrast to mutations that lead to constitutive overexpression of defense responses, which generally cause dwarfism.

Thus, what is needed is the systematic identification of genes useful to confer resistance to pathogens.

Summary of the Invention

The invention provides an isolated nucleic acid molecule (polynucleotide), e.g., DNA, comprising a plant or fungal nucleotide sequence, the expression of which is altered in response to stress, e.g., pathogen infection.

5 For example, the invention provides a nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising at least a portion of a key effector gene(s) responsible for host resistance to particular pathogens. To provide resistance or tolerance to a pathogen in a plant, this sequence may be overexpressed individually, in the sense or antisense orientation, or in

10 combination with other sequences, to confer improved disease resistance or tolerance to a plant relative to a plant that does not comprise and/or express the sequence. The overexpression may be constitutive, or it may be preferable to express the effector gene(s) from an inducible promoter including a promoter which is responsive to external stimuli, such as chemical application, or to

15 pathogen infection, e.g., so as to avoid possible deleterious effects on plant growth. In one embodiment of the invention, the promoter employed to express the nucleotide sequence of the invention may be one that mediates rapid and transient transcription after pathogen infection. Thus, the invention also provides an isolated nucleic acid molecule comprising a plant nucleotide

20 sequence which alters, e.g., increases or decreases, the transcription of plant genes, e.g., open reading frames, in response to stress, e.g., pathogen infection.

As described herein, *Arabidopsis* plants of differing genotypes were infected with different strains of an oomycete, *P. parasitica*. RNA was isolated from each plant/pathogen pair and employed to prepare probes which were hybridized to a gene

25 chip having nucleic acid sequences (probe sets) corresponding to approximately 8,200 *Arabidopsis* genes. Genes were then identified that were upregulated or downregulated in response to infection, including genes that were dependent on *RPP7* or *RPP8*, which act via unconventional signaling cascades and are not dependent on defense regulators such as EDS1, NDR1, PAD4, NPR1, RAR1, PBS3 or salicylic acid (SA). Among the

30 genes showing strong *Peronospora*-induced expression changes, clusters of genes were identified that were specifically upregulated by *RPP7* or *RPP8*, or both. In particular in one analysis, the expression of 184 genes (SEQ ID NOs:1-211 and 792) related to 217 probe sets was upregulated by either *RPP7* or *RPP8*, or both, while in another analysis the expression of genes related to 194 probe sets (SEQ ID NOs:212-399 and 793) was

upregulated by either *RPP7* or *RPP8*, or both. Further, as described below, promoters of genes that were rapidly and transiently transcribed after *P. parasitica* infection and were *RPP7/8*-dependent were significantly enriched with both novel sequence motifs and potential binding sites of known transcription factors. Specifically, the promoters were significantly enriched with two novel sequence motifs (referred to as "motif 1" and "motif 2"), one of which was similar to binding sites for Myb transcription factors, sequence motifs related to WRKY binding sites, and two other novel sequence motifs ("motif 3" and "motif 4"). Moreover, comparisons between expression signatures of wild type plants as well as the *RPP7* loss of function mutants, and *edm1*, *edm2* and *edm3* mutants, allow for predictions regarding the *RPP7* pathway hierarchy.

In addition, more than 200 genes (SEQ ID NOs:75, 214, 228, 301, 339, 400-684, 792-795) were identified that were specifically controlled by the *RPP4*-dependent pathway, which mediates resistance of the *Arabidopsis* ecotype Col-0 to the *Peronospora* isolate Emoy2. According to their response to SA, an important mediator of local and systemic defense responses, and the protein biosynthesis inhibitor cycloheximide (CHX), these genes were further subcategorized into immediate early and secondary response genes. A set of immediate early SA responsive genes (SEQ ID NOs:150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615, and 526) was found to consist exclusively of regulatory genes. Such genes are likely controlled by transcription factors acting closely downstream of SA. One highly conserved motif in the promoters of these immediate early genes was similar to binding sites of WRKY transcription factors (SEQ ID NOs:757-765). Other conserved promoter motifs appeared to be novel and may facilitate the cloning of their cognate transcription factors. A cluster of SA/CHX super-induced genes was found to show elevated expression ground states in the *npr1* mutant (SEQ ID NOs:214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447 and 551) suggesting an NPR1-dependent de-repression mechanism in the control of some SA responsive immediate early genes.

Thus, the invention provides an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to a pathogen that induces a response mediated by *R* genes, including pathogens such as bacteria, fungi, oomycetes, viruses, nematodes and insects, e.g., aphids (see Hammond-Kosack and Jones (1997), which is specifically incorporated by

reference herein). For example, the plant or fungal nucleotide sequence encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to infection by an oomycete such as *Peronospora*, and is *RPP4*-,
5 *RPP7*-, and/or *RPP8*-dependent. These sequences can be identified by employing an array of nucleic acid samples, e.g., a plurality of oligonucleotides, each plurality corresponding to a different plant gene, on a solid substrate, e.g., a DNA chip, and probes corresponding to nucleic acid from pathogen-infected (e.g., wild-type) plant cells and to nucleic acid from uninfected plant cells or
10 plant cells having a mutation which alters the response to pathogen infection. Thus, genes, the expression of which are altered by pathogen infection, can be systematically identified. Preferably, the nucleotide sequence is from plant DNA, either a dicot or a monocot, which encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by an open reading
15 frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. More preferably, the nucleotide sequence is from plant DNA that is substantially similar to an *Arabidopsis* nucleic acid segment having any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. The term "substantially similar", when used herein with respect to a polypeptide
20 means a polypeptide corresponding to a reference polypeptide, wherein the polypeptide has substantially the same structure and function as the reference polypeptide, e.g., where only changes in amino acid sequence are those which do not affect the polypeptide function. When used for a polypeptide or an amino acid sequence, the percentage of identity between the substantially similar and
25 the reference polypeptide or amino acid sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, up to at least 99%, where the reference polypeptide is an *Arabidopsis* polypeptide encoded by an open reading
30 frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. However, the percent of identity between the substantially similar and the reference polypeptide may be less than 65% as long as the two polypeptides have the same or similar function, e.g., catalyze the same or similar reaction. Another indication that two polypeptides are substantially similar to

each other is that an agent, e.g., an antibody, which specifically binds to one of the polypeptides, specifically binds to the other.

In its broadest sense, the term "substantially similar", when used herein with respect to a nucleotide sequence, means a nucleotide sequence
5 corresponding to a reference nucleotide sequence, wherein the corresponding sequence is from a gene that encodes a polypeptide having substantially the same structure and function as the polypeptide encoded by a gene comprising the reference nucleotide sequence. The term "substantially similar" is specifically intended to include nucleotide sequences wherein the sequence has been
10 modified to optimize expression in particular cells. The percentage of identity between the substantially similar nucleotide sequence and the reference nucleotide sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%,
15 96%, 97%, 98%, up to at least 99%, wherein the reference sequence is preferably any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. Sequence comparisons may be carried out using a Smith-Waterman sequence alignment algorithm (see e.g., Waterman (1995) or <http://www.uto.usc.edu/software/seqaln/index.html>). The localS program, version 1.16, is
20 preferably used with following parameters: match: 1, mismatch penalty: 0.33, open-gap penalty: 2, extended-gap penalty: 2. Further, a nucleotide sequence that is "substantially similar" to a reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C,
25 more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC,
30 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

Hence, the isolated nucleic acid molecules of the invention also include the orthologs of the *Arabidopsis* sequences disclosed herein, i.e., the corresponding nucleic acid molecules in organisms other than *Arabidopsis*,

including, but not limited to, plants other than *Arabidopsis*, preferably cereal plants, e.g., corn, wheat or rice, as well as rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugarbeet, and in fungi. An ortholog is a gene from a different species that
5 encodes a product having the same function as the product encoded by a gene from a reference organism. The encoded ortholog products likely have at least 70% amino acid sequence identity to each other. Hence, the invention includes an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 70% identity to a polypeptide encoded by one or
10 more of the *Arabidopsis* sequences, although it is also envisioned that orthologous genes to those disclosed herein may encode a polypeptide with less than 70%, e.g., less than 65% amino acid sequence identity, but which polypeptide has the same or similar function. Databases such GenBank or one found at <http://bioserver.myongjiac.kr/rjce.html> (for rice) may be employed to
15 identify sequences related to the *Arabidopsis* sequences, e.g., orthologs in cereal crops such as rice. Alternatively, recombinant DNA techniques such as hybridization or PCR may be employed to identify sequences related to the *Arabidopsis* sequences.

Thus, the invention preferably includes an isolated nucleic acid molecule
20 comprising a plant or fungal nucleotide sequence that encodes a polypeptide that has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, amino acid sequence identity to an *Arabidopsis* polypeptide encoded by an open reading
25 frame comprising any one of SEQ ID NOs: 1-684 and 792-795, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795. In one embodiment, the isolated nucleic acid molecule is not SEQ ID NOs: 1-684 and
30 792-795. The invention also provides anti-sense nucleic acid molecules corresponding to the open reading frames or genes identified as responsive to pathogen infection. Also provided are expression cassettes, e.g., recombinant vectors, and host cells, comprising the nucleic acid molecule of the invention in either sense or antisense orientation.

Also provided is an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising a nucleic acid sequence having at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, nucleic acid sequence similarity to an *Arabidopsis* open reading frame comprising any one of SEQ ID NOs: 1-684 and 792-795, the complement thereof, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795.

The nucleic acid molecules of the invention, their encoded polypeptides and compositions thereof, are useful to provide resistance to pathogens and as a diagnostic for the presence or absence of the pathogen by correlating the expression level or pattern of expression of one or more of the nucleic acid molecules of the invention or one or more of the polypeptides encoded thereby. As one embodiment of the invention includes isolated nucleic acid molecules that have increased expression in response to pathogen infection, the invention further provides compositions and methods for enhancing resistance to pathogen infection. The compositions of the invention include plant or fungal nucleotide sequences and the amino acid sequences for the polypeptides or partial-length polypeptides encoded thereby which are useful to provide tolerance or resistance to a plant to a pathogen, preferably by preventing or inhibiting pathogen infection. The resistance or tolerance may be accomplished by decreasing or eliminating expression of a plant gene necessary for pathogen infection and/or replication or by overexpressing a gene product that inhibits pathogen infection and/or replication. Methods of the invention involve stably transforming a plant with one or more of at least a portion of these nucleotide sequences which confer tolerance or resistance operably linked to a promoter capable of driving expression of that nucleotide sequence in a plant cell. By "portion" or "fragment", as it relates to a nucleic acid molecule, sequence or segment of the invention, when it is linked to other sequences for expression, is meant a sequence having at least 80 nucleotides, more preferably at least 150 nucleotides, and still more preferably at least 400 nucleotides. If not employed for expressing, a "portion" or "fragment" means at least 9, preferably 12, more

preferably 15, even more preferably at least 20, consecutive nucleotides, e.g., probes and primers (oligonucleotides), corresponding to the nucleotide sequence of the nucleic acid molecules of the invention. By "resistant" is meant a plant which exhibits substantially no phenotypic changes as a consequence of infection with the pathogen. By "tolerant" is meant a plant which, although it may exhibit some phenotypic changes as a consequence of infection, does not have a substantially decreased reproductive capacity or substantially altered metabolism. Thus, some of the isolated nucleic acid molecules of the invention are useful in a method of combating a pathogen in an agricultural crop. The method comprises introducing to a plant, plant cell, or plant tissue an expression cassette comprising a nucleic acid molecule of the invention so as to yield a transformed differentiated plant, transformed cell or transformed tissue. Transformed cells or tissue can be regenerated to provide a transformed differentiated plant. The transformed differentiated plant preferably expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to pathogen infection relative to a corresponding nontransformed plant. The present invention also provides a transformed plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields under conditions of pathogen infection and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

The invention also includes recombinant nucleic acid molecules which have been modified so as to comprise codons other than those present in the unmodified sequence. The recombinant nucleic acid molecules of the invention include those in which the modified codons specify amino acids that are the same as those specified by the codons in the unmodified sequence, as well as those that specify different amino acids, i.e., they encode a variant polypeptide having one or more amino acid substitutions relative to the polypeptide encoded by the unmodified sequence.

The invention further includes a nucleotide sequence which is complementary to one (hereinafter "test" sequence) which hybridizes under stringent conditions with the nucleic acid molecules of the invention as well as RNA which is encoded by the nucleic acid molecule. When the hybridization is performed under stringent conditions, either the test or nucleic acid molecule of invention is preferably supported, e.g., on a membrane or DNA chip. Thus, either a denatured test or nucleic acid molecule of the invention is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of, e.g., between 55 and 70°C, in double strength citrate buffered saline (SC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon the degree of stringency required such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one-tenth strength SC containing 0.1% SDS.

The present invention also provides a method to identify a gene, the expression of which is altered in response to an external stimulus, e.g., pathogen infection. The method comprises contacting a plurality of samples comprising portions or fragments of isolated nucleic acid molecules with a probe which corresponds to a population of a nucleic acid sequences, the expression of which is altered in response to an external stimulus, so as to form a binary complex. Each sample corresponds to a different gene. Then complex formation is detected or determined. The method may be employed with nucleic acid samples and probes from any organism, e.g., any prokaryotic or eukaryotic organism. Preferably, the nucleic acid sample and probes are from a plant, such as a dicot or monocot. For example, the method comprises contacting a solid substrate comprising a plurality of samples comprising portions or fragments of isolated plant nucleic acid with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from a pathogen infected plant so as to form a complex. Preferred pathogens are those which induce an *R*-gene dependent resistance response. Each individual sample comprises one or more nucleic acid sequences corresponding to a plant gene, e.g., a pool of oligonucleotides corresponding to the same gene or a portion of that gene. The plurality of samples is provided on a DNA chip. A second plurality of samples on a solid substrate, i.e., a DNA chip, each comprising a plurality of samples comprising portions or fragments of

isolated plant nucleic acid is contacted with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from an uninfected or mutant plant or plant cells so as to form a complex. Then complex formation with nucleic acid from infected cells and from uninfected or mutant cells is compared.

5 The invention also provides a method for identifying a plant cell infected with a pathogen, e.g., one that induces a *RPP4*-, *RPP7*- and/or *RPP8*-dependent resistance response. The method comprises contacting nucleic acid obtained from a plant cell suspected of being infected with the pathogen with at least one, preferably at least two, oligonucleotides under conditions effective to amplify at
10 least a portion of a nucleotide sequence in the isolated plant nucleic acid which is substantially similar to at least one of SEQ ID NOs: 1-684 and 792-795, so as to yield an amplified product. Then the presence of the amplified product is detected or determined. The presence of the amplified product, e.g., in an amount that is different than the amount of the corresponding amplified product
15 from an uninfected or mutant plant, corresponding to one or more of SEQ ID NOs: 1-684 and 792-795 or an ortholog thereof, is indicative of pathogen infection.

 The invention provides an additional method for identifying a plant cell infected with a pathogen. The method comprises hybridizing a probe selected
20 from SEQ ID NOs: 1-684 and 792-795 to nucleic acid obtained from a plant cell suspected of being infected with a pathogen. The amount of the probe hybridized to nucleic acid obtained from a cell suspected of being infected with a pathogen is compared to hybridization of the probe to nucleic acid isolated from an uninfected or mutant cell. A change in the amount of the hybridized probe in
25 nucleic acid isolated from a cell suspected of being infected by a pathogen relative to the amount of hybridized probe in nucleic acid isolated from an uninfected or mutant cell is indicative of infection.

 Also provided is an isolated nucleic acid molecule comprising a nucleotide sequence that directs transcription, e.g., a promoter, of a linked
30 nucleic acid segment in a host cell, such as a plant cell, wherein transcription is altered, e.g., increased, in response to a pathogen infection. Preferably, the pathogen is *R*-dependent, and more preferably, one that triggers a response that is dependent on *RPP4*, *RPP7* and/or *RPP8*, such as an oomycete (for example, *Peronospora*). It is preferred that the nucleotide sequence is from plant genomic

DNA which has at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, nucleotide sequence identity to a sequence of a promoter from an
5 *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, e.g., SEQ ID NOs:774-788, or comprising motifs such as one of SEQ ID NOs:685-773. Thus, the invention also includes orthologs of *Arabidopsis* promoters.

Preferably, the nucleotide sequence includes the promoter region from a gene corresponding to SEQ ID NOs: 1-770 and 792-795, which region preferably
10 includes at least one copy of at least one of the following, e.g., a nucleic acid sequence comprising one of SEQ ID NOs:685-697 ("motif 1"), SEQ ID NOs:698-709 ("motif 2"), GGT/CCCA ("motif 3"), GNCCAAA ("motif 4"), or SEQ ID NOs:710-713, 714-756, or 757-773. The promoter sequence is preferably about 25 to 2000, e.g., 50 to 500 or 100 to 1400, nucleotides in length.

15 In one embodiment of the invention, the isolated nucleic acid molecule comprises a plant nucleotide sequence which is the promoter region for any one of SEQ ID NOs: 1-684 and 792-795, or is structurally related to the promoter for SEQ ID NOs: 1-684 and 792-795, i.e., is an orthologous promoter, and is linked to a plant structural gene or open reading frame. Hence, the present invention
20 further provides an expression cassette or a recombinant vector containing the nucleic acid molecule, and the vector may be a plasmid. Such cassettes or vectors, when present in a plant, plant cell or plant tissue result in transcription of the linked nucleic acid segment in the plant, plant tissue or plant cell. Transcription of the linked segment is altered in response to pathogen infection,
25 including *Peronospora* infection. For promoters with motif 1, transcription of linked segments may be altered in response to agents or other stimuli that induce Myb-like transcription factors.

Generally, the promoters of the invention may be employed to express a nucleic acid segment that is operably linked to the promoter, for example, an
30 open reading frame or a portion thereof, an anti-sense construct or a transgene. The open reading frame may be obtained from an insect resistance gene, a bacterial disease resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a

mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a positive selectable marker, a gene affecting plant agronomic characteristics, i.e., yield, standability and the like, or an environment or stress resistance gene, i.e., one or more genes
5 that confer herbicide resistance or tolerance, insect resistance or tolerance, disease resistance or tolerance (viral, bacterial, fungal, oomycete, or nematode), stress tolerance or resistance (as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, salt stress, or oxidative stress), increased yields, food content and makeup, physical appearance, male
10 sterility, drydown, standability, prolificacy, starch properties or quantity, oil quantity and quality, amino acid or protein composition, and the like.

Preferably, the promoters of the invention include a consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743,
15 250 to about 743, 400 to about 743, 600 to about 743, of the promoter sequences from genes comprising any one of SEQ ID NOs:685-788, 714-756; and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

In a particular embodiment of the invention said consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500,
20 contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, has at least 75%, preferably 80%, more preferably 90% and most preferably 95% sequence identity with a corresponding consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500; contiguous nucleotides, e.g., 40
25 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs:685-788, 714-756, and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

The expression cassettes or vectors of the invention may optionally
30 include other regulatory sequences, e.g., transcription terminator sequences, introns and/or enhancers, and may be contained in a host cell. The expression cassette or vector may augment the genome of a transformed plant or may be maintained extrachromosomally. The expression cassette or vector may further have a Ti plasmid and be contained in an *Agrobacterium tumefaciens* cell; it may

be carried on a microparticle, wherein the microparticle is suitable for ballistic transformation of a plant cell; or it may be contained in a plant cell protoplast. Further, the expression cassette can be contained in a plant, plant cell or plant tissue from a dicot or a monocot. In particular, the plant may be a cereal plant.

5 The present invention further provides a method of augmenting a plant genome by contacting plant cells with an expression cassette or vector of the invention, i.e., one having a nucleotide sequence that directs transcription of a linked nucleic acid segment in a plant cell, wherein transcription of the linked segment is altered in response to a pathogen such as an oomycete, e.g.,
10 *Peronospora*, infection, and wherein the nucleic sequence is from plant DNA that has at least 65%, and more preferably at least 70%, identity to the sequence of a promoter from an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, so as to yield transformed plant cells; and regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the
15 differentiated transformed plant expresses the linked fragment in the cells of the plant in response to infection. The present invention also provides a plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in
20 which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and
25 probes.

The invention also provides a method of plant breeding, e.g., to prepare a crossed fertile transgenic plant. The method comprises crossing a fertile transgenic plant comprising a particular nucleic acid molecule of the invention with itself or with a second plant, e.g., one lacking the particular nucleic acid
30 molecule, to prepare the seed of a crossed fertile transgenic plant comprising the particular nucleic acid molecule. The seed is then planted to obtain a crossed fertile transgenic plant. The plant may be a monocot or a dicot. In a particular embodiment, the plant is a cereal plant.

The crossed fertile transgenic plant may have the particular nucleic acid molecule inherited through a female parent or through a male parent. The second plant may be an inbred plant. The crossed fertile transgenic may be a hybrid. Also included within the present invention are seeds of any of these
5 crossed fertile transgenic plants.

The present invention also provides a method to identify a nucleotide sequence that directs transcription of nucleic acid in the genome of a plant cell in response to pathogen exposure, by contacting a probe comprising plant nucleic acid, e.g., cRNA, isolated from tissues of a plant contacted with the pathogen,
10 with a plurality of isolated nucleic acid samples on a plurality of solid substrates, wherein each sample is a plurality of oligonucleotides corresponding to at least a portion of a plant gene, so as to form a complex between at least a portion of the probe and a nucleic acid sample(s) having sequences that are structurally related to the sequences in the probe. Then complex formation is determined or
15 detected to determine which samples represent genes comprising promoters that are responsive to infection with the pathogen. The probe and/or samples may be nucleic acid from a dicot or from a monocot.

A method to shuffle the nucleic acid molecules of the invention is provided. This method involves fragmentation of a (parent) nucleic acid
20 molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-684 and 792-795, the ortholog thereof, or the corresponding gene thereof, followed by religation. This method allows for the production of polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule. Accordingly, the invention provides cells and transgenic plants
25 containing nucleotide sequences produced through shuffling that encode polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule.

A computer readable medium containing the nucleic acid sequences of the invention as well as methods of use for the computer readable medium are
30 provided. This medium allows a nucleic acid molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795 to be used as a reference sequence to search against databases. This medium also allows for computer-based manipulation of a nucleic acid sequence

corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795, and the corresponding gene or polypeptide encoded by the nucleic acid sequence.

5

Brief Description of the Figures

Figure 1 depicts *RPP*-dependent defense pathways.

Figure 2 depicts nucleotide sequences including the promoter region and motifs therein for genes, the expression of which is altered in response to pathogen infection (SEQ ID NOs: 774-788).

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Figure 3 is a schematic of the overlap in genes that are induced early after *P. parasitica* infection and in a *RPP8*-specific manner, genes that are induced late after infection and in a *RPP8*-specific manner, and genes induced early and late after infection in a *RPP7*-specific manner.

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Figure 4 shows a schematic of *RPP4*-pathway, *RPP7*-pathway and *RPP8*-upregulated transcription factor genes.

Detailed Description of the Invention

Definitions

20

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base which is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated.

25

Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzner et al., 1991; Ohtsuka et al., 1985; Rossolini et al., 1994). A "nucleic acid fragment" is a fraction of a given nucleic acid molecule. In higher plants, deoxyribonucleic

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acid (DNA) is the genetic material while ribonucleic acid (RNA) is involved in the transfer of information contained within DNA into proteins. The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. The terms "nucleic acid", "nucleic acid molecule", "nucleic acid fragment" or "nucleic acid sequence or segment" may also be used interchangeably with gene, cDNA, DNA and RNA encoded by a gene.

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or an "isolated" or "purified" polypeptide is a DNA molecule or polypeptide that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or polypeptide may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In one embodiment, an "isolated" nucleic acid is free of sequences that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein or polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention, or biologically active portion thereof, is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein-of-interest chemicals. Fragments and variants of the disclosed nucleotide sequences and proteins or partial-length proteins encoded thereby are also encompassed by the present invention. By "fragment" or "portion" is meant a full length or less than

full length of the nucleotide sequence encoding, or the amino acid sequence of, a polypeptide or protein. Alternatively, fragments or portions of a nucleotide sequence that are useful as hybridization probes generally do not encode fragment proteins retaining biological activity. Thus, fragments or portions of a
5 nucleotide sequence may range from at least about 9 nucleotides, about 12 nucleotides, about 20 nucleotides, about 50 nucleotides, about 100 nucleotides or more.

The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences
10 and/or the regulatory sequences required for their expression. For example, gene refers to a nucleic acid fragment that expresses mRNA, functional RNA, or specific protein, including regulatory sequences. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including
15 cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

"Naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a
20 protein or nucleotide sequence present in an organism (including a virus), which can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

A "marker gene" encodes a selectable or screenable trait.

"Selectable marker" is a gene whose expression in a cell gives the cell a
25 selective advantage. The selective advantage possessed by the cells transformed with the selectable marker gene may be due to their ability to grow in the presence of a negative selective agent, such as an antibiotic or a herbicide, compared to the growth of non-transformed cells. The selective advantage possessed by the transformed cells, compared to non-transformed cells, may also
30 be due to their enhanced or novel capacity to utilize an added compound as a nutrient, growth factor or energy source. Selectable marker gene also refers to a gene or a combination of genes whose expression in a cell gives the cell both a negative and/or a positive selective advantage.

The term "chimeric" refers to any gene or DNA that contains 1) DNA

sequences, including regulatory and coding sequences, that are not found together in nature, or 2) sequences encoding parts of proteins not naturally adjoined, or 3) parts of promoters that are not naturally adjoined. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are
5 derived from different sources, or comprise regulatory sequences and coding sequences derived from the same source, but arranged in a manner different from that found in nature.

A "transgene" refers to a gene that has been introduced into the genome by transformation and is stably maintained. Transgenes may include, for
10 example, DNA that is either heterologous or homologous to the DNA of a particular plant to be transformed. Additionally, transgenes may comprise native genes inserted into a non-native organism, or chimeric genes. The term "endogenous gene" refers to a native gene in its natural location in the genome of an organism. A "foreign" gene refers to a gene not normally found in the host
15 organism but that is introduced by gene transfer.

The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

By "variants" is intended substantially similar sequences. For nucleotide sequences, variants include those sequences that, because of the degeneracy of
20 the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those
25 generated, for example, by using site-directed mutagenesis which encode the native protein, as well as those that encode a polypeptide having amino acid substitutions. Generally, nucleotide sequence variants of the invention will have at least 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g.,
30 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98%, sequence identity to the native (endogenous) nucleotide sequence.

"DNA shuffling" is a method to introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The

DNA molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA preferably encodes a variant polypeptide modified with respect to the polypeptide encoded by the template DNA, and may
5 have an altered biological activity with respect to the polypeptide encoded by the template DNA.

The nucleic acid molecules of the invention can be optimized for enhanced expression in plants of interest. See, for example, EPA035472; WO91/16432; Perlak et al., 1991; and Murray et al., 1989. In this manner, the
10 genes or gene fragments can be synthesized utilizing plant-preferred codons. See, for example, Campbell and Gowri, 1990 for a discussion of host-preferred codon usage. Thus, the nucleotide sequences can be optimized for expression in any plant. It is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may
15 also be used. Variant nucleotide sequences and proteins also encompass sequences and protein derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different coding sequences can be manipulated to create a new polypeptide possessing the desired properties. In this manner, libraries of recombinant polynucleotides are
20 generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer, 1994; Stemmer, 1994; Cramer et al., 1997; Moore et al., 1997; Zhang et al., 1997; Cramer et al., 1998; and
25 U.S. Patent Nos. 5,605,793 and 5,837,458.

"Conservatively modified variations" of a particular nucleic acid sequence refers to those nucleic acid sequences that encode identical or essentially identical amino acid sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences.
30 Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the

encoded protein. Such nucleic acid variations are "silent variations" which are one species of "conservatively modified variations." Every nucleic acid sequence described herein which encodes a polypeptide also describes every possible silent variation, except where otherwise noted. One of skill will
5 recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each "silent variation" of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

"Recombinant DNA molecule" is a combination of DNA sequences that
10 are joined together using recombinant DNA technology and procedures used to join together DNA sequences as described, for example, in Sambrook et al., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (1989).

The terms "heterologous DNA sequence," "exogenous DNA segment" or "heterologous nucleic acid," each refer to a sequence that originates from a
15 source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the
20 terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" DNA sequence is a DNA sequence that is naturally
25 associated with a host cell into which it is introduced.

"Wild-type" refers to the normal gene, or organism found in nature without any known mutation.

"Genome" refers to the complete genetic material of an organism.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or
30 *Agrobacterium* binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

Specifically included are shuttle vectors by which is meant a DNA vehicle capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eukaryotic (e.g. higher plant, mammalian, yeast or fungal cells).

5 "Cloning vectors" typically contain one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector. Marker genes typically
10 include genes that provide tetracycline resistance, hygromycin resistance or ampicillin resistance.

"Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of
15 interest which is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the
20 nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. The expression of the nucleotide sequence in the expression cassette may be under
25 the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, the promoter can also be specific to a particular tissue or organ or stage of development.

Such expression cassettes will comprise the transcriptional initiation
30 region of the invention linked to a nucleotide sequence of interest. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene of interest to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

The transcriptional cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau et al., 1991; Proudfoot, 1991; Sanfacon et al., 1991; Mogen et al., 1990; Munroe et al., 1990; Ballas et al., 1989; Joshi et al., 1987.

An oligonucleotide corresponding to a nucleic acid molecule of the invention may be about 30 or fewer nucleotides in length (e.g., 9, 12, 15, 18, 20, 21 or 24, or any number between 9 and 30). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16-24 nucleotides in length may be preferred. Those skilled in the art are well versed in the design of primers for use processes such as PCR. If required, probing can be done with entire restriction fragments of the gene disclosed herein which may be 100's or even 1000's of nucleotides in length.

"Coding sequence" refers to a DNA or RNA sequence that codes for a specific amino acid sequence and excludes the non-coding sequences. It may constitute an "uninterrupted coding sequence", i.e., lacking an intron, such as in a cDNA or it may include one or more introns bounded by appropriate splice junctions. An "intron" is a sequence of RNA which is contained in the primary transcript but which is removed through cleavage and re-ligation of the RNA within the cell to create the mature mRNA that can be translated into a protein.

The terms "open reading frame" and "ORF" refer to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence. The terms "initiation codon" and "termination codon" refer to a unit of three adjacent nucleotides ('codon') in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation).

A "functional RNA" refers to an antisense RNA, ribozyme, or other RNA that is not translated.

The term "RNA transcript" refers to the product resulting from RNA polymerase catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without introns and that can be translated into protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA.

"Regulatory sequences" and "suitable regulatory sequences" each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, promoters, translation leader sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. As is noted above, the term "suitable regulatory sequences" is not limited to promoters. However, some suitable regulatory sequences useful in the present invention will include, but are not limited to constitutive plant promoters, plant tissue-specific promoters, plant development specific promoters, inducible plant promoters and viral promoters.

"5' non-coding sequence" refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency (Turner et al., 1995).

"3' non-coding sequence" refers to nucleotide sequences located 3' (downstream) to a coding sequence and include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al., 1989.

The term "translation leader sequence" refers to that DNA sequence portion of a gene between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency.

The term "mature" protein refers to a post-translationally processed polypeptide without its signal peptide. "Precursor" protein refers to the primary product of translation of an mRNA. "Signal peptide" refers to the amino terminal extension of a polypeptide, which is translated in conjunction with the polypeptide forming a precursor peptide and which is required for its entrance into the secretory pathway. The term "signal sequence" refers to a nucleotide sequence that encodes the signal peptide.

The term "intracellular localization sequence" or "signal sequence" refers to a nucleotide sequence that encodes an intracellular targeting signal. An "intracellular targeting signal" is an amino acid sequence that is translated in conjunction with a protein and directs it to a particular sub-cellular compartment. "Endoplasmic reticulum (ER) stop transit signal" refers to a carboxy-terminal extension of a polypeptide, which is translated in conjunction with the polypeptide and causes a protein that enters the secretory pathway to be retained in the ER. "ER stop transit sequence" refers to a nucleotide sequence that encodes the ER targeting signal. Other intracellular targeting sequences encode targeting signals active in seeds and/or leaves and vacuolar targeting signals.

"Promoter" refers to a nucleotide sequence, usually upstream (5') to its coding sequence, which controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription. "Promoter" includes a minimal promoter that is a short DNA sequence comprised of a TATA-box and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. "Promoter" also refers to a nucleotide sequence that includes a minimal promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence which can stimulate promoter activity and may be an innate

element of the promoter or a heterologous element inserted to enhance the level or tissue specificity of a promoter. It is capable of operating in both orientations (normal or flipped), and is capable of functioning even when moved either upstream or downstream from the promoter. Both enhancers and other upstream promoter elements bind sequence-specific DNA-binding proteins that mediate their effects. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even be comprised of synthetic DNA segments. A promoter may also contain DNA sequences that are involved in the binding of protein factors which control the effectiveness of transcription initiation in response to physiological or developmental conditions.

The "initiation site" is the position surrounding the first nucleotide that is part of the transcribed sequence, which is also defined as position +1. With respect to this site all other sequences of the gene and its controlling regions are numbered. Downstream sequences (i.e. further protein encoding sequences in the 3' direction) are denominated positive, while upstream sequences (mostly of the controlling regions in the 5' direction) are denominated negative.

Promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation are referred to as "minimal or core promoters." In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription. A "minimal or core promoter" thus consists only of all basal elements needed for transcription initiation, e.g., a TATA box and/or an initiator.

"Constitutive expression" refers to expression using a constitutive or regulated promoter. "Conditional" and "regulated expression" refer to expression controlled by a regulated promoter.

"Constitutive promoter" refers to a promoter that is able to express the gene that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant. Each of the transcription-activating elements do not exhibit an absolute tissue-specificity, but mediate transcriptional activation in most plant parts at a level of $\geq 1\%$ of the level reached in the part of the plant in which transcription is most active.

"Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and

include both tissue-specific and inducible promoters. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. New promoters of various types useful in plant cells are constantly being discovered, numerous examples may be found in the compilation by Okamuro et al., 1989. Since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of different lengths may have identical promoter activity.

Typical regulated promoters useful in plants include but are not limited to safener-inducible promoters, promoters derived from the tetracycline-inducible system, promoters derived from salicylate-inducible systems, promoters derived from alcohol-inducible systems, promoters derived from glucocorticoid-inducible system, promoters derived from pathogen-inducible systems, and promoters derived from ecdysone-inducible systems.

"Tissue-specific promoter" refers to regulated promoters that are not expressed in all plant cells but only in one or more cell types in specific organs (such as leaves or seeds), specific tissues (such as embryo or cotyledon), or specific cell types (such as leaf parenchyma or seed storage cells). These also include promoters that are temporally regulated, such as in early or late embryogenesis, during fruit ripening in developing seeds or fruit, in fully differentiated leaf, or at the onset of senescence.

"Inducible promoter" refers to those regulated promoters that can be turned on in one or more cell types by an external stimulus, such as a chemical, light, hormone, stress, or a pathogen.

"Operably-linked" refers to the association of nucleic acid sequences on single nucleic acid fragment so that the function of one is affected by the other. For example, a regulatory DNA sequence is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (i.e., that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can be operably-linked to regulatory sequences in sense or antisense orientation.

"Expression" refers to the transcription and/or translation of an endogenous gene or a transgene in plants. For example, in the case of antisense constructs, expression may refer to the transcription of the antisense DNA only. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA. Expression may also refer to the production of protein.

"Altered levels" refers to the level of expression in transgenic cells or organisms that differs from that of normal or untransformed cells or organisms.

"Overexpression" refers to the level of expression in transgenic cells or organisms that exceeds levels of expression in normal or untransformed cells or organisms.

"Antisense-inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of protein from an endogenous gene or a transgene.

"Co-suppression" and "transwitch" each refer to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar transgene or endogenous genes (U.S. Patent No. 5,231,020).

"Gene silencing" refers to homology-dependent suppression of viral genes, transgenes, or endogenous nuclear genes. Gene silencing may be transcriptional, when the suppression is due to decreased transcription of the affected genes, or post-transcriptional, when the suppression is due to increased turnover (degradation) of RNA species homologous to the affected genes. (English et al., 1996). Gene silencing includes virus-induced gene silencing (Ruiz et al., 1998).

"Silencing suppressor" gene refers to a gene whose expression leads to counteracting gene silencing and enhanced expression of silenced genes. Silencing suppressor genes may be of plant, non-plant, or viral origin. Examples include, but are not limited to HC-Pro, P1-HC-Pro, and 2b proteins. Other examples include one or more genes in TGMV-B genome.

"Transcription stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as polyadenylation signal sequences, capable of terminating transcription. Examples include the 3' non-regulatory regions of genes encoding nopaline synthase and the small subunit of ribulose biphosphate carboxylase.

"Translation stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as one or more termination codons in all three frames, capable of terminating translation. Insertion of a translation stop fragment adjacent to or near the initiation codon at the 5' end of the coding sequence will result in no translation or improper translation. Excision of the translation stop fragment by site-specific recombination will leave a site-specific sequence in the coding sequence that does not interfere with proper translation using the initiation codon.

The terms "*cis*-acting sequence" and "*cis*-acting element" refer to DNA or RNA sequences whose functions require them to be on the same molecule. An example of a *cis*-acting sequence on the replicon is the viral replication origin.

The terms "*trans*-acting sequence" and "*trans*-acting element" refer to DNA or RNA sequences whose function does not require them to be on the same molecule.

"Chromosomally-integrated" refers to the integration of a foreign gene or DNA construct into the host DNA by covalent bonds. Where genes are not "chromosomally integrated" they may be "transiently expressed." Transient expression of a gene refers to the expression of a gene that is not integrated into the host chromosome but functions independently, either as part of an autonomously replicating plasmid or expression cassette, for example, or as part of another biological system such as a virus.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically
5 introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms are the algorithm of Myers and
10 Miller, 1988; the local homology algorithm of Smith et al., 1981; the homology alignment algorithm of Needleman and Wunsch, 1970; the search-for-similarity-method of Pearson and Lipman, 1988; the algorithm of Karlin and Altschul, 1990, modified as in Karlin and Altschul, 1993.

Computer implementations of these mathematical algorithms can be
15 utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics
20 Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al., 1988; Higgins et al., 1989; Corpet et al., 1988; Huang et al., 1992; and Pearson et al., 1994. The ALIGN program is based on the algorithm of Myers and Miller, *supra*. The
25 BLAST programs of Altschul et al., 1990, are based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high
30 scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., 1990). These initial neighborhood word hits act as seeds for initiating searches to find

longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al., 1997. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al., *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g. BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, $M=5$, $N=-4$, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989). See <http://www.ncbi.nlm.nih.gov>. Alignment may also be performed manually by inspection.

For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein is preferably made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By

5 "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

(c) As used herein, "sequence identity" or "identity" in the context of two
10 nucleic acid or polypeptide sequences makes reference to a specified percentage of residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window, as measured by sequence comparison algorithms or by visual inspection. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions
15 which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted
20 upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity.
25 Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

30 (d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal

alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, and most preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 70%; more preferably at least 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions (see below). Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%,

75%, 76%, 77%, 78%, or 79%, preferably 80%, 81%, 82%, 83%, 84%, 85%,
86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or
94%, or even more preferably, 95%, 96%, 97%, 98% or 99%, sequence identity
to the reference sequence over a specified comparison window. Preferably,
5 optimal alignment is conducted using the homology alignment algorithm of
Needleman and Wunsch, 1970. An indication that two peptide sequences are
substantially identical is that one peptide is immunologically reactive with
antibodies raised against the second peptide. Thus, a peptide is substantially
identical to a second peptide, for example, where the two peptides differ only by
10 a conservative substitution.

For sequence comparison, typically one sequence acts as a reference
sequence to which test sequences are compared. When using a sequence
comparison algorithm, test and reference sequences are input into a computer,
subsequence coordinates are designated if necessary, and sequence algorithm
15 program parameters are designated. The sequence comparison algorithm then
calculates the percent sequence identity for the test sequence(s) relative to the
reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are
substantially identical is that the two molecules hybridize to each other under
20 stringent conditions. The phrase "hybridizing specifically to" refers to the
binding, duplexing, or hybridizing of a molecule only to a particular nucleotide
sequence under stringent conditions when that sequence is present in a complex
mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to
complementary hybridization between a probe nucleic acid and a target nucleic
25 acid and embraces minor mismatches that can be accommodated by reducing the
stringency of the hybridization media to achieve the desired detection of the
target nucleic acid sequence.

"Stringent hybridization conditions" and "stringent hybridization wash
conditions" in the context of nucleic acid hybridization experiments such as
30 Southern and Northern hybridizations are sequence dependent, and are different
under different environmental parameters. Longer sequences hybridize
specifically at higher temperatures. The T_m is the temperature (under defined
ionic strength and pH) at which 50% of the target sequence hybridizes to a
perfectly matched probe. Specificity is typically the function of post-

hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, 1984; $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with >90% identity are sought, the T_m can be decreased 10°C . Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at $1, 2, 3$, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at $6, 7, 8, 9$, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at $11, 12, 13, 14, 15$, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

An example of highly stringent wash conditions is 0.15 M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2X SSC wash at 65°C for 15 minutes (see, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1X SSC at 45°C for 15 minutes.

An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6X SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, more preferably about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C and at least about 60°C for long robes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2X (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.

The following are examples of sets of hybridization/wash conditions that may be used to clone orthologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5

M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with
5 washing in 0.1X SSC, 0.1% SDS at 65°C.

By "variant" polypeptide is intended a polypeptide derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native
10 protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

Thus, the polypeptides of the invention may be altered in various ways
15 including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the polypeptides can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel, 1985; Kunkel et al., 1987; U.
20 S. Patent No. 4,873,192; Walker and Gaastra, 1983, and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff et al., 1978, herein incorporated by reference. Conservative
25 substitutions, such as exchanging one amino acid with another having similar properties, are preferred.

Thus, the genes and nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant forms. Likewise, the polypeptides of the invention encompass both naturally occurring proteins as well as variations and modified forms thereof. Such variants will continue to
30 possess the desired activity. The deletions, insertions, and substitutions of the polypeptide sequence encompassed herein are not expected to produce radical changes in the characteristics of the polypeptide. However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of

doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays.

Individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%,
5 more typically less than 1%) in an encoded sequence are "conservatively modified variations," where the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative
10 substitutions for one another: Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I); Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine (N), Glutamine (Q). See also, Creighton, 1984. In addition,
15 individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also "conservatively modified variations."

"Production tissue" refers to mature, harvestable tissue consisting of non-dividing, terminally-differentiated cells. It excludes young, growing tissue
20 consisting of germline, meristematic, and not-fully-differentiated cells.

"Germline cells" refer to cells that are destined to be gametes and whose genetic material is heritable.

The word "plant" refers to any plant, particularly to seed plant, and "plant cell" is a structural and physiological unit of the plant, which comprises a cell
25 wall but may also refer to a protoplast. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

"Plant tissue" includes differentiated and undifferentiated tissues or plants, including but not limited to roots, stems, shoots, leaves, pollen, seeds,
30 tumor tissue and various forms of cells and culture such as single cells, protoplast, embryos, and callus tissue. The plant tissue may be in plants or in organ, tissue or cell culture.

The term "altered plant trait" means any phenotypic or genotypic change in a transgenic plant relative to the wild-type or non-transgenic plant host.

The term "transformation" refers to the transfer of a nucleic acid fragment into the genome of a host cell, resulting in genetically stable inheritance. Host cells containing the transformed nucleic acid fragments are referred to as "transgenic" cells, and organisms comprising transgenic cells are referred to as "transgenic organisms". Examples of methods of transformation of plants and plant cells include *Agrobacterium*-mediated transformation (De Blaere et al., 1987) and particle bombardment technology (Klein et al., 1987; U.S. Patent No. 4,945,050). Whole plants may be regenerated from transgenic cells by methods well known to the skilled artisan (see, for example, Fromm et al., 1990).

"Transformed," "transgenic," and "recombinant" refer to a host cell or organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome generally known in the art and are disclosed in Sambrook et al., 1989. See also Innis et al., 1995; and Gelfand, 1995; and Innis and Gelfand, 1999. Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially mismatched primers, and the like. For example, "transformed," "transformant," and "transgenic" plants or calli have been through the transformation process and contain a foreign gene integrated into their chromosome. The term "untransformed" refers to normal plants that have not been through the transformation process.

A "transgenic plant" is a plant having one or more plant cells that contain an expression vector.

"Transiently transformed" refers to cells in which transgenes and foreign DNA have been introduced (for example, by such methods as *Agrobacterium*-mediated transformation or biolistic bombardment), but not selected for stable maintenance.

"Stably transformed" refers to cells that have been selected and regenerated on a selection media following transformation.

"Transient expression" refers to transgene expression in cells, e.g., after transformation with recombinant virus or by such methods as *Agrobacterium*-mediated transformation, electroporation, or biolistic bombardment, but not selected for its stable maintenance.

"Genetically stable" and "heritable" refer to chromosomally-integrated genetic elements that are stably maintained in the plant and stably inherited by progeny through successive generations.

5 "Primary transformant" and "T0 generation" refer to transgenic plants that are of the same genetic generation as the tissue which was initially transformed (i.e., not having gone through meiosis and fertilization since transformation).

"Secondary transformants" and the "T1, T2, T3, etc. generations" refer to transgenic plants derived from primary transformants through one or more meiotic and fertilization cycles. They may be derived by self-fertilization of
10 primary or secondary transformants or crosses of primary or secondary transformants with other transformed or untransformed plants.

"Significant increase" is an increase that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater.

15 "Significantly less" means that the decrease is larger than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater.

I. The Nucleic Acid Molecules of the Invention and Polypeptide Encoded

20 Thereby

This invention relates to isolated plant, e.g., *Arabidopsis* and rice, nucleic acid molecules, sequences and segments (fragments), the expression of which is altered in response to pathogen infection, as well as the endogenous plant promoters for those expressed molecules, sequences or segments. However, the
25 expression of these genes may also be altered in response to non-pathogens, e.g., in response to environmental stimuli. The nucleic acid molecules can be used in pathogen control strategies, e.g., by overexpressing nucleic acid molecules which can confer tolerance to a cell, or by altering the expression of host genes which are required for pathogen infection, e.g., by "knocking out" the expression of at
30 least one genomic copy of the gene. Plants having genetic disruptions in host genes may be less susceptible to infection, e.g., due to a decrease or absence of a host protein needed for infection, or, alternatively, hypersusceptible to infection. Plants that are hypersusceptible to infection may be useful to prepare transgenic

plants as the expression of the gene(s) which was disrupted may be related to gene silencing.

Preferred sources for the nucleic acid molecules of the invention include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Wolffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wolffella* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*, *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*).

Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt, *Biosystematic Investigation on the Family of Duckweeds: The family of*

Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*), Western hemlock (*Tsuga canadensis*), Sitka spruce (*Picea glauca*), redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula,

Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia.

- Other vegetable sources (and databases to identify orthologs of the invention) for the nucleic acid sequences of the invention include those are shown in Table 1.

Table 1

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber		http://www.cucurbit.org/
	<i>Cucumis melo</i>	Melon		http://genome.cornell.edu/cgc/
	<i>Citrullus lanatus</i>	Watermelon		
	<i>Cucurbita pepo</i>	Squash – summer		
	<i>Cucurbita maxima</i>	Squash - winter		
	<i>Cucurbita moschata</i>	Pumpkin /butternut		
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	<ul style="list-style-type: none"> 15x BAC on variety Heinz 1706 order from Clemson Genome center (www.genome.clemson.edu) 11.6x BAC of <i>L. cheesmanii</i> (originates from J. Giovannoni) available from Clemson genome center (www.genome.clemson.edu) EST collection 	genome.cornell.edu/solgenes http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=solgenes http://genome.cornell.edu/tgc/ http://tgrc.ucdavis.edu/

			<p>from TIGR (www.tigr.org/tb/lgi/index.html)</p> <ul style="list-style-type: none"> • EST collection from Clemson Genome Center (www.genome.clemson.edu) • TAG 99:254-271, 1999 (esculentum x pennelli) • TAG 89:1007-1013, 1994 (peruvianum) • Plant Cell Reports 12:293-297, 1993 (RAPDs) • Genetics 132:1141-1160, 1992 (potato x tomato) • Genetics 120:1095-1105, 1988 (RFLP potato and tomato) • Genetics 115:387-393, 1986 (esculentum x pennelli isozyme and cDNAs) 	
	<i>Capsicum annuum</i>	Pepper		http://neptune.netimages.com/~chile/science.html
	<i>Capsicum frutescens</i>	Chile pepper		
	<i>Solanum melongena</i>	Eggplant		
	(<i>Nicotiana tabacum</i>)	(Tobacco)		
	(<i>Solanum tuberosum</i>)	(Potato)		
	(<i>Petunia x hybrida hort. ex E. Vilm.</i>)	(Petunia)	4x BAC of <i>Petunia hybrida</i> 7984 available from	

			Clemson genome center (www.genome.clemson.edu)	
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Brassicaceae	<i>Brassica oleracea</i> L. var. <i>italica</i>	Broccoli		http://res.agr.ca/ecorc/cwmt/crucifer/traits/index.htm http://geneous.cit.cornell.edu/cabbage/aboutcab.html
	<i>Brassica oleracea</i> L. var. <i>capitata</i>	Cabbage		
	<i>Brassica rapa</i>	Chinese Cabbage		
	<i>Brassica oleracea</i> L. var. <i>botrytis</i>	Cauliflower		
	<i>Raphanus sativus</i> var. <i>niger</i>	Daikon		
	(<i>Brassica napus</i>)	(Oilseed rape)		http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb
		Arabidopsis	12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=agr
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Umbelliferae	<i>Daucus carota</i>	Carrot		
Compositae	<i>Lactuca sativa</i>	Lettuce		
	<i>Helianthus annuus</i>	(Sunflower)		
Total				
Chenopodiaceae	<i>Spinacia oleracea</i>	Spinach		
	(<i>Beta vulgaris</i>)	(Sugar Beet)		
Total				

Leguminosae	<i>Phaseolus vulgaris</i>	Bean	4.3x BAC available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=beangenex
	<i>Pisum sativum</i>	Pea		
	(<i>Glycine max</i>)	(Soybean)	7.5x and 7.9x BACs available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase
Total			http://www.nal.usda.gov/pgdic/Map_projects/	
Gramineae	<i>Zea mays</i>	Sweet Corn	Novartis BACs for Mo17 and B73 have been donated to Clemson Genome Center (www.genome.clemson.edu)	
	(<i>Zea mays</i>)	(Field Corn)		http://www.agron.missouri.edu/mnl/
Total			http://www.nal.usda.gov/pgdic/Map_projects/	
Liliaceae	<i>Allium cepa</i>	Onion		
		Leek		
		(Garlic)		
		(Asparagus)		
Total			http://www.nal.usda.gov/pgdic/Map_projects/	

Preferred forage and turf grass nucleic acid sources for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop. Preferably, the nucleic acid sources are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.), and even more preferably corn and soybean.

According to one embodiment, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence obtained or obtainable

from any plant gene which encodes a polypeptide having at least 70% amino acid sequence identity to a polypeptide encoded by SEQ ID NOs. 1-684 or 789-795, or a promoter for said gene. Thus, based on the *Arabidopsis* nucleic acid sequences of the present invention, orthologs of those sequences may be identified or isolated from the genome of any desired organism, preferably from another plant, according to well known techniques based on their sequence similarity to the *Arabidopsis* coding sequences, e.g., hybridization, PCR or computer generated sequence comparisons. For example, all or a portion of a particular *Arabidopsis* sequence is used as a probe that selectively hybridizes to other gene sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen source organism. Further, suitable genomic and cDNA libraries may be prepared from any cell or tissue of an organism. Such techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g., Sambrook et al., 1989) and amplification by PCR using oligonucleotide primers preferably corresponding to sequence domains conserved among related polypeptide or subsequences of the nucleotide sequences provided herein (see, e.g., Innis et al., 1990). These methods are particularly well suited to the isolation of gene sequences from organisms closely related to the organism from which the probe sequence is derived. The application of these methods using the *Arabidopsis* coding sequences as probes is well suited for the isolation of gene sequences from any source organism, preferably other plant species. In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art as discussed hereinabove.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P , or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the

sequence of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook et al., 1989. In general, sequences that hybridize to the sequences disclosed herein will have at least 40% to 50%, about
5 60% to 70% and even about 80% 85%, 90%, 95% to 98% or more identity with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

The nucleic acid molecules of the invention can also be identified by, for
10 example, a search of known databases for genes encoding polypeptides having a specified amino acid sequence identity. Methods of alignment of sequences for comparison are well known in the art and are described hereinabove.

II. Expression Cassettes of the Invention

15 The present invention also encompasses expression cassettes, preferably in the form of a recombinant vectors comprising the nucleic acid sequences of the invention. In such vectors, the expression cassette comprises regulatory elements for expression of the nucleotide sequences in a host cell capable of expressing the nucleotide sequences. Such regulatory elements usually comprise
20 promoter and termination signals and preferably also comprise elements allowing efficient translation of polypeptides encoded by the nucleic acid sequences of the present invention. For efficient initiation of translation, sequences adjacent to the initiating methionine may require modification. For example, they can be modified by the inclusion of sequences known to be
25 effective in plants. Joshi (1987) has suggested an appropriate consensus for plants and Clontech suggests a further consensus translation initiator (1993/1994 catalog, page 210). These consensus are suitable for use with the nucleotide sequences of this invention. The sequences are incorporated into constructions comprising the nucleotide sequences, up to and including the ATG (whilst
30 leaving the second amino acid unmodified), or alternatively up to and including the GTC subsequent to the ATG (with the possibility of modifying the second amino acid of the transgene).

Vectors comprising the nucleic acid sequences are usually capable of replication in particular host cells, e.g., as extrachromosomal molecules, and are

therefore used to amplify the nucleic acid sequences of this invention in the host cells. In a preferred embodiment, host cells for such vectors are plant cells.

A. Promoters and Enhancers

Expression of the nucleotide sequences in transgenic plants is driven by promoters shown to be functional in plants. The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. In many cases, expression in multiple tissues is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

These promoters include, but are not limited to, constitutive, inducible, temporally regulated, developmentally regulated, chemically regulated, stress-responsive, tissue-preferred and tissue-specific promoters. Promoter sequences are known to be strong or weak. A strong promoter provides for a high level of gene expression, whereas a weak promoter provides for a very low level of gene expression. An inducible promoter is a promoter that provides for the turning on and off of gene expression in response to an exogenously added agent, or to an environmental or developmental stimulus. A bacterial promoter such as the P_{tac} promoter can be induced to varying levels of gene expression depending on the level of isothiopropylgalactoside added to the transformed bacterial cells. An isolated promoter sequence that is a strong promoter for heterologous nucleic acid is advantageous because it provides for a sufficient level of gene expression to allow for easy detection and selection of transformed cells and provides for a high level of gene expression when desired.

Preferred promoters that are expressed constitutively include promoters from genes encoding actin or ubiquitin and the CaMV 35S and 19S promoters. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the nucleic acid sequence or encoded polypeptide to be synthesized only when the crop plants are treated with the inducing chemicals. Preferred technology for chemical induction of gene expression is detailed in the published application EP

0 332 104 (to Ciba-Geigy) and U.S. Patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

Tissue-specific or tissue-preferential promoters useful in the present invention. Also useful are promoters which confer seed-specific expression, such as those disclosed by Schernthaner et al., 1988; anther (tapetal) specific promoter B6 (Huffman et al.); and pistil-specific promoters such as a modified S13 promoter (Dzelkalns et al., 1993).

Preferred tissue specific expression patterns include green tissue-specific, root-specific, stem-specific, and flower-specific. Promoters suitable for expression in green tissue include many which regulate genes involved in photosynthesis and many of these have been cloned from both monocotyledons and dicotyledons. A preferred promoter is the maize PEPC promoter from the phosphoenol carboxylase gene (Hudspeth & Grula, 1989). A preferred promoter for root-specific expression is that described by de Framond (1991; EP 0 452 269 to Ciba-Geigy). A preferred stem specific promoter is that described in U.S. Patent No. 5,625,136 (to Ciba-Geigy) and which drives expression of the maize *trpA* gene.

Other promoters which direct specific or enhanced expression in certain plant tissues will be known to those of skill in the art in light of the present disclosure. These include, for example, the *rbcS* promoter, specific for green tissue; the *ocs*, *nos*, and *mas* promoters which have higher activity in roots or wounded leaf tissue; a truncated (-90 to +8) 35S promoter which directs enhanced expression in roots, an tubulin gene that directs expression in roots and promoters derived from zein storage protein genes which direct expression in endosperm. It is particularly contemplated that one may advantageously use the 16 bp *ocs* enhancer element from the octopine synthase (*ocs*) gene (Bonchez et al., 1989), especially when present in multiple copies, to achieve enhanced expression in roots.

Preferred plant promoters include, but are not limited to, a promoter such as the CaMV 35S promoter, an enhanced 35S promoter or others such as CaMV 19S, *nos*, *Adh1*, sucrose synthase, α -tubulin, ubiquitin, actin, *cab*, PEPCase or those associated with the R gene complex. Further suitable promoters include the U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein

protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a 27 kD zein protein, the A20 promoter from the gene encoding a 19 kD -zein protein, inducible promoters, such as the light inducible promoter derived from the pea *rbcS* gene and the actin promoter from rice; seed specific promoters, such as the phaseolin promoter from beans, may also be used. Other promoters useful in the practice of the invention are known to those of skill in the art.

Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990,) corn alcohol dehydrogenase 1 (Vogel et al., 1992; Dennis et al., 1984), corn light harvesting complex (Simpson, 1985; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985; Rochester et al., 1986), pea small subunit RuBP carboxylase (Poulsen et al., 1986; Cashmore et al., 1983), Ti plasmid mannopine synthase (Langridge et al., 1989), Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991), α -tubulin, cab (Sullivan et al., 1989), PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters (Chandler et al., 1989), and chalcone synthase promoters (Franken et al., 1991).

Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

Several tissue-specific regulated genes and/or promoters have been reported in plants. These include genes encoding the seed storage proteins (such as napin, cruciferin, beta-conglycinin, and phaseolin) zein or oil body proteins (such as oleosin), or genes involved in fatty acid biosynthesis (including acyl carrier protein, stearyl-ACP desaturase, and fatty acid desaturases (fad 2-1)), and other genes expressed during embryo development (such as Bce4, see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific

expression is the pea vicilin promoter (Czako et al., 1992. (See also U.S. Pat. No. 5,625,136, herein incorporated by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from Arabidopsis (Gan et al., 1995, 270 (5244), 1986-8).

A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. 4,943,674, the disclosure of which is hereby incorporated by reference. cDNA clones that are preferentially expressed in cotton fiber have been isolated (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in U.S. Patent No. 4,535,060, U.S. Patent No. 4,769,061, U.S. Patent No. 4,801,590, and U.S. Patent No. 5,107,065, which disclosures are incorporated herein by reference.

Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an example of a developmentally-regulated fiber cell protein is E6 (John et al., 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

The tissue-specificity of some "tissue-specific" promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with "leaky" expression by a combination of different tissue-specific promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379). Several inducible promoters ("gene switches") have been reported. Many are described in the review by Gatz (1996 and 1997). These include tetracycline repressor system, *Lac* repressor system, copper-inducible systems, salicylate-inducible systems (such as the PR1a system), glucocorticoid- (Aoyama, 1997) and ecdysone-inducible systems. Also included are the benzene sulphonamide- (U.S. Patent No. 5,364,780) and alcohol- (WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters. Other studies have focused on genes inducibly regulated in response to

environmental stress or stimuli such as increased salinity, drought, pathogen and wounding. (Graham et al., 1985; Graham et al., 1985, Smith et al., 1986).

Accumulation of metallocarboxypeptidase-inhibitor protein has been reported in leaves of wounded potato plants (Graham et al., 1981). Other plant genes have
5 been reported to be induced methyl jasmonate, elicitors, heat-shock, anaerobic stress, or herbicide safeners.

Frequently it is desirable to have continuous or inducible expression of a DNA sequence throughout the cells of an organism in a tissue-independent manner. For example, increased resistance of a plant to infection by soil- and air
10 borne pathogens might be accomplished by genetic manipulation of the plant's genome to comprise a continuous promoter operably linked to a heterologous or homologous pathogen-resistance gene such that pathogen-resistance proteins are continuously expressed throughout the plant's tissues.

Alternatively, it might be desirable to inhibit expression of a native DNA
15 sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive expression of the antisense sequence produces an RNA transcript that interferes with translation of the
20 mRNA of the native DNA sequence.

Other elements include those that can be regulated by endogenous or exogenous agents, e.g., by DNA binding proteins such as zinc finger proteins, including naturally occurring zinc finger proteins or chimeric zinc finger proteins (see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO
25 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311) or myb-like transcription factors. For example, a chimeric zinc finger protein may include amino acid sequences which bind to a specific DNA sequence (the zinc finger) and amino acid sequences that activate (e.g., GAL 4 sequences) or repress the transcription of the sequences linked to the specific
30 DNA sequence.

B. 5' and 3' Sequences

In addition to promoters, a variety of 3 transcriptional terminators are also available for use in the present invention. Transcriptional terminators are responsible for the termination of transcription and correct mRNA

polyadenylation. The 3' nontranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the tml terminator, the nopaline synthase terminator, the pea rbcS E9⁺ terminator, the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato, although other 3' elements known to those of skill in the art can also be employed.

The 5' regulatory region of the expression cassette may also include other enhancing sequences. Numerous sequences have been found to enhance gene expression in transgenic plants. These include sequences which have been shown to enhance expression such as intron sequences (e.g., from *Adhl*, *bronzel* or the sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other leaders known in the art include but are not limited to: Picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5 noncoding region) (Elroy-Stein et al., 1989); Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison et al., 1986); MDMV leader (Maize Dwarf Mosaic Virus); Human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak et al., 1991); Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling et al., 1987; Tobacco mosaic virus leader (TMV), (Gallie et al., 1989; and Maize Chlorotic Mottle Virus leader (MCMV) (Lommel et al., 1991. See also, Della-Cioppa et al., 1987.

C. Targeting Sequences

It may be preferable to target expression of the nucleotide sequences of the present invention to different cellular localizations in the plant. In some cases, localization in the cytosol may be desirable, whereas in other cases, localization in some subcellular organelle, e.g., the nucleus, may be preferred. Subcellular

localization of transgene encoded enzymes is undertaken using techniques well known in the art. Typically, the DNA encoding the target peptide from a known organelle-targeted gene product is manipulated and fused upstream of the nucleotide sequence. Many such target sequences are known for the chloroplast and their functioning in heterologous constructions has been shown. The expression of the nucleotide sequences of the present invention is also targeted to the endoplasmic reticulum or to the vacuoles of the host cells. Techniques to achieve this are well-known in the art.

D. Marker Genes

10 In order to improve the ability to identify transformants, one may desire to employ a selectable or screenable marker gene as, or in addition to, the preselected nucleic acid sequence or segment. "Marker genes" are genes that impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker. 15 Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can 'select' for by chemical means, i.e., through the use of a selective agent (e.g., a herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing, i.e., by 'screening' (e.g., the R-locus trait). Of course, many examples of suitable 20 marker genes are known to the art and can be employed in the practice of the invention.

Included within the terms selectable or screenable marker genes are also genes which encode a "secretable marker" whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include 25 markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected by their catalytic activity. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA; small active enzymes detectable in extracellular solution (e.g., α -amylase, β -lactamase, phosphinothricin 30 acetyltransferase); and proteins that are inserted or trapped in the cell wall (e.g., proteins that include a leader sequence such as that found in the expression unit of extensin or tobacco PR-S).

With regard to selectable secretable markers, the use of a gene that encodes a polypeptide that becomes sequestered in the cell wall, and which polypeptide

includes a unique epitope is considered to be particularly advantageous. Such a secreted antigen marker would ideally employ an epitope sequence that would provide low background in plant tissue, a promoter-leader sequence that would impart efficient expression and targeting across the plasma membrane, and
5 would produce protein that is bound in the cell wall and yet accessible to antibodies. A normally secreted wall protein modified to include a unique epitope would satisfy all such requirements.

Elements of the present disclosure are exemplified in detail through the use of particular marker genes. However in light of this disclosure, numerous other
10 possible selectable and/or screenable marker genes will be apparent to those of skill in the art in addition to the one set forth herein below. Therefore, it will be understood that the following discussion is exemplary rather than exhaustive. In light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the present invention renders possible the
15 introduction of any gene, including marker genes, into a recipient cell to generate a transformed plant cell, e.g., a monocot cell.

Possible selectable markers for use in connection with the present invention include, but are not limited to, a *neo* gene, which codes for kanamycin resistance and can be selected for using kanamycin, G418, a gene encoding
20 resistance to bleomycin, and the like; a *bar* gene which codes for bialaphos resistance; a gene which encodes an altered EPSP synthase protein thus conferring glyphosate resistance; a nitrilase gene such as *bxn* from *Klebsiella ozaenae* which confers resistance to bromoxynil; a mutant acetolactate synthase gene (ALS) which confers resistance to imidazolinone, sulfonylurea or other
25 ALS-inhibiting chemicals (European Patent Application 154,204, 1985); a methotrexate-resistant DHFR gene; a dalapon dehalogenase gene that confers resistance to the herbicide dalapon; or a mutated anthranilate synthase gene that confers resistance to 5-methyl tryptophan. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a
30 suitable chloroplast transit peptide, CTP (European Patent Application 0 218 571, 1987).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the *bar* gene from *Streptomyces*

hygroscopicus or the *pat* gene from *Streptomyces viridochromogenes* (U.S. Patent No. 5,550,318). The enzyme phosphinothricin acetyltransferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, causing rapid accumulation of ammonia and cell death. The success in using this selective system in conjunction with monocots was particularly surprising because of the major difficulties which have been reported in transformation of cereals.

Screenable markers that may be employed include, but are not limited to, a β -glucuronidase or *uidA* gene (GUS) which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues; a β -lactamase gene, which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a *xy/E* gene which encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene; a tyrosinase gene which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to form the easily detectable compound melanin; a β -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene, which allows for bioluminescence detection; or an aequorin gene, which may be employed in calcium-sensitive bioluminescence detection, or a green fluorescent protein.

Genes from the maize R gene complex are contemplated to be particularly useful as screenable markers. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. Maize strains can have one, or as many as four, R alleles which combine to regulate pigmentation in a developmental and tissue specific manner. A gene from the R gene complex was applied to maize transformation, because the expression of this gene in transformed cells does not harm the cells. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line carries dominant alleles for genes encoding the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2), but carries a recessive allele at the R locus, transformation of any cell from that line with R will result in red pigment formation. Exemplary lines include Wisconsin 22

which contains the rg-Stadler allele and TR112, a K55 derivative which is r-g, b, Pl. Alternatively any genotype of maize can be utilized if the C1 and R alleles are introduced together.

5 A further screenable marker contemplated for use in the present invention is firefly luciferase, encoded by the *lux* gene. The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation counting, fluorescent spectrophotometry, low-light video cameras, photon counting cameras or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening.

E. Other Sequences

A vector of the invention can also further comprise plasmid DNA. Plasmid vectors include additional DNA sequences that provide for easy selection, amplification, and transformation of the expression cassette in 15 prokaryotic and eukaryotic cells, e.g., pUC-derived vectors such as pUC8, pUC9, pUC18, pUC19, pUC23, pUC119, and pUC120, pSK-derived vectors, pGEM-derived vectors, pSP-derived vectors, or pBS-derived vectors. The additional DNA sequences include origins of replication to provide for autonomous replication of the vector, additional selectable marker genes, 20 preferably encoding antibiotic or herbicide resistance, unique multiple cloning sites providing for multiple sites to insert DNA sequences or genes encoded in the expression cassette, and sequences that enhance transformation of prokaryotic and eukaryotic cells.

Another vector that is useful for expression in both plant and prokaryotic 25 cells is the binary Ti plasmid (as disclosed in Schilperoort et al., U.S. Patent No. 4,940,838) as exemplified by vector pGA582. This binary Ti plasmid vector has been previously characterized by An, cited *supra*. This binary Ti vector can be replicated in prokaryotic bacteria such as *E. coli* and *Agrobacterium*. The *Agrobacterium* plasmid vectors can be used to transfer the expression cassette to 30 dicot plant cells, and under certain conditions to monocot cells, such as rice cells. The binary Ti vectors preferably include the nopaline T DNA right and left borders to provide for efficient plant cell transformation, a selectable marker gene, unique multiple cloning sites in the T border regions, the *co/E1* replication of origin and a wide host range replicon. The binary Ti vectors carrying an

expression cassette of the invention can be used to transform both prokaryotic and eukaryotic cells, but is preferably used to transform dicot plant cells.

Virtually any DNA may be used for delivery to recipient cells to ultimately produce fertile transgenic plants in accordance with the present invention. For example, DNA segments in the form of vectors and plasmids, or linear DNA fragments, in some instance containing only the DNA element to be expressed in the plant, and the like, may be employed.

Vectors, plasmids, cosmids, YACs (yeast artificial chromosomes) and DNA segments for use in transforming such cells will, of course, generally comprise the cDNA, gene or genes which one desires to introduce into the cells. These DNA constructs can further include structures such as promoters, enhancers, polylinkers, or even regulatory genes as desired. The DNA segment or gene chosen for cellular introduction will often encode a protein which will be expressed in the resultant recombinant cells, such as will result in a screenable or selectable trait and/or which will impart an improved phenotype to the regenerated plant. However, this may not always be the case, and the present invention also encompasses transgenic plants incorporating non-expressed transgenes.

20 III. Transformation

The expression cassettes of the present invention can be introduced into a host cell, e.g., a plant cell, in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of cell, e.g., monocotyledonous or dicotyledonous, targeted for transformation. Vectors which may be used to transform plant tissue with the expression cassettes of the present invention include both *Agrobacterium* vectors and ballistic vectors, as well as vectors suitable for DNA-mediated transformation, e.g., direct uptake or via electroporation. However, cells other than plant cells may be transformed with the expression cassettes of the invention.

Suitable methods of transforming plant cells include, but are not limited to, microinjection (Crossway et al., 1986), direct DNA transfer to plant cells by PEG precipitation; liposomes; electroporation (Riggs et al., 1986, *Agrobacterium*-mediated transformation (Hinchee et al., 1988), direct gene transfer (Paszkowski et al., 1984), and ballistic particle acceleration using

devices available from Agracetus, Inc., Madison, Wis. and BioRad, Hercules, Calif. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al., 1988). Also see, Weissinger et al., 1988; Sanford et al., 1987 (onion); Christou et al., 1988 (soybean); McCabe et al., 1988 (soybean); Datta et al., 1990 (rice); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Fromm et al., 1990 (maize); and Gordon-Kamm et al., 1990 (maize); Svab et al., 1990 (tobacco chloroplast); Koziel et al., 1993 (maize); Shimamoto et al., 1989 (rice); Christou et al., 1991 (rice); European Patent Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., 1993 (wheat); Weeks et al., 1993 (wheat).

In one embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al., 1994.

The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate orthologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for transformation (Svab et al., 1990; Staub et al., 1992). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub et al., 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial *aadA* gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3'-adenyltransferase (Svab et al., 1993). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a

homoplastidic state. Plastid expression, in which genes are inserted by orthologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplastic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

Agrobacterium tumefaciens cells containing a vector comprising an expression cassette of the present invention, wherein the vector comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an *Agrobacterium tumefaciens* as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell. Numerous *Agrobacterium* vector systems useful in carrying out the present invention are known. For example, U.S. Pat. No. 4,459,355 discloses a method for transforming susceptible plants, including dicots, with an *Agrobacterium* strain containing the Ti plasmid. The transformation of woody plants with an *Agrobacterium* vector is disclosed in U.S. Patent No. 4,795,855. Further, U.S. Patent No. 4,940,838 to Schilperoort et al. discloses a binary *Agrobacterium* vector (i.e., one in which the *Agrobacterium* contains one plasmid having the vir region of a Ti plasmid but no T region, and a second plasmid having a T region but no vir region) useful in carrying out the present invention.

It is particularly preferred to use the binary type vectors of Ti and Ri plasmids of *Agrobacterium spp.* Ti-derived vectors transform a wide variety of higher plants, including monocotyledonous and dicotyledonous plants, such as soybean, cotton, rape, tobacco, and rice (Pacciotti et al., 1985; Byrne et al., 1987; Sukhapinda et al., 1987; Lorz et al., 1985; Potrykus, 1985; Park et al., 1985; Hiei et al., 1994. The use of T-DNA to transform plant cells has received extensive study and is amply described (EP 120516; Hoekema, 1985; Knauf, et al., 1983; and An. et al., 1985. For introduction into plants, the nucleotide sequences of the invention can be inserted into binary vectors as described in the examples.

Transformation of plants can be undertaken with a single DNA molecule or multiple DNA molecules (i.e., co-transformation), and both these techniques are suitable for use with the expression cassettes of the present invention.

Numerous transformation vectors are available for plant transformation, and the
 5 expression cassettes of this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation.

Preferred plant cells for transformation include, but are not limited to, cells from plant such as corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B.*
 10 *juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus*
 15 *tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa
 20 (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.),
 25 oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L.*
 30 *valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wofiella* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*, *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*).

Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt,

5 Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis*

10 such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and

15 chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*);

20 redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils,

25 chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula,

30 blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry,

nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens,
 5 Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Other vegetables are in Table 1.

10 Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

Preferably, plants of the present invention are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean,
 15 barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, and the like), and even more preferably rice, corn and soybean.

In a preferred embodiment, the host cells are monocot or dicot cells, including, but are not limited to, wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince,
 20 cherry, apricot, pepper, melon, lettuce, cauliflower, *Brassica*, e.g., broccoli, cabbage, brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry,
 25 chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut, nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g.,
 30 lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia,

Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. More preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be
5 regenerated into a transgenic plant.

Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term "organogenesis," as used herein, means a process by which shoots and roots are developed sequentially from meristematic centers; the
10 term "embryogenesis," as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen,
15 embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem).

The choice of plant tissue source for transformation will depend on the nature of the host plant and the transformation protocol. Useful tissue sources
20 include callus, suspension culture cells, protoplasts, leaf segments, stem segments, tassels, pollen, embryos, hypocotyls, tuber segments, meristematic regions, and the like. The tissue source is selected and transformed so that it retains the ability to regenerate whole, fertile plants following transformation, i.e., contains totipotent cells. Type I or Type II embryonic maize callus and
25 immature embryos are preferred *Zea mays* tissue sources. Selection of tissue sources for transformation of monocots is described in detail in U.S. Application Serial No. 08/112,245 and PCT publication WO 95/06128 (incorporated herein by reference).

For certain plant species, different antibiotic or herbicide selection markers
30 may be preferred. Selection markers used routinely in transformation include the *nptII* gene which confers resistance to kanamycin and related antibiotics (Messing & Vierra, 1982); Bevan et al., 1983), the *bar* gene which confers resistance to the herbicide phosphinothricin (White et al., 1990, Spencer et al., 1990), the *hph* gene which confers resistance to the antibiotic hygromycin

(Blochinger & Diggelmann), and the *dhfr* gene, which confers resistance to methotrexate (Bourouis et al., 1983).

Thus, the present invention also provides a transformed (transgenic) plant cell, *in planta* or *ex planta*, including, but not limited to, a transformed plant cell
 5 from plants such as corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet
 10 (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos
 15 nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond
 20 (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wofieldia* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*,
 30 *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*). Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt,

Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (5 *Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), 10 carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga 15 menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, 20 soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g., 25 trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, 30 apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens,

Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia, as well
 5 as from vegetables including those described in Table 1.

In a preferred embodiment, the transformed cells, include, but are not limited to, transformed wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince, cherry, apricot, pepper, melon, lettuce, cauliflower, *Brassica*, e.g., broccoli, cabbage,
 10 brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry, chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut,
 15 nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field
 20 bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia, Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura,
 25 Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. Preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be regenerated into a transgenic plant.

30 IV. Identification of Transgenic Plants

To confirm the presence of the preselected nucleic acid segment(s) or "transgene(s)" in the regenerating plants, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays well known to those of skill in the art, such as Southern and Northern blotting, *in situ*

hybridization and nucleic acid-based amplification methods such as PCR or RT-PCR; "biochemical" assays, such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant, e.g., for disease or pest resistance.

DNA may be isolated from cell lines or any plant parts to determine the presence of the preselected nucleic acid segment through the use of techniques well known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

The presence of nucleic acid elements introduced through the methods of this invention may be determined by polymerase chain reaction (PCR). Using this technique discrete fragments of nucleic acid are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a preselected nucleic acid segment is present in a stable transformant, but does not prove integration of the introduced preselected nucleic acid segment into the host cell genome. In addition, it is not possible using PCR techniques to determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that using PCR techniques it would be possible to clone fragments of the host genomic DNA adjacent to an introduced preselected DNA segment.

Positive proof of DNA integration into the host genome and the independent identities of transformants may be determined using the technique of Southern hybridization. Using this technique specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition it is possible through Southern hybridization to demonstrate the presence of introduced preselected DNA segments in high molecular weight DNA, i.e., confirm that the introduced preselected DNA segment has been integrated into the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR, e.g., the presence of a preselected DNA segment, but also demonstrates integration into the genome and characterizes each individual transformant.

It is contemplated that using the techniques of dot or slot blot hybridization which are modifications of Southern hybridization techniques one could obtain the same information that is derived from PCR, e.g., the presence of a preselected DNA segment.

5 Both PCR and Southern hybridization techniques can be used to demonstrate transmission of a preselected DNA segment to progeny. In most instances the characteristic Southern hybridization pattern for a given transformant will segregate in progeny as one or more Mendelian genes (Spencer et al., 1992); Laursen et al., 1994) indicating stable inheritance of the gene. The
10 nonchimeric nature of the callus and the parental transformants (R_0) was suggested by germline transmission and the identical Southern blot hybridization patterns and intensities of the transforming DNA in callus, R_0 plants and R_1 progeny that segregated for the transformed gene.

Whereas DNA analysis techniques may be conducted using DNA isolated
15 from any part of a plant, RNA may only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used for detection and quantitation of RNA produced from introduced preselected DNA segments. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes
20 such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information
25 about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

While Southern blotting and PCR may be used to detect the preselected
30 DNA segment in question, they do not provide information as to whether the preselected DNA segment is being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced preselected DNA segments or evaluating the phenotypic changes brought about by their expression.

Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or
5 denaturing gel electrophoresis or isoelectric focussing, or by chromatographic techniques such as ion exchange or gel exclusion chromatography. The unique structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations of approaches may be employed with even greater specificity such as Western
10 blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid sequencing following purification. Although these are among the most commonly employed, other procedures may be additionally
15 used.

Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and quantifying the loss of substrates or the
20 generation of products of the reactions by physical or chemical procedures. Examples are as varied as the enzyme to be analyzed.

Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical
25 composition, morphology, or physiological properties of the plant. Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays.

30 V. Utility

Once an expression cassette of the invention has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. Particularly preferred plants of the invention

include the agronomically important crops listed above. The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction and can thus be maintained and propagated in progeny plants. The present invention also relates to a transgenic plant cell, tissue, organ, seed or plant part obtained from the transgenic plant. Also included within the invention are transgenic descendants of the plant as well as transgenic plant cells, tissues, organs, seeds and plant parts obtained from the descendants.

Preferably, the expression cassette in the transgenic plant is sexually transmitted. In one preferred embodiment, the coding sequence is sexually transmitted through a complete normal sexual cycle of the R0 plant to the R1 generation. Additionally preferred, the expression cassette is expressed in the cells, tissues, seeds or plant of a transgenic plant in an amount that is different than the amount in the cells, tissues, seeds or plant of a plant which only differs in that the expression cassette is absent.

The transgenic plants produced herein are thus expected to be useful for a variety of commercial and research purposes. Transgenic plants can be created for use in traditional agriculture to possess traits beneficial to the grower (e.g., agronomic traits such as resistance to water deficit, pest resistance, herbicide resistance or increased yield), beneficial to the consumer of the grain harvested from the plant (e.g., improved nutritive content in human food or animal feed), or beneficial to the food processor (e.g., improved processing traits). In such uses, the plants are generally grown for the use of their grain in human or animal foods. However, other parts of the plants, including stalks, husks, vegetative parts, and the like, may also have utility, including use as part of animal silage or for ornamental purposes. Often, chemical constituents (e.g., oils or starches) of maize and other crops are extracted for foods or industrial use and transgenic plants may be created which have enhanced or modified levels of such components.

Transgenic plants may also find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements

encoded by the expression cassette may be transferred, e.g., from maize cells to cells of other species, e.g., by protoplast fusion.

The transgenic plants may have many uses in research or breeding, including creation of new mutant plants through insertional mutagenesis, in order to identify beneficial mutants that might later be created by traditional mutation and selection. An example would be the introduction of a recombinant DNA sequence encoding a transposable element that may be used for generating genetic variation. The methods of the invention may also be used to create plants having unique "signature sequences" or other marker sequences which can be used to identify proprietary lines or varieties.

Thus, the transgenic plants and seeds according to the invention can be used in plant breeding which aims at the development of plants with improved properties conferred by the expression cassette, such as tolerance of viruses or other pests, or other stresses. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate descendant plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

VI. A Computer Readable Medium

The invention also provides a computer readable medium having stored thereon a data structure containing nucleic acid sequences having at least 70% sequence identity to a nucleic acid sequence selected from those listed in SEQ ID Nos: 1-795 as well as complementary, ortholog, and variant sequences thereof. Storage and use of nucleic acid sequences on a computer readable medium is well known in the art. (See for example U.S. Patent Nos. 6,023,659; 5,867,402; 5,795,716) Examples of such medium include, but are not limited to, magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory. Accordingly, the nucleic acid sequences contained on the computer readable medium may be compared through use of a module that receives the sequence information and compares it to other sequence information. Examples of other sequences to which the nucleic acid sequences of the invention may be compared include those maintained by the National Center for Biotechnology Information (NCBI)(<http://www.ncbi.nlm.nih.gov/>) and the Swiss Protein Data Bank. A computer is an example of such a module that can read and compare nucleic acid sequence information. Accordingly, the invention also provides the method of comparing a nucleic acid sequence of the invention to another sequence. For example, a sequence of the invention may be submitted to the NCBI for a Blast search as described herein where the sequence is compared to sequence information contained within the NCBI database and a comparison is returned. The invention also provides nucleic acid sequence information in a computer readable medium that allows the encoded polypeptide to be optimized for a desired property. Examples of such properties include, but are not limited to, increased or decreased: thermal stability, chemical stability, hydrophylicity, hydrophobicity, and the like. Methods for the use of computers to model polypeptides and polynucleotides having altered activities are well known in the art and have been reviewed. (Lesyng et al., 1993; Surles et al., 1994; Koehl et al., 1996; Rossi et al., 2001).

The invention will be further described by the following examples which is not intended to limit the scope of the invention.

Example 1GeneChip Standard ProtocolQuantitation of total RNA

Total RNA from plant tissue is extracted and quantified.

- 5 1. Quantify total RNA using GeneQuant

1OD₂₆₀=40 mg RNA/ml; A260/A280=1.9 to about 2.1

2. Run gel to check the integrity and purity of the extracted RNA

Synthesis of double-stranded cDNA

- 10 Gibco/BRL SuperScript Choice System for cDNA Synthesis (Cat#1B090-019)

was employed to prepare cDNAs. T7-(dT)₂₄ oligonucleotides were prepared

and purified by HPLC. (5'-

- 15 GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-(dT)₂₄-
3'(SEQ ID NO:800).

Step 1. Primer hybridization:

Incubate at 70°C for 10 minutes

Quick spin and put on ice briefly

- 20 Step 2. Temperature adjustment:

I Incubate at 42°C for 2 minutes

Step 3. First strand synthesis:

DEPC-water- 1 µl

RNA (10 µg final)-10 µl

- 25 T7=(dT)₂₄ Primer (100 pmol final)-1 µl pmol

5X 1st strand cDNA buffer-4 µl

0.1M DTT (10 mM final)- 2 µl

10 mM dNTP mix (500 µM final)-1 µl

Superscript II RT 200 U/µl- 1 µl

- 30 Total of 20 µl

Mix well

Incubate at 42°C for 1 hour

Step 4. Second strand synthesis:

Place reactions on ice, quick spin

- DEPC-water- 91 μ l
 5X 2nd strand cDNA buffer- 30 μ l
 mM dNTP mix (250 mM final) - 3 μ l
E. coli DNA ligase (10 U/ μ l)-1 μ l
 5 *E. coli* DNA polymerase I-10 U/ μ l- 4 μ l
 RnaseH 2U/ μ l -1 μ l
 T4 DNA polymerase 5 U/ μ l-2 μ l
 0.5 M EDTA (0.5 M final)--10 μ l
 Total 162 μ l
 10 Mix/spin down/incubate 16°C for 2 hours

Step 5. Completing the reaction:

Incubate at 16°C for 5 minutes

Purification of double stranded cDNA

- 15 1. Centrifuge PLG (Phase Lock Gel, Eppendorf 5 Prime, Inc., PI-188233)
 at 14,000X, transfer 162 μ l of cDNA to PLG
 2. Add 162 μ l of Phenol:Chloroform:Isoamyl alcohol (pH 8.0), centrifuge
 2 minutes
 3. Transfer the supernatant to a fresh 1.5 ml tube, add
 20 Glycogen (5 mg/ml) 2
 0.5 M NH₄OAc (0.75xVol) 120
 ETOH (2.5xVol, -20 °C) 400
 4. Mix well and centrifuge at 14,000X for 20 minutes
 5. Remove supernatant, add 0.5 ml 80% EtOH (-20°C)
 25 6. Centrifuge for 5 minutes, air dry or by speed vac for 5-10 minutes
 7. Add 44 μ l DEPC H₂O

Analyze of quantity and size distribution of cDNA

Run a gel using 1 μ l of the double-stranded synthesis product

30 Synthesis of biotinylated cRNA

(use Enzo BioArray High Yield RNA Transcript Labeling Kit Cat#900182)

Purified cDNA	22 μ l
10X Hy buffer	4 μ l
10X biotin ribonucleotides	4 μ l

10X DTT	4 μ l
10X Rnase inhibitor mix	4 μ l
20X T7 RNA polymerase	2 μ l
Total	40 μ l

- 5 Centrifuge 5 seconds, and incubate for 4 hours at 37°C
Gently mix every 30-45 minutes

Purification and quantification of cRNA

(use Qiagen Rneasy Mini kit Cat# 74103)

- 10 Determine concentration and dilute to 1 μ g/ μ l concentration

Fragmentation of cRNA

cRNA (1 μ g/ μ l)	15 μ l
5X Fragmentation Buffer*	6 μ l
15 DEPC H ₂ O	9 μ l
	30 μ l

*5x Fragmentation Buffer

1M Tris (pH8.1)	4.0 ml
20 MgOAc	0.64 g
KOAc	0.98 g
DEPC H ₂ O	
Total	20 ml
Filter Sterilize	

25

Array wash and staining

Stringent Wash Buffer**

Non-Stringent Wash Buffer***

SAPE Stain****

- 30 Antibody Stain*****

Wash on fluidics station using the appropriate antibody amplification protocol

**Stringent Buffer: 12X MES 83.3 ml, 5 M NaCl 5.2 ml, 10% Tween 1.0 ml, H₂O 910 ml,

Filter Sterilize

***Non-Stringent Buffer: 20X SSPE 300 ml, 10% Tween 1.0 ml, H₂O 698 ml,
Filter Sterilize, Antifoam 1.0.

****SAPE stain: 2X Stain Buffer 600 µl, BSA 48 µl, SAPE 12µl, H₂O 540 µl.

5 *****Antibody Stain: 2X Stain Buffer 300 µl, H₂O 266.4 µl, BSA 24 ul, Goat
IgG 6 µl, Biotinylated Ab 3.6 µl

Example 2Identification of *Arabidopsis* Genes Induced by *Peronospora* Infection

10

To define the transcriptional profile for *Peronospora*-induced and/or
RPP7- and *RPP8*- dependent genes, four *Arabidopsis* lines were infected with
one of two different *P. parasitica* isolates (see Table 2). One *Arabidopsis* line
was Col-0::*RPP8* which carries the cloned *RPP8* genomic clone (*RPP8* mediates
15 resistance of the ecotype La-er against Emco5; McDowell et al. 1998) and is
Emco5 resistant. Wild-type Col-0 plants are Emco5 susceptible. *RPP7* mediates
resistance of *Arabidopsis* against the *Peronospora* isolate Hiks1, and occurs
naturally in Col-0. Another *Arabidopsis* line had a loss of function *rpp7* mutant
allele (Col-0 (*rpp7*)) (McDowell et al., 2000). Finally, three mutants in the
20 signaling pathway for *RPP7*, i.e., they lack a *RPP7*-mediated response, were
identified, i.e., *edm1*, *edm2* and *edm3*, and a line with one of the mutant alleles,
i.e., *edm1*, was used.

RNA samples were collected from two week old seedlings at three time
points, 0, 12 and 24 hours post infection with 100,000 spores/ml. Twelve hours
25 post-inoculation was determined to be an appropriate time point for analysis of
both incompatible interactions, based on trypan blue staining of HR sites and
PR-1 and *sen1* induction. Forty-eight hours post-inoculation was determined to
be a time point where both compatible interactions exhibit dense hyphal growth
and both *PR-1* and *sen1* expression. Three independent sets of RNA were
30 pooled.

Table 2

	<u>Plant</u>	<u><i>Peronospora</i> isolate</u>	<u>Time of RNA collection</u>
	Col-0 (<i>RPP7</i> , <i>incomp.</i>)	Hiks1	0, 12, 48 hours
35	Col-0 (<i>rpp7</i> , <i>comp.</i>)	Hiks1	0, 12, 48 hours

Col-0 (<i>edm1</i> , <i>comp.</i>)	Hiks1	0, 12, 48 hours
Col-0 (<i>tgRPP8</i> , <i>incomp.</i>)	Emco5	0, 12, 48 hours
Col-0 (<i>rpp8</i> , <i>comp.</i>)	Emco5	0, 12, 48 hours

5 RNAs were labeled as described in Example 1 and hybridized to an Affymetrix Gene Chip having sequences corresponding to about 8,200 *Arabidopsis* genes. The data collected from these chips was employed to determine:

- 1) the difference, if any, between *RPP7* and *RPP8* triggered signaling (and how these profiles compare to other profiles, for example, to the profiles of *RPM1* and *RPS2*);
- 2) which portion of the transcriptional response is *R* dependent;
- 3) which genes are either commonly or uniquely induced during two different compatible interactions;
- 4) which genes are specifically activated during the incompatible interactions (gleaned by comparison with isogenic compatible controls) and, hence, may be important for the plant's defense against *Peronospora*;
- 5) which genes whose expression is a prerequisite for induced defense reactions against *Peronospora*; and
- 6) which genes are specifically repressed during the incompatible interactions, which may be required for successful Oomycete infections.

Results

Genes Expressed Early and Transiently After Infection

The normalized "average difference" (AD) from the chip experiments were processed as follows. All values together with the respective gene identifiers were loaded in EXCEL. Genes having, for a given treatment, AD values of 25 or less were considered as being not expressed. To reduce spurious background fluctuation, this cut off level was elevated to 75 for most of the analyses and normalized all AD values of 75 or less. For all five infection time courses, the AD values were divided by the corresponding 0 hour time point AD value. To visualize differences in gene expression ground states between the four experimental *Arabidopsis* lines, the following ratios were calculated for the 0 hour AD values: Col-0 (from Emco5 series)/Col-0-*RPP8* and *rpp7*/Col-0 (from Hiks1 series) and *edm1*/Col-0 (from Hiks1 series). These ratios indicate whether

a given gene is up- or down-regulated by the *RPP7* or *RPP8* pathway, respectively. The resulting set of 18 expression ratio series was then loaded into CLUSTER (Eisen et al., 1998). The AD values were log transformed (base 2) and filtered to include only genes in the final data set that showed at least a 3-
 5 fold expression change (which equals a 1.6-fold change of the log transformed values). These criteria were fulfilled by 464 genes that define the final data set. With this data set Average linkage clustering was performed (uncentered correlation). The resulting clustergram was displayed using TREEVIEW (Eisen et al., 1998). A second clustergram was generated in the same way applying a cut
 10 off value of 50 on the normalized AD values. This clustergram includes 619 genes (probe sets).

Based on these clustergrams, gene clusters showing distinct expression behaviors were defined. Cluster cR7/R8 (see Table 3) contained genes that are early and transiently upregulated early and transiently after *P. parasitica*
 15 infection of *Arabidopsis* in an *RPP7/8* dependent manner. Upregulation by the *RPP8* pathway was generally stronger. Strong induced expression of cR7/R8 genes was detectable 12 hours after Emco5 infection in Col-0(*tgRPP8*) plants (incompatible interaction), whereas no elevated expression can be observed 48
 20 hours post infection in the same plants (as compared to untreated control plants). Only weakly elevated or no elevated expression was detected at all tested time points in Col-0 plants (compatible interaction). After Hiks1 infection, elevated expression of these genes was only observed in Col-0 plants (incompatible
 25 interaction) after 12 hours. At no other time point following Hiks1 infection was substantially elevated expression of these genes observed. The expression ground state of these genes is similar in all four *Arabidopsis* lines.

Table 3

20245 s at	cut off = 75
18716 At	
18022 at	
14609 at	
17014 s at	
17051 s at	
19640 at	
14248 at	
13176_at	

15978 at cut off +50
 17014 s at
 14609 at
 13764 at
 16649 s at Subcluster A
 13215 s at
 17653 at
 17008 at
 15042 at
 12778_r_at

14614 at
 17051 s at
 14248 at Subcluster B
 20245 s at
 19640 at
 18716 at
 18022_at

17500 s at
 13217 s at
 18928 at

The cR7/R8 cluster was originally defined using the clustergram based on a cut off value of 75 and comprised only 9 genes. Applying a cut off value of 50, the cluster became larger, comprising 21 genes, which could be divided into two subclusters (Table 4). Subcluster cR7/R8 A includes genes strongly and transiently upregulated by the *RPP8* pathway, but either not, or only faintly, upregulated by the *RPP7* pathway. Members of subcluster B showed pronounced upregulation by both *RPP* pathways after 12 hours and also elevated expression during compatible Emco5 infections in Col-0.

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Table 4

Subcluster AGene-identifier (probe set)

15978_at

17014_s_at*

14609_at

16649_s_at+

13215_s_at+

17653_at

17008_at

Related to

X68592.6_at

atu05206_s_at

AC002340.147_at

athorf_s_at

CafferoylCoAmethyltrans_s_a
t

AL035679.144_at

AC006585.212_at

15042_at	AL021961.3_at
12778_r_at	AC006577.16_r_at

Subcluster B

<u>Gene-identifier (probe set)</u>	<u>Related to</u>
14614_at	AC004165.66_at
17051_s_at	af098947_s_at
14248_at	PAD3_at
20245_s_at	AC005309.97_s_at
19640_at	AC004561.78_at
18716_at	X91916_at
18022_at	AJ010971_at
17500_s_at [†]	athcallga_s_at
13217_s_at [†]	calmodulinlike_s_at
18928_at	AC002333.181_at

* Genes printed in **bold** were identified using a cut off value of 75; all others were identified using a cut off value of 50.

[†]The probe sets 16649 and 13215 as well as 17500 and 13217 correspond to the same genes.

Thus, the predominant feature of genes of the cR7/R8 cluster is more pronounced expression along with *RPP7* and *RPP8* mediated *Peronospora* resistance in comparison to the corresponding compatible interactions. Expression of these genes peaks in around 12 hours post infection and returns to ground state by 48 hours post infection. Hence, increased transcript levels of these genes coincide with the time window of decision between disease or resistance. Within 48 hours after infection with each tested *Peronospora* isolate, the plant either responds with HR and hinders development of oomycete hyphae or allows successful infection.

Identification of Conserved Sequence Motifs Within cR7/R8 Upstream Regions

To identify potential *cis*-elements involved in the specific regulation of cR7/R8 genes, stretches comprising 1.1 to 1.2 kb localized directly upstream of the translation start sites of coding regions from this cluster were collected from genomic *Arabidopsis* sequences (see Figure 2). Two motif search algorithms were used to recognize conserved motifs: AlignAce (Roth et al., 1998) and MEME (Bailey and Elkan, 1994). A search with AlignAce (default settings) revealed two conserved motifs within a set of 8 promoters comprising 7 from the originally defined cR7R8 using a cut off value of 75 and the promoter of a gene encoding a putative Myb-like transcription factor (Martin & Paz-Ares, 1997)

(probe set 13176, SEQ ID NO:36), which shows a similar expression behavior as cR7/R8. The AlignAce output is shown below in Table 5:

Table 5

Motif 1	MAP Score:	SEQ ID NO.	Corresponding Probe Set
*****	6.87857		
CAACAATTAT	0 36 1	685	17014
CAACTATGTC	0 981 1	686	17014
CAACAATGAC	1 934 0	687	20245
CAACAATGAC	2 271 1	688	14609
AAACAATGAT	2 1184 1	689	14609
CAACATTGAC	3 163 0	690	17051
CAACATTGTT	3 298 0	691	17051
CAACAATGTT	4 613 1	692	19640
CAACTATGAT	4 791 0	693	19640
CAACAATGAT	4 1064 0	694	19640
CAAAAATGAT	7 397 0	695	17008
CAACATTGAT	7 415 1	696	17008
CATATCA/TA/TTGAC (Consensus)		697	N.A.

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Motif 2	MAP Score:	SEQ ID NO.	Corresponding Probe Set
***** **	2.22382		
TTTGGGCAAAA	1 368 0	698	20245
GTTGGGTCAAA	1 739 0	699	20245
GATGGGCACAA	2 691 0	700	14609
GATGGGCCAAA	3 700 0	701	17051
GATGGGTATAA	4 344 0	702	19640
GATGGGACTAA	5 98 1	703	14248
TTTGGGCCTAA	5 971 1	704	14248
TATGGGCCCAA	5 1012 0	705	14248
CTTGGGACAAA	7 579 1	706	17008
GATGGGTCAAC	7 1009 0	707	17008
CATGGGAATAA	7 1072 1	708	17008
NATTGGGNC/ANAA (Consensus)		709	N.A.

For each motif, examples from cR7/R8 promoters are listed. Nucleotides evaluated by AlignAce as being conserved are indicated by a "*" above the examples. Besides motifs 1 and 2, a variety of additional ones were found by AlignAce, which, however, consisted almost exclusively of Ts and As. These motifs probably do not constitute functional *cis*-elements. Promoter sequences

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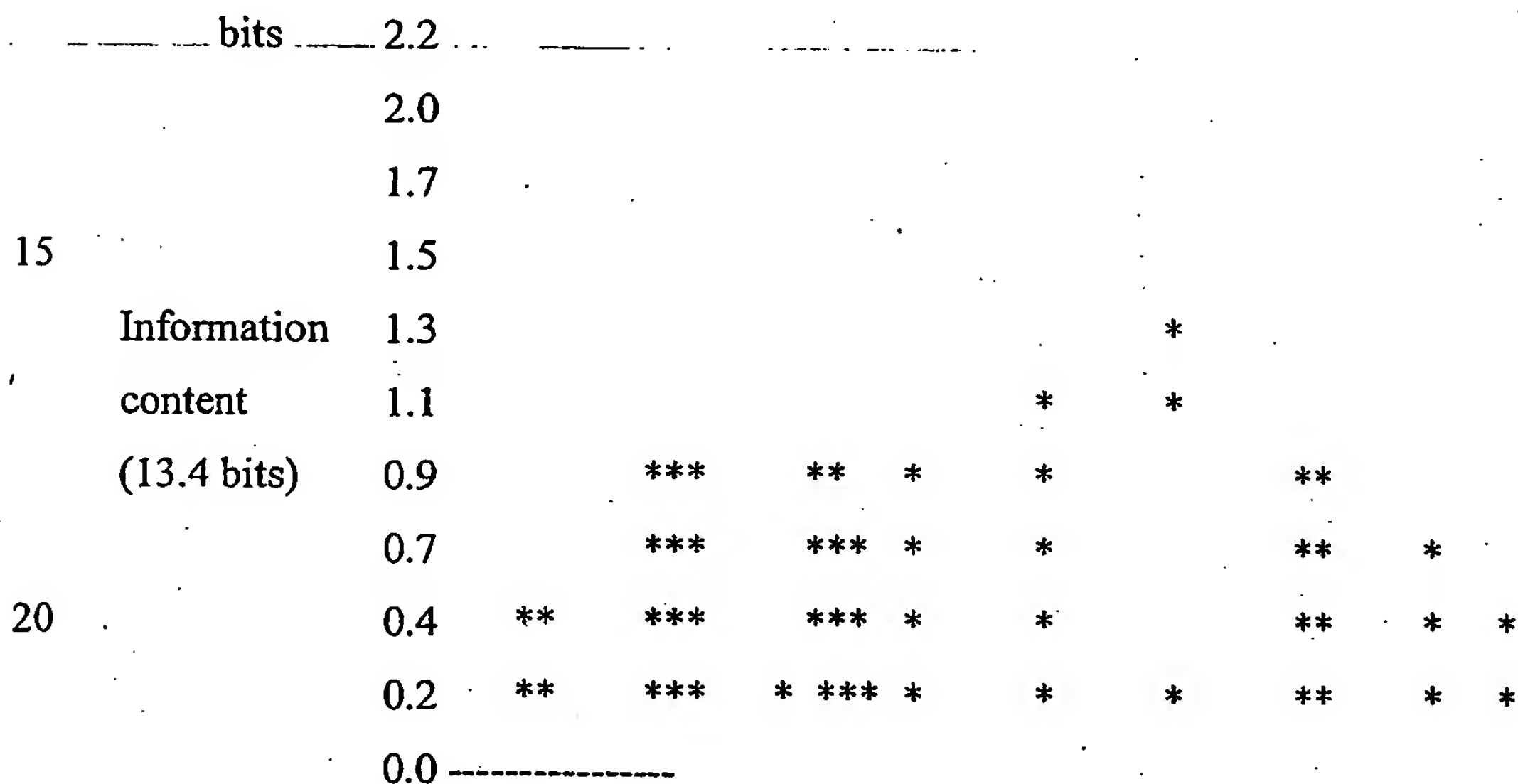
are generally enriched in As or Ts (A/T content in cR7R8 promoters is 70%) and regulatory *cis*-elements usually contain also Cs or Gs.

Motif 1 (CAACA/TA/TTGA/TC/T, SEQ ID NO:710) resembles the type I Myb binding site consensus (MBS;T/CAACT/GG), which is bound by animal and some plant Myb transcription factors (Yang & Klessig, 1996). The 3' portion of the motif 1 consensus allows overlap with binding sites of WRKY (TTTGACC/T; Eulgem et al., 2000) or TGA-bZIP transcription factors (TGACG; Schindler et al. 1992). Interestingly, a gene encoding a putative Myb-like transcription factor (gene identification number 13176) is upregulated along with cR7/R8 genes in an *RPP7/RPP8*-dependent, early and transient manner. The factor encoded by this gene may be a regulator of cR7/R8 genes. Motif 1 is particularly enriched in promoters of the originally defined cR7/R8 cluster (cut off = 75). This motif, which consists of six strictly defined positions and four positions allowing two base pairs each, should occur by random roughly once per 20,000 bp in each of both possible orientations (assuming a T/A content of 70% and a G/C content of 30%). In the 8,441 bp of cR7/R8 promoter sequences, the motif occurs 9 times (roughly 20 times the statistically expected frequency). Consistent with the statistical expectation, motif 1 occurs only two times within 15,873 bp from a set of control promoters of genes showing no defense related expression (data not shown).

In the extended set of cR7/R8 genes (cut off = 50), the enrichment of motif 1 is less striking. It occurs only 9 times within 16,519 bp in total and, more importantly, none of the promoters added to the set by lowering the cut off value contains this motif. Thus, if motif 1 is involved in the specific regulation of cR7/R8 genes it cannot alone be responsible for the particular expression features of these genes, and may rather be responsible for the more pronounced R7/R8-triggered expression of members of the originally defined cluster (cut off = 75).

Motif 2 (A/TTGGGNC/ANAA; SEQ ID NO:711) does not resemble any other known plant *cis*-element. The consensus sequence consists of six strictly defined positions, two positions with two alternatives and two positions with four alternatives; and, hence, should occur by random once per 10,000 bp. Motif 2 can be found 10 times within 8,441 bp of the promoters from the originally defined cR7/R8 (cut off = 75) and 14 times within 16,519 bp of the extended

cR7/R8 promoter set. Thus, its occurrence in cR7/R8 promoters is roughly 10 times the statistical expectation. Motif 2 is absent in the 15,873 bp of promoters of genes showing no defense related expression (data not shown). It is, however, also enriched in the promoters of previously defined clusters of defense related genes, such as the PR1 regulon (SAR genes) and SOMc3 (genes up regulated in Ws-0 after infection with avirulent Noco2; data not shown). The latter two clusters may also include genes sharing expression features with cR7/R8 genes. In addition to AlignAce, a motif 2-like sequence was also recognized by MEME. Within the extended set of cR7/R8 promoters, MEME found the following sequence stretch to be conserved:



Multilevel Consensus sequence T/C TTT G/C A/T/G C/T
 25 CCAAG/A/CAA/GAC/A (SEQ ID NO:712)

The reverse complement of this consensus sequence is (positions with three alternatives were given as "N") given below with motif 2 for comparison:

30 MEME motif: G/T T C/T T N T T G G G N G/C A A A A/C (SEQ ID NO:713)
 Motif 2: T G G G N A N/C A A (SEQ ID NO:714)

MEME was run using the default settings of “advanced MEME” choosing the options “one motif per sequence”, “narrow motifs” and “additional strand: reverse complement”.

To confirm these results, Northern blots using probes of representatives of each cluster are performed. In addition, T-DNA lines are screened for knock out in Myb-like gene (AL031394.56_at) and selected members of cR7/R8, such as RNS1 (atu05206_s_at) or the gene encoding a calmodulin-like protein (identification number 13217_s_at). Also, yeast one hybrid screens are performed to clone transcription factors binding to motifs 1 and 2, or other identified motifs. Transgenic *Arabidopsis* plants carrying fusions of GUS with a representative promoter from cR7/R8 can be used to further evaluate the functional significance of motifs 1 and 2, and to perform a genetic screening for mutants impaired in regulation of cR7/R8 genes.

15 Genes Induced by *Peronospora* Infection in a Manner that Requires *RPP7* or *RPP8*

The data sets described above were employed to identify genes that were induced by *Peronospora* infection and were RPP7/8-dependent. All expression values less than 5 were set to 5. Using ratios calculated in Excel, and database sorting using Access, a subset of genes was identified whose expression depends on RPP7 or RPP8 using the following criteria:

Col Hiks1 12 hour/Col untreated > 2.5 AND Col Hiks1 12 hour > 30
AND Col Hiks1 12 hour/Col rpp7 Hiks1 12 hour > 2
OR
25 Col Hiks1 48 hour/Col untreated > 2.5 AND Col Hiks1 48 hour > 30
AND Col Hiks1 48 hour/Col rpp7 Hiks1 48 hour > 2
OR
Col RPP8 Emco5 12 hour/Col RPP8 no treatment > 2.5 AND Col RPP8
Emco5 12 hour > 30 AND Col RPP8 Emco5 12 hour/Col (rpp8) Emco5
30 12 hour > 2
OR
Col RPP8 Emco5 48 hour/Col RPP8 no treatment AND Col RPP8
Emco5 48 hour > 30 AND Col RPP8 Emco5 48 hour/Col (rpp8) Emco5
48 hour > 2

This yielded 217 probe sets ("RPP7 or 8") which correspond to sequences, the expression of which were increased by at least 2.5 fold and were *RPP7*- or *RPP8*-dependent (Table 6).

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Table 6

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
12360_at (AL022347.131_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
12556_at (AL079344.155_AT)	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
12630_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]

12777_i_at (AC006577.16_I_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12778_r_at (AC006577.16_R_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12779_f_at (AC006577.16_F_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1 (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]
12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]

13154_s_at (AC002333.210_S_AT)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13198_i_at (ATTS0190_I_AT)	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
13631_at (AC002387.185_AT)	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13697_at (NI16_AT)	No hits found.

13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
13880_s_at (AL049480.183_S_AT)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
14096_at (AC002291.12_AT)	No hits found.
14110_i_at (AL035528.279_I_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14111_s_at (AL035528.279_S_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14116_at (AF077407.30_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
14141_at (NOVARTIS31_AT)	No hits found less than or equal to 1e-15.
14145_at (NOVARTIS35_AT)	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
14146_at (NOVARTIS36_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
14201_at (NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15.
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]

14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb A1100027 come from this gene.
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14254_s_at (PAL1-MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14256_f_at (PAL1-INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana]
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana]
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
14682_i_at (WT1012A_RC_I_AT)	No hits found.
14691_at (WT1096_AT)	No hits found.

14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
14709_at (WT788_AT)	No hits found less than or equal to 1e-15.
14763_at (X86958.1_AT)	emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
15532_r_at (AL078637.191_R_AT)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]
15616_s_at (ATHPRO25A_S_AT)	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
15629_s_at (AB003280_S_AT)	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]

15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]
15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16061_s_at (AB004796_S_AT)	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
16150_s_at (ATHPEAR_S_AT)	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]
16257_at (AC004138.105_AT)	gb AAC32915.1 (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16360_at (AL031187.126_AT)	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]
16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	gb AAC48925.1 (U05206) ribonuclease [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]
17068_s_at (ATHRLPKA_S_AT)	gb AAA32857.1 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana]
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1; 3-glucanase-class I precursor [Arabidopsis thaliana]

17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
17499_s_at (AF107726_S_AT)	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
17653_at (AL035679.144_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
17775_at (AC004392.2_AT)	gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
17840_s_at (AC002333.223_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
17843_s_at (AC002391.150_S_AT)	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]
18022_at (AJ010971_AT)	emb CAB52675.1 (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]
18551_at (AC002391.163_AT)	gb AAB87112.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
18567_at (AC004411.25_AT)	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana] gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]
18625_at (AC005278.22_AT)	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
18716_at (X91916_AT)	gb AAC33239.1 (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
18844_at (AC005315.131_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC16927.1 (AC002338) putative laccase [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
18946_at (Y11788.1_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18969_g_at (AF163823.4_G_AT)	emb CAB41722.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
19158_at (X95738.2_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
19171_at (AC002335.160_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
19177_at (X99923.1_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
19182_at (AL031804.245_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	

19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
20232_s_at (AL022347.12_S_AT)	emb CAA18460.1 (AL022347) protein kinase-like protein [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate

	synthase alpha subunit [Arabidopsis thaliana]
20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]
20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
20429_s_at (Z97336.167_S_AT)	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	gb AAC98070.1 (AC005896) putative C2H2- type zinc finger protein [Arabidopsis thaliana]
20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]

The functions of RPP7 and RPP8 are independent of *PAD4*, *NDR1*, *NahG*, *COI1*, and *EDS1*. Consequently, it is unlikely that genes whose expression is reduced in *pad4* or *NahG* backgrounds are important for RPP7- or RPP8- mediated resistance. Although data from *Peronospora* infection of *pad4* or *nahG* plants was not available, data from *Pseudomonas syringae* (ES4326) infection of *pad4* and *NahG* plants was available and employed to determine which genes depended on *PAD4* or were interfered with by *NahG*. Resistance to *P. syringae* mediated by *RPS2* requires *NDR1* function. Genes whose expression requires *RPS2* are less likely to be important for RPP7 or RPP8 mediated resistance than genes whose expression is independent of *RPS2*. Gene expression data was available for wild-type plants infected with *Pseudomonas syringae* pv. tomato DC3000 *avrRpt2*, and *rps2* mutant plants infected with *Pseudomonas syringae* pv. tomato DC3000 *avrRpt2*, 6 hours after infection.

EDM1 is required for resistance mediated by RPP7. Thus, genes whose expression requires *EDM1* are likely to be important for RPP7-mediated resistance. Gene expression data was available for an *edm1* mutant (see above).

The data from the 7 additional data sets (Col Psm ES4326 30 hour; Col Mock 30 hour; Col *NahG* Psm ES4226 30 hour; Col *pad4* Psm ES4326 30 hour; Col water control; Col DC3000 *avrRpt2* and *rps2* DC3000 *avrPrt2* was added to the 217 probe sets in "RPP7 or 8". The following sets were identified:

edm1:

Col edm1 Hiks1 12 hour/Col Hiks1 12 hour < 0.5 OR Col edm1 Hiks1
48 hour/Col Hiks1 48 hour < 0.5.

rps2:

- 5 Col DC3000 *avrRpt2* 6 hour/Col water control > 2 AND *rps2* DC3000
avrRpt2 6 hour/Col DC3000 *avrRpt2* 6 hour < 0.5.

pad4 or NahG:

- 10 Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col pad4 Psm
ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.
OR
Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col NahG Psm
ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.

- 15 There are 8 possible combinations of these three sets. Access was used to divide
the 217 probe sets into 8 sets, numbered 2-9 (considering the whole set of 217
probe sets as set 1) as shown in Tables 7 and 8:

Table 7

20	<u>Set</u>	<u>Content</u>	<u>Number of probe</u>
		<u>sets</u>	
	2	RPP7 or 8 not edm1 not rps2 not pad4 or NahG	62 probe sets
	3	edm1 not rps2 not pad4 or NahG	50 probe sets
	4	rps2 not edm1 not pad4 or NahG	14 probe sets
25	5	pad4 or NahG not edm1 not rps2	21 probe sets
	6	edm1 and rps2 not pad4 or NahG	23 probe sets
	7	edm1 and pad4 or NahG not rps2	25 probe sets
	8	rps2 and pad4 or NahG not edm1	8 probe sets
	9	edm1 and rps2 and pad4 or NahG	<u>14 probe sets</u>
30	Total		217 probe sets

Table 8

2 RPP7 or 8 not edm1 not rps2
not pad4 or NahG

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
12556_at (AL079344.155_AT)	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657
12777_i_at (AC006577.16_I_AT)	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657
12779_f_at (AC006577.16_F_AT)	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana]
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13880_s_at (AL049480.183_S_AT)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023:172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]
14111_s_at (AL035528.279_S_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]

14145_at (NOVARTIS35_AT)	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana]
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana]
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]
16257_at (AC004138.105_AT)	gb AAC32915.1 (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]
16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]

17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475, gb ATTS4362 come from this gene. [Arabidopsis thaliana]
17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]
18625_at (AC005278.22_AT)	gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]
18844_at (AC005315.131_AT)	gb AAC33239.1 (AC005315) putative ligand- gated ion channel protein [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	gb AAC16927.1 (AC002338) putative laccase [Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAB41722.1 (AL049730) pEARLI 1- like protein [Arabidopsis thaliana]
19158_at (X95738.2_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]

Duplicates

12777 and 12779 (lipase)

12889 and 20291 (ASA1)

12908 and 16536 (ERF5)

17464 and 19982 (RLK5)

18216 and 18217 (T22C5.18)

18908 and 18909 (subtilisin-like protease)

20238 and 20239 (beta-fructofuranosidase)

3 edm1 without rps2 without pad4orNahG

ProbeSet	Description
12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]

12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
12778_r_at (AC006577.16_R_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1 (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13198_i_at (ATT0190_I_AT)	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
13631_at (AC002387.185_AT)	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
14096_at (AC002291.12_AT)	No hits found.
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]
14254_s_at (PAL1-MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
14691_at (WT1096_AT)	No hits found.
14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]

15532_r_at (AL078637.191_R_AT)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana] dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
15629_s_at (AB003280_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana] dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
16609_s_at (AB008104_S_AT)	
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana] gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	
	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
17008_at (AC006585.212_AT)	
	gb AAC48925.1 (U05206) ribonuclease [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	
17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana] dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	
	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]
17653_at (AL035679.144_AT)	
17744_s_at (AC004684.168_S_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
17843_s_at (AC002391.150_S_AT)	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana] emb CAB52675.1 (AJ010971) glucose-6- phosphate 1-dehydrogenase [Arabidopsis thaliana]
18022_at (AJ010971_AT)	
	gb AAB87112.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
18551_at (AC002391.163_AT)	
	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana] emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
18716_at (X91916_AT)	
18946_at (Y11788.1_AT)	
	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
19171_at (AC002335.160_AT)	
	emb CAA68191.1 (X99923) male sterility 2- like protein [Arabidopsis thaliana]
19177_at (X99923.1_AT)	
	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
19182_at (AL031804.245_AT)	
	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	

19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
20232_s_at (AL022347.12_S_AT)	emb CAA18460.1 (AL022347) protein kinase-like protein [Arabidopsis thaliana]
20429_s_at (Z97336.167_S_AT)	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
20641_at (X91919.1_AT)	emb CAA63012.1 (X91919) LEA76 homologue type1 [Arabidopsis thaliana] Arabidopsis thaliana. ESTs gb N97082, gb Z27056 and gb Z29902 come from this gene.

Duplicates -----

12905 and 16609 (ERF2)

13188 and 16981 (thioredoxin h)

12891 and 12892 (ACC
synthase)

14838 (phosphoribosyl
anthranilate transferase) has a
duplicate in set 2 (14620).
Counted in set 2

14254 (PAL1) has a duplicate in
set 2 (14256) Counted in set 2.

12778 (lipase) has duplicates in
set 2 (12777 and 12779) Counted
in set 2.

4 rps2 without edm1 without pad4orNahG

ProbeSet

Description

12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
12360_at (AL022347.131_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13154_s_at (AC002333.210_S_AT)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]
14141_at (NOVARTIS31_AT)	No hits found less than or equal to 1e-15.

15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]

Duplicates

12360 and 20223 (serine
threonine kinase)
13685 and 20365 (similar to
Mlo)

5 pad4orNahG without rps2 without edm1

ProbeSet

	Description
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]

14146_at (NOVARTIS36_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]
16360_at (AL031187.126_AT)	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1, 3- glucanase class I precursor [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]

Duplicates:

15778 and 15779 (zinc finger
protein)

**6 edm1 and rps2 without
pad4orNahG**

ProbeSet

ProbeSet	Description
12630_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T43869 come from from this gene. [Arabidopsis thaliana]
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]

13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
14116_at (AF077407.30_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14682_i_at (WT1012A_RC_I_AT)	No hits found.
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16061_s_at (AB004796_S_AT)	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S- linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5- trisphosphate 5-Phosphatase [Arabidopsis thaliana]

19640_at (AC004561.78_AT) gb|AAC95192.1| (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Duplicates

13187 and 13189 (thioredoxin h)
There are two duplicates of this in set 3 (13188 and 16981) Count it in set 3.

13215 and 16649 (putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase)

13285 and 16091 (heat shock protein 83)

13217 (calmodulin-like) has a duplicate in set 3 (17500). Count in set 3

16105 (hsf4) has a duplicate in set 4 (13273) Count in set 4

7 pad4orNahG and edm1 without rps2

ProbeSet

Description

14110_i_at (AL035528.279_I_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
14709_at (WT788_AT)	No hits found less than or equal to 1e-15.
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
15616_s_at (ATHPRO25A_S_AT)	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
16150_s_at (ATHPEAR_S_AT)	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]
17068_s_at (ATHRLPKA_S_AT)	gb AAA32857.1 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana]
17499_s_at (AF107726_S_AT)	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
17775_at (AC004392.2_AT)	gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18969_g_at (AF163823.4_G_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]

Duplicates

14249 and 14250 (PAD4)

14704 and 15846 and 15847
(unknown protein)

18968 and 18969
(endoxyloglucan transferase)

20287 and 20288 (class IV
chitinase)

14110 (putative disease-
resistance gene) is an incomplete
probe set with very low signal. It
has a duplicate (14111) in set 2.
Count in set 2.

14672 (trp synthase alpha) has a
duplicate in set 2 (17487)
Counted in set 2.

**8 rps2 and pad4orNahG
without edm1**

ProbeSet	Description
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis emb CAA07352.1 (AJ006960) peroxidase
17930_s_at (AJ006960.4_S_AT)	[Arabidopsis thaliana]
19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]

Duplicates:

14635 and 17128 (PR-1)

**9 edm1 and rps2 and
pad4orNahG**

ProbeSet	Description
12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]

12989_s_at (AC004077.149_S_AT) 13697_at (NI16_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana] No hits found.
14201_at (NOVARTIS73_AT) 14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15. No hits found less than or equal to 1e-15.
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana] emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
14638_s_at (PRXCB_S_AT)	emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
14763_at (X86958.1_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
15116_f_at (AF121356_F_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
17544_s_at (ATU40856_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
17840_s_at (AC002333.223_S_AT)	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
18567_at (AC004411.25_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
20269_at (AC002387.237_AT)	

Duplicates

12879 and 17544 (AIG1)

14201 and 14202 (Novartis 73)

14638 (peroxidase) has a
duplicate in set 7 (15970).

Counted in set 7.

The first set (set 2 above) do not require *EDM1* and are not affected by *rps2*, *pad4* or *NahG*. These genes are less likely to be important for resistance mediated by *RPP7* and *RPP8* than the genes in the second set (set 3 above). The

5 genes in the second set require *EDM1* but are not affected by *rps2*, *pad4* or *NahG*. These genes are more likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the third set (set 4 above) are affected by *rps2*, do not require *EDM1*, and are not affected by *pad4* or *NahG*. The genes in the

10 fourth (set 5 above), seventh (set 8 above) and eight (set 9 above) sets include genes that are affected by *pad4* or *NahG*, and so are less likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the sixth set (set 7 above) require *RPP7* or *RPP8* for increased expression after infection by

Peronospora and are affected by *rps2*. These genes are also less likely to be important for resistance mediated by *RPP7* and *RPP8*.

Duplicates were identified by sorting "RPP7 or 8" by description, which put duplicated genes adjacent to one another. Most duplicates were in the same set, but there were nine cases of duplicates that had one probe set in one set, and another in another set. Examination of the data revealed that in these cases, the expression values were close to the cut-offs used to define the various sets. If one copy met the criteria, e.g., for *rps2*-dependent, but the other copy did not, the gene was classified as not *rps2*-dependent. Duplicates are noted. One hundred eighty-four unique genes remained (SEQ ID NOs:1-211 and 792, Table 9 and Table 10).

Table 9

SEQ ID NO	ProbeSet	Description
1	12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
2	12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
3	12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
4	12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
5	12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
6	12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
7	12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
8	12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
9	12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
10	12360_at (AL022347.131_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
11	20223_at (AL022347.145_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]

- 12 12500_s_at (AF081067.3_S_AT) gb|AAC32192.1| (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
- 13 12521_at (AF049236.28_AT) gb|AAC14413.1| (AF049236) unknown [Arabidopsis thaliana]
- 14 12538_at (AF033205.2_AT) gb|AAC02973.1| (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
- 15 12556_at (AL079344.155_AT) emb|CAB45330.1| (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
- 16 12574_at (X82624.2_AT) emb|CAA57944.1| (X82624) SRG2At [Arabidopsis thaliana]
- 17 12630_at (AF024504.13_AT) gb|AAF18681.1|AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
- 18 12642_at (AC006920.138_AT) gb|AAD22285.1|AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
- 19 12777_i_at (AC006577.16_I_AT) gb|AAD25772.1|AC006577_8 (AC006577) Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb|T44453, gb|T04815, gb|T45993, gb|R30138, gb|AI099570 and gb|T22281 come from this gene. [Arabidopsis thaliana]
- 20 12778_r_at (AC006577.16_R_AT) gb|AAD25772.1|AC006577_8 (AC006577) Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb|T44453, gb|T04815, gb|T45993, gb|R30138, gb|AI099570 and gb|T22281 come from this gene. [Arabidopsis thaliana]
- 21 12779_f_at (AC006577.16_F_AT) gb|AAD25772.1|AC006577_8 (AC006577) Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb|T44453, gb|T04815, gb|T45993, gb|R30138, gb|AI099570 and gb|T22281 come from this gene. [Arabidopsis thaliana]
- 22 12879_s_at (AIG1_S_AT) gb|AAC49282.1| (U40856) AIG1 [Arabidopsis thaliana]
- 23 17744_s_at (AC004684.168_S_AT) gb|AAC23646.1| (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
- 24 12889_s_at (ASA1_S_AT) gb|AAA32738.1| (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
- 25 20291_s_at (M92353.4_S_AT) gb|AAA32738.1| (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]

26	12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
27	12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
28	12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
29	16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
30	12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
31	16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
32	12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1 (AF021244) coronatine- induced protein 1 [Arabidopsis thaliana]
33	12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis- related protein 1 [Arabidopsis thaliana]
34	12989_s_at (AC004077.149_S_A T)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
35	13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
36	13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
37	13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]
38	13154_s_at (AC002333.210_S_A T)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
39	13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
40	13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
41	13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
42	13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
43	16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
44	13198_i_at (ATT50190_I_AT)	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

45	13215_s_at (CAFFEROYLCOAM ETHYLTRANS_S_A T)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
46	16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
47	13217_s_at (CALMODULINLIK E_S_AT)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
48	17500_s_at (ATHCALLGA_S_A T)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
49	13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
50	16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
51	13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
52	13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
53	16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
54	13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
	13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
55	13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
56	13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
57	13631_at (AC002387.185_AT)	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
58	13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
59	13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]

		gb AAD25552.1 AC005850_9 (AC005850)
	20365_s_at	Highly Similar to Mlo proteins [Arabidopsis
60	(AC005850.19_S_AT)	thaliana]
61	13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
no cds	13697_at (NI16_AT)	No hits found.
	13751_at	gb AAF16751.1 AC010155_4 (AC010155)
62	(NOVARTIS127_AT)	F3M18.8 [Arabidopsis thaliana]
	13764_at	gb AAD39641.1 AC007591_6 (AC007591)
63	(NOVARTIS22_AT)	F9L1.6 [Arabidopsis thaliana]
	13818_s_at	gb AAD15433.1 (AC006218) putative
	(AC006218.175_S_A	aspartate aminotransferase [Arabidopsis
64	T)	thaliana]
	13880_s_at	emb CAB39611.1 (AL049480) possible
	(AL049480.183_S_A	apospory-associated like protein
65	T)	[Arabidopsis thaliana]
	13966_at	emb CAA17775.1 (AL022023) putative
66	(AL022023.172_AT)	protein [Arabidopsis thaliana]
		gb AAC78535.1 (AC005662) putative
	14083_at	embryo-abundant protein [Arabidopsis
67	(AC005662.56_AT)	thaliana]
	14096_at	
68	(AC002291.12_AT)	No hits found.
	14110_i_at	emb CAB36854.1 (AL035528) putative
	(AL035528.279_I_AT	disease resistance protein [Arabidopsis
69)	thaliana]
	14111_s_at	emb CAB36854.1 (AL035528) putative
	(AL035528.279_S_A	disease resistance protein [Arabidopsis
70	T)	thaliana]
		gb AAC26243.1 (AF077407) contains
		similarity to sugar transporters (Pfam:
	14116_at	sugar_tr.hmm, score: 395.39) [Arabidopsis
71	(AF077407.30_AT)	thaliana]
	14141_at	
72	(NOVARTIS31_AT)	No hits found less than or equal to 1e-15.
		dbj BAA22813.1 (D26015) CND41,
	14145_at	chloroplast nucleoid DNA binding protein
73	(NOVARTIS35_AT)	[Nicotiana tabacum]
	14146_at	gb AAD25550.1 AC005850_7 (AC005850)
74	(NOVARTIS36_AT)	Hypothetical protein [Arabidopsis thaliana]
	14148_at	gb AAF34713.1 AF224762_1 (AF224762)
75	(NOVARTIS38_AT)	SigA binding protein [Arabidopsis thaliana]
	14201_at	
76	(NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
	14202_at	
	(NOVARTIS73_RC_	
77	AT)	No hits found less than or equal to 1e-15.
	14223_at	emb CAA19683.1 (AL024486) putative
78	(NOVARTIS9_AT)	protein [Arabidopsis thaliana]

79	14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]
80	14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
81	14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
82	14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
83	14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
84	14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
85	14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana]
86	14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
87	14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
88	14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
89	14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
90	14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
91	14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
92	14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
93	14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana]
94	14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
95	17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
96	14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]

97	15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
98	14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
99	17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
100	14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
101	14682_i_at (WT1012A_RC_I_AT)	No hits found.
102	14691_at (WT1096_AT)	No hits found.
103	14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
104	15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
105	15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
106	14709_at (WT788_AT)	No hits found less than or equal to 1e-15. emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
107	14763_at (X86958.1_AT)	
108	14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
109	15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
110	15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
111	15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine- ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
112	15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
113	15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
114	15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
115	15523_s_at (AL078637.213_S_A T)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
116	15532_r_at (AL078637.191 R A	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]

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- 117 15616_s_at
(ATHPRO25A_S_AT) emb|CAA08794.1| (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
dbj|BAA24440.1| (AB010407)
- 118 15629_s_at
(AB003280_S_AT) phosphoglycerate dehydrogenase
[Arabidopsis thaliana]
gb|AAD10829.1| (AF117063) putative
- 119 15641_s_at
(AF117063_S_AT) inositol polyphosphate 5-phosphatase At5P2
[Arabidopsis thaliana]
gb|AAB80922.1| (AF022658) putative c2h2
- 120; 682 15665_s_at
(AF022658_S_AT) zinc finger transcription factor [Arabidopsis thaliana]
- 121 15778_at
(X98676.2_AT) emb|CAA67234.1| (X98676) zinc finger protein [Arabidopsis thaliana]
- 122 15779_g_at
(X98676.2_G_AT) emb|CAA67234.1| (X98676) zinc finger protein [Arabidopsis thaliana]
- 123 15859_at
(AC006587.164_AT) gb|AAD15461.1| (AC006067) unknown protein [Arabidopsis thaliana]
- 124 15978_at
(X68592.6_AT) gb|AAD15461.1| (AC006067) unknown protein [Arabidopsis thaliana]
- 125 16053_i_at
(Y14251.4_I_AT) emb|CAA74639.1| (Y14251) glutathione S-transferase [Arabidopsis thaliana]
- 126 16061_s_at
(AB004796_S_AT) gb|AAB97145.1| (AF000977) MEK1
[Arabidopsis thaliana] thaliana]
gb|AAD34615.1|AF153283_1 (AF153283)
- 127 16083_s_at
(AF153283_S_AT) putative progesterone-binding protein homolog [Arabidopsis thaliana]
- 128 16150_s_at
(ATHPEAR_S_AT) emb|CAB41718.1| (AL049730) pEARLI 1
[Arabidopsis thaliana]
- 129 16232_s_at
(AL080252.77_S_AT) emb|CAB45796.1| (AL080252) putative protein [Arabidopsis thaliana]
gb|AAC32915.1| (AC004138) putative
- 130 16257_at
(AC004138.105_AT) nucleoside triphosphatase [Arabidopsis thaliana]
- 131 16298_at
(AL021890.71_AT) emb|CAA17152.1| (AL021890) putative protein [Arabidopsis thaliana]
- 132 16299_at
(AL024486.185_AT) emb|CAA19705.1| (AL024486) putative protein [Arabidopsis thaliana]

gb|AAD40144.1|AF149413_25 (AF149413)
contains similarity to protein kinase domains.
(Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10)
- 133 16357_at
(AF149413.38_AT) [Arabidopsis thaliana]
emb|CAA20203.1| (AL031187) receptor-like
- 134 16360_at
(AL031187.126_AT) serine/threonine protein kinase ARK3
[Arabidopsis thaliana]

- 135 16365_at (AC003974.136_AT) gb|AAC04495.1| (AC003974) putative disease resistance protein [Arabidopsis thaliana]
- 136 16578_s_at (ATHRPRP1B_S_AT) emb|CAB68132.1| (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
- 137 16817_s_at (AL096882.91_S_AT) emb|CAB51412.1| (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
- 138 16914_s_at (AL049500.57_S_AT) emb|CAB39936.1| (AL049500) osmotin precursor [Arabidopsis thaliana]
- 139 16995_at (AC002391.188_AT) gb|AAB87114.1| (AC002391) unknown protein [Arabidopsis thaliana]
- 140 17008_at (AC006585.212_AT) gb|AAD23027.1|AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
- 141 17014_s_at (ATU05206_S_AT) gb|AAC48925.1| (U05206) ribonuclease [Arabidopsis thaliana]
- 142 17051_s_at (AF098947_S_AT) gb|AAD09952.1| (AF098947) CTF2B [Arabidopsis thaliana]
- 143 17068_s_at (ATHRLPKA_S_AT) gb|AAA32857.1| (M84658) receptor-like protein kinase [Arabidopsis thaliana]
- 144 17083_s_at (ATU18770_S_AT) gb|AAD25838.1|AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
- 145 17097_s_at (ATU66345_S_AT) gb|AAC49697.1| (U66345) calreticulin [Arabidopsis thaliana]
- 146 17278_at (AC000107.5_AT) gb|AAD36959.1|AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
- 147 17413_s_at (AJ006961.4_S_AT) emb|CAA67551.1| (X99097) peroxidase [Arabidopsis thaliana]
- 148 17464_at (AC000132.72_AT) gb|AAB60752.1| (AC000132) Similar to A. thaliana receptor-like protein kinase (gb|RLK5_ARATH). ESTs gb|ATTS0475,gb|ATTS4362 come from this gene. [Arabidopsis thaliana]
- 149 17485_s_at (Z97340.345_S_AT) emb|CAB10405.1| (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]
- 150 17499_s_at (AF107726_S_AT) gb|AAD19610.1| (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
- 151 17511_s_at (AF067605_S_AT) gb|AAB71482.1| (AC002294) similar to S-linalool synthase gp|U58314|1491939 [Arabidopsis thaliana]
- 152 17522_s_at (D78606_S_AT) dbj|BAA28538.1| (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
- 153 17544_s_at (ATU40856_S_AT) gb|AAC49282.1| (U40856) AIG1 [Arabidopsis thaliana]

- 154 17653_at (AL035679.144_AT) emb|CAB38823.1| (AL035679) putative protein [Arabidopsis thaliana]
gb|AAC28500.1| (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb|AF020814 from Pisum sativum. [Arabidopsis thaliana]
- 155 17775_at (AC004392.2_AT)
- 156 17840_s_at (AC002333.223_S_AT) gb|AAB64049.1| (AC002333) putative endochitinase [Arabidopsis thaliana]
- 157 17843_s_at (AC002391.150_S_AT) gb|AAB87109.1| (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
- 158 17899_at (Z97339.197_AT) emb|CAB10339.1| (Z97339) hypothetical protein [Arabidopsis thaliana]
- 159 17930_s_at (AJ006960.4_S_AT) emb|CAA07352.1| (AJ006960) peroxidase [Arabidopsis thaliana]
- 160 18012_s_at (AJ002295_S_AT) emb|CAB59428.1| (AJ002295) inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]
- 161 18022_at (AJ010971_AT) emb|CAB52675.1| (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
- 162 18054_at (AJ238846_AT) emb|CAB54517.1| (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
- 163 18216_at (X95573.2_AT) gb|AAF24959.1|AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
- 164 18217_g_at (X95573.2_G_AT) gb|AAF24959.1|AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
- 165 18551_at (AC002391.163_AT) gb|AAB87112.1| (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
- 166 18567_at (AC004411.25_AT) gb|AAC34217.1| (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
- 167 18590_at (AJ222713.4_AT) emb|CAA10955.1| (AJ222713) unnamed protein product [Arabidopsis thaliana]
- 168; 665 18591_at (X74756.2_AT) emb|CAA52772.1| (X74756) ATAF2 [Arabidopsis thaliana]
- 169 18625_at (AC005278.22_AT) gb|AAC72125.1| (AC005278) ESTs gb|H36966, gb|R65511, gb|T42324 and gb|T20569 come from this gene. [Arabidopsis thaliana]
- 170 18716_at (X91916_AT) gb|AAF26754.1|AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
- 171 18844_at (AC005315.131_AT) gb|AAC33239.1| (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
- 172 18908_i_at (AF055848.2_I_AT) gb|AAC62611.1| (AF055848) subtilisin-like protease [Arabidopsis thaliana]

173	18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
174	18946_at (Y11788.1_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
175	18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
176	18969_g_at (AF163823.4_G_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
177	18983_s_at (AL049730.104_S_A T)	emb CAB41722.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
178	19158_at (X95738.2_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
179	19171_at (AC002335.160_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
180	19177_at (X99923.1_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
181	19182_at (AL031804.245_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
182	19229_at (AC003027.39_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
183	19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
184	19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
185	19415_at (AL080253.32_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
186	19594_i_at (X98321.2_I_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
187	19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
188	19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
189	19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]
190	19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
191	19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
192	19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

193	19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
194	19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
195	19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
196	20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
197	20232_s_at (AL022347.12_S_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
198	20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
199	20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
200	20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
201	20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
202	20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
203	20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
204	20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
205	20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
206	20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
207	20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
208	20429_s_at (Z97336.167_S_AT)	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
209	20620_g_at (AC005896.161_G_A T)	gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
210	20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]
211	20641_at (X91919.1_AT)	emb CAA63012.1 (X91919) LEA76 homologue type1 [Arabidopsis thaliana] Arabidopsis thaliana. ESTs gb N97082, gb Z27056 and gb Z29902 come from this gene.
789	18224_s_at (AL021890.57_S_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
790	16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]

		gb AAC17040.1 (AC002986) Similarity to
		A. thaliana gene product F21M12.20,
		gb AC000132. EST gb Z25651 comes from
		this gene. [Arabidopsis thaliana]
791	19982_at (AC002986.28_AT)	gb AAC16927.1 (AC002338) putative
367	18920_at (AC002338.11_AT)	laccase [Arabidopsis thaliana]
212	12324_i_at	AC007212
793	12345_at	L36246
213	12500_s_at	AF081067
214; 662	12505_s_at	AC005309
215	12608_i_at	S70188
216	12642_at	AC006920
217	12746_i_at	AL096882
218	12748_f_at	AL096882
219	12761_s_at	AC006577
220	12773_at	AC005727
221	12778_r_at	AC006577
222	12798_at	AC003028
223	12802_at	AL022373
	12842_s_at	No hits found less than or equal to 1e-15
224	12843_s_at	AC007195
	12845_s_at	AJ004810
225	12879_s_at	U40856
226	12891_at	U73786
227	12892_g_at	U73786
228; 658	12904_s_at	AB008103
229	12905_s_at	AB008104
230	12908_s_at	AB008107
231	12909_s_at	Z97343
232	12911_s_at	X84229
233	12916_s_at	AF021244
234	13138_at	AL096882
235	13177_at	AL049640
236	13178_at	U93215
237	13187_i_at	U35829
238	13189_s_at	U35829
239	13198_i_at	AL021749
240	13212_s_at	AL137080
241	13217_s_at	AL049862
242	13258_s_at	AC005309
243	13273_s_at	U68017
244	13284_s_at	AJ002551
245	13604_at	AC000104
246	13615_at	AC002332
247	13617_at	AC006592
248	13718_at	Z72152
249	13771_at	AC006593
250	13785_at	AC007087
251	14052_at	AC004122

252	14096_at	AC002291
253	14097_at	AC005309
254	14116_at	AF077407
255	14141_at	AC011437
256; 683	14148_at	AF224762
257	14196_at	AC012563
258	14201_at	AL163972
259	14219_at	AC068667
260	14223_at	AL024486
261	14248_at	AC007357
262	14250_r_at	AL050300
263	14595_at	AL022580
264	14608_at	AC007357
265	14614_at	AC004165
266	14621_at	AC004747
267	14627_i_at	X76609
268	14628_r_at	X76609
269	14635_s_at	AC005398
270	14636_s_at	AC013258
271	14643_s_at	AC006836
272	14672_s_at	U18993
273	14675_s_at	D85191
274	14691_at	AP002046
275	14704_s_at	AC006067
276	14706_r_at	AL137189
277	14709_at	AP002046
278	14711_s_at	AF085279
279	14731_s_at	AF014960
280	14784_at	AC005310
281	14951_at	AL049481
282	15057_at	AL035440
283	15085_s_at	AL031018
284	15105_s_at	Z14987
285	15116_f_at	AF121356
286	15125_f_at	D85190
287	15141_s_at	D85191
288	15145_s_at	D64155
289	15154_s_at	AL096860
290	15161_s_at	U90522
291	15178_s_at	U43489
292	15216_s_at	U75198
293	15431_at	AL030978
294	15496_at	AC006282
295	15523_s_at	AL078637
296	15593_s_at	U54561
297	15611_s_at	L22567
298	15616_s_at	AJ009696
299	15622_s_at	U43945

300	15629_s_at	AB010407
301	15665_s_at	AF022658
302	15680_s_at	D42061
303	15846_at	AC006067
304	15847_g_at	AC006067
305	15866_s_at	AC005770
306	15950_at	AC006429
307	15954_at	U72155
308	15978_at	X68592
309	16038_s_at	L04173
310	16063_s_at	AB008103
311	16105_s_at	U68017
312	16150_s_at	AL049730
313	16153_s_at	AC013258
314	16393_s_at	AC006436
315	16412_s_at	AL022603
316	16442_s_at	AJ002551
317	16504_s_at	Z97335
318	16510_at	AL034567
319	16536_s_at	AB008107
320	16539_s_at	Z97343
321	16569_s_at	L23968
322	16578_s_at	AL137080
323	16609_s_at	AB008104
324	16620_s_at	AF051338
325	16637_s_at	Z97336
326	16817_s_at	AL096882
327	16864_i_at	AL133248
328	16951_i_at	AC005662
329	16952_s_at	AC005662
330	16981_s_at	U35829
331	17014_s_at	U05206
332	17033_s_at	U83179
333	17054_s_at	AF134128
334	17073_s_at	AC006836
335	17119_s_at	AF132212
336	17123_s_at	AF106087
337	17128_s_at	AC005398
338	17187_at	AF128396
339; 669	17303_s_at	AC005499
340; 663	17379_at	AC018721
341	17386_at	AC006264
342	17413_s_at	X99097
343	17499_s_at	AF107726
344	17500_s_at	AL049862
345	17544_s_at	U40856
346	17567_at	AL162751
347	17886_at	AC004484

348	17899_at	Z97339
349	17917_s_at	AC004261
350	17961_at	AC007323
351	17963_at	AL049730
352	18003_at	AF188334
	18064_r_at	No hits found
	18069_at	No hits found
	18070_r_at	No hits found
353	18216_at	AC012375
354	18217_g_at	AC012375
355	18235_at	AC000348
356	18252_at	AL096882
357	18255_at	AC005770
358	18272_at	AF002109
359	18533_at	AL021684
360	18556_at	AC006264
361	18590_at	AJ222713
362	18591_at	X74756
363	18607_s_at	U78721
364	18635_at	AC004005
365	18716_at	AC007396
366	18876_at	AF002109
367	18920_at	AC002338
368	18928_at	AC002338
369	19034_at	AL021768
370	19171_at	AC002335
371	19178_at	AB035137
372	19182_at	AL031804
373	19251_at	AL035538
374	19640_at	AC004561
375	19977_at	AL049659
376	20017_at	AC004521
377	20034_i_at	A71607
378	20201_at	AL078470
379	20227_s_at	AB027252
380	20269_at	AC002387
381	20297_at	AC007153
382	20314_s_at	AL096882
383	20335_s_at	Y14208
384	20429_s_at	Z97336
385	20585_s_at	AC005309
386	20641_at	X91919
387	12333_at	AJ286345
388	14028_at	
389	14295_s_at	Z54356
390	14965_at	AC002329
391	15969_s_a	AJ133036
392	15982_s_a	X98190

393	16461_I_at	AC004683
394	16462_s_a	AC004683
395	16514_at	AL035538
396	17549_s_a	L37126
397	18706_s_a	X75782
398	19594_i_at	X98321
399	20555_s_a	AL080318
400	16212_at	gb AAD17366.1 (AF128396) similar to human phosphotyrosyl phosphatase activator PTPA (GB:X73478) [Arabidopsis thaliana]
794	14985_s_at	gb AAC32233.2 (AC005168) unknown protein [Arabidopsis thaliana]
401	16411_s_at	emb CAB71046.1 (AL137898) shaggy-like kinase beta [Arabidopsis thaliana]
402	15920_i_at	gb AAD39561.1 AC007067_1 (AC007067) T10O24.1 [Arabidopsis thaliana]
403	16299_at	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
404	18445_at	gb AAC98458.1 (AC005851) putative glucosyltransferase [Arabidopsis thaliana]
405	19215_at	gb AAC23400.1 (AC004005) putative methyl chloride transferase [Arabidopsis thaliana]
406	16439_at	emb CAA50905.1 (X72022) ORF1 [Arabidopsis thaliana]
407	16047_at	gb AAD20710.1 (AC006300) unknown protein [Arabidopsis thaliana]
408	18003_at	gb AAF01328.1 AF188334_1 (AF188334) Toll/interleukin-1 receptor-like protein [Arabidopsis thaliana]
409	20429_s_at	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
410	17917_s_at	gb AAD12002.1 (AC004261) calcium binding protein (CaBP-22) [Arabidopsis thaliana]
411	17963_at	emb CAB41717.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
412	16150_s_at	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
413	20239_g_at	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
414	20238_at	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
415	15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
416	18591_at	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]

417	14116_at	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
418	12759_at	gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb 84105 and gb AI100071 come from this gene. [Arabidopsis thaliana]
419	19060_at	gb AAC18809.1 (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]
420	12998_at	emb CAB41863.1 (AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]
421	13172_s_at	gb AAD30608.1 AC007369_18 (AC007369) Sugar transporter [Arabidopsis thaliana]
422	14709_at	No hits found less than or equal to 1e-15.
423	15931_at	gb AAD41420.1 AC007727_9 (AC007727) F8K7.9 [Arabidopsis thaliana]
424	20369_s_at	emb CAB41109.1 (AL049656) ammonium transport protein (AMT1) [Arabidopsis thaliana]
425	14201_at	No hits found less than or equal to 1e-15.
426	14691_at	No hits found.
75	14148_at	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
426	16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2 [Arabidopsis thaliana]
427	13625_s_at	emb CAB42924.1 (AL049862) putative disease resistance protein [Arabidopsis thaliana]
428	13702_s_at	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
429	17886_at	gb AAC14530.1 (AC004484) unknown protein [Arabidopsis thaliana]
430	12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase [Arabidopsis thaliana]
431	12353_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase [Arabidopsis thaliana]
432	17899_at	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]

433	18894_at	emb CAB43665.1 (AL050352) Ca ²⁺ -transporting ATPase-like protein [Arabidopsis thaliana]
434	14978_at	gb AAB64024.1 (AC002333) putative glucosyltransferase [Arabidopsis thaliana]
435	14223_at	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
436	16109_s_at	gb AAC05342.1 (AC002521) putative protein kinase [Arabidopsis thaliana]
437	18820_at	gb AAD28055.1 AC007166_3 (AC007166) putative protein kinase [Arabidopsis thaliana]
438	20345_at	gb AAC72865.1 (AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]
439	14170_at	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]
440	15143_s_at	gb AAD38519.1 AF138281_1 (AF138281) phospholipase D-gamma-2 [Arabidopsis thaliana]
441	17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
442	20590_at	emb CAB37511.1 (AL035540) Phospholipase like protein [Arabidopsis thaliana]
443	14608_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana]
444	13550_at	emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
445	13355_at	emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana]
446	13564_at	gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis thaliana]
447	19845_g_at	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
448	12764_f_at	gb AAC32912.1 (AC004138) putative glutathione S-transferase [Arabidopsis thaliana]
449	17922_at	gb AAB16855.1 (U71122) pyruvate decarboxylase [Arabidopsis thaliana]

450	15982_s_at	emb CAA66863.1 (X98190) peroxidase ATP2a [Arabidopsis thaliana]
451	12227_at	gb AAD39285.1 AC007576_8 (AC007576) Unknown protein [Arabidopsis thaliana]
452	20555_s_at	emb CAB45975.1 (AL080318) copper amine oxidase like protein (fragment2) [Arabidopsis thaliana]
453	19844_at	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
454	13985_s_at	gb AAC31242.1 (AC004747) unknown protein [Arabidopsis thaliana]
455	13548_at	gb AAD41421.1 AC007727_10 (AC007727) ESTs gb N96028, gb F14286, gb T20680, gb F14443, gb AA657300 and gb N65244 come from this gene. [Arabidopsis thaliana]
456	15611_s_at	gb AAA32775.1 (L22567) cor78 [Arabidopsis thaliana]
457	19840_s_at	gb AAD25759.1 AC007060_17 (AC007060) Strong similarity to F19I3.2 gi 3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb AC004238. EST gb R90518 comes from this gene.
458	15985_at	emb CAA67340.1 (X98808) peroxidase ATP3a [Arabidopsis thaliana]
459	14584_at	gb AAD32844.1 AC007658_3 (AC007658) unknown protein [Arabidopsis thaliana]
460	15422_at	gb AAD36948.1 AF069441_8 (AF069441) hypothetical protein [Arabidopsis thaliana]
461	20150_at	gb AAB61076.1 (AF007271) A_TM021B04.14 gene product [Arabidopsis thaliana]
462	18844_at	gb AAC33239.1 (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
463	16360_at	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
464	20292_at	gb AAB87113.1 (AC002391) putative protein kinase [Arabidopsis thaliana]
465	14554_at	gb AAC18798.1 (AC003671) F17O7.4 [Arabidopsis thaliana]
466	18604_at	gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]

467	16061_s_at	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
468	14145_at	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
469	16144_s_at	dbj BAA04870.1 (D21843) MAP kinase [Arabidopsis thaliana]
470	17097_s_at	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
471	19718_at	gb AAB71447.1 (AC000098) Similar to Arabidopsis Fe(II) transport protein (gb U27590). [Arabidopsis thaliana]
472	14298_g_at	gb AAC25507.1 (AC003979) T22J18.6 [Arabidopsis thaliana]
473	12307_at	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
474	20232_s_at	emb CAA18460.1 (AL022347) protein kinase-like protein [Arabidopsis thaliana]
475	19322_at	gb AAF19738.1 AC012463_12 (AC012463) T2E6.14 [Arabidopsis thaliana]
476	14224_at	gb AAF07386.1 AC010675_9 (AC010675) putative peptide transporter [Arabidopsis thaliana]
477	14270_at	gb AAD39269.1 AC007203_1 (AC007203) Putative UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]
478	15479_at	emb CAB39671.1 (AL049483) putative protein [Arabidopsis thaliana]
479	14090_i_at	gb AAD41981.1 AC006438_13 (AC006438) unknown protein [Arabidopsis thaliana]
480	16162_s_at	gb AAB05099.1 (U39944) BELL1 [Arabidopsis thaliana]
481	20149_at	gb AAB70415.1 (AC000106) Similar to Beta integral membrane protein (gb U43629). [Arabidopsis thaliana]
482	12765_at	gb AAD15574.1 (AC006340) unknown protein [Arabidopsis thaliana]
214	12505_s_at	gb AAC63643.1 (AC005309) putative CONSTANS-like B-box zinc finger protein [Arabidopsis thaliana]
483	13140_at	gb AAC79588.1 (AC005727) putative RING zinc finger ankyrin protein [Arabidopsis thaliana]
484	15022_at	gb AAC72124.1 (AC005278) ESTs gb H37641 and gb AA651422 come from this gene. [Arabidopsis thaliana]

485	16306_at	emb CAB41935.1 (AL049751) putative protein [Arabidopsis thaliana] gb AAC26246.1 (AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
486	18611_at	emb CAB43428.1 (AL050300) putative protein [Arabidopsis thaliana]
487	20199_at	emb CAA18626.1 (AL022580) putative protein [Arabidopsis thaliana]
488	14595_at	gb AAD31337.1 AC007354_10 (AC007354) Strong similarity to gb Y09533 involved in starch metabolism from Solanum tuberosum and contains a PF 01326 Pyruvate phosphate dikinase, PEP/pyruvate binding domain. EST gb N96757 comes from this gene.
489	12532_at	[Arabidopsis thaliana] emb CAB41162.1 (AL049659) putative protein [Arabidopsis thaliana]
490	19977_at	gb AAC79594.1 (AC005727) putative membrane channel protein [Arabidopsis thaliana]
491	12773_at	gb AAD32870.1 AC005489_8 (AC005489) F14N23.8 [Arabidopsis thaliana]
492	19632_at	emb CAA16957.1 (AL021811) putative protein [Arabidopsis thaliana]
493	19359_s_at	emb CAA78712.1 (Z14988) glycine rich protein [Arabidopsis thaliana] thaliana]
494	14716_f_at	gb AAC19269.1 (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
495	13648_at	gb AAD41977.1 AC006438_9 (AC006438) unknown protein [Arabidopsis thaliana]
496	12768_at	gb AAC69134.1 (U78721) putative auxin-regulated protein [Arabidopsis thaliana]
497	16422_at	gb AAC26203.1 (AF053747) dormancy-associated protein [Arabidopsis thaliana]
498	15131_s_at	emb CAB38829.1 (AL035679) drought-inducible cysteine proteinase RD19A precursor
499	14659_s_at	emb CAB38829.1 (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]
500	14658_s_at	emb CAB36513.1 (AL035440) putative protein [Arabidopsis thaliana]
501	15057_at	emb CAB56039.1 (AJ133786) gigantea protein [Arabidopsis thaliana]
502	17581_g_at	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
503	18567_at	

504	17047_s_at	gb AAC68674.1 (AF078825) RING-H2 finger protein RHA3b [Arabidopsis thaliana]
505	15105_s_at	emb CAA78711.1 (Z14987) glycine rich protein [Arabidopsis thaliana]
506	14196_at	gb AAF16557.1 AC012563_10 (AC012563) unknown protein [Arabidopsis thaliana]
507	17599_s_at	gb AAD50976.1 AF170494_1 (AF170494) ionotropic glutamate receptor ortholog GLR6 [Arabidopsis thaliana]
508	18556_at	gb AAD29803.1 AC006264_11 (AC006264) cyclophilin (CYP2) [Arabidopsis thaliana]
509	16486_at	gb AAB04606.1 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana]
510	18272_at	gb AAB95293.1 (AF002109) unknown protein [Arabidopsis thaliana]
795	12219_at	gb AAD31373.1 AC006053_15 (AC006053) unknown protein [Arabidopsis thaliana]
511	20446_s_at	gb AAC80600.1 (AC005106) T25N20.21 [Arabidopsis thaliana]
512	12561_at	emb CAA16701.1 (AL021687) putative protein [Arabidopsis thaliana]
513	12060_at	gb AAD46000.1 AC005916_12 (AC005916) Contains similarity to gb AF113001 silencing mediator of retinoic acid and thyroid hormone receptor alpha and gb AF109179 cyclin T1 from Mus musculus. ESTs gb N95317, gb Z29139 and gb Z30853 come from this gene. [Arabidopsis thaliana]
514	18235_at	gb AAB61480.1 (AC000348) T7N9.4 [Arabidopsis thaliana]
515	14021_r_at	emb CAA04134.1 (AJ000497) Starch branching enzyme II [Arabidopsis thaliana]
516	14020_i_at	emb CAA04134.1 (AJ000497) Starch branching enzyme II [Arabidopsis thaliana] emb CAA44630.1 (X62818) Metallothionein-like protein [Arabidopsis thaliana]
517	16011_s_at	gb AAD09232.1 (U83179) unknown [Arabidopsis thaliana]
518	17033_s_at	
519	16050_at	gb AAD24630.1 AC006919_10 (AC006919) putative fructose biphosphate aldolase [Arabidopsis thaliana]

520	19692_at	gb AAC14039.1 (AC003981) F22O13.13 [Arabidopsis thaliana]
521	19181_s_at	gb AAC39464.1 (AF053065) late embryogenesis abundant protein homolog [Arabidopsis thaliana]
792	13435_at	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
522	17128_s_at	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
523	14635_s_at	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
524	15846_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
525	15847_g_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
526	14704_s_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
527	17456_at	gb AAB80678.1 (AC002332) putative steroid dehydrogenase [Arabidopsis thaliana]
528	14895_s_at	emb CAB10562.1 (Z97344) acetylornithine deacetylase [Arabidopsis thaliana]
529	19979_at	gb AAB95235.1 (AC002130) F1N21.7 [Arabidopsis thaliana]
530	20325_s_at	emb CAA78152.1 (Z12162) protein phosphatase 1A [Arabidopsis thaliana]
531	18234_at	gb AAB61479.1 (AC000348) T7N9.3 [Arabidopsis thaliana]
532	16474_s_at	emb CAA35838.1 (X51474) kin1 [Arabidopsis thaliana]
533	18701_s_at	emb CAA38894.1 (X55053) cold regulated [Arabidopsis thaliana]
534	13785_at	gb AAD23000.1 AC007087_19 (AC007087) cold-regulated protein cor15b precursor [Arabidopsis thaliana]
535	20387_at	gb AAC23422.1 (AC004005) putative methionine aminopeptidase [Arabidopsis thaliana]
536	13178_at	gb AAB63086.1 (U93215) unknown protein [Arabidopsis thaliana]
537	12103_at	gb AAD30603.1 AC007369_13 (AC007369) Unknown protein [Arabidopsis thaliana]
538	13225_s_at	emb CAA42483.1 (X59814) Cold and ABA regulated gene [Arabidopsis thaliana]

539	17003_at	gb AAB95275.1 (AF002109) putative LIM-domain protein [Arabidopsis thaliana]
540	15878_at	emb CAA19880.1 (AL031032) putative protein [Arabidopsis thaliana]
541	13004_at	gb AAD03574.1 (AC003952) putative senescence-related protein [Arabidopsis thaliana]
542	14052_at	gb AAC34333.1 (AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]
543	15798_at	gb AAC05351.1 (AC002521) putative receptor-like protein kinase [Arabidopsis thaliana]
793	12345_at	gb AAB67985.1 (L36246) anoxia-induced protein [Arabidopsis thaliana]
544	16818_s_at	emb CAA20206.1 (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]
545	13916_at	gb AAC62136.1 (AC005169) unknown protein [Arabidopsis thaliana]
666	20342_at	emb CAB41311.1 (AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
546	20421_at	emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
547	14250_r_at	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
548	14249_i_at	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
549	17544_s_at	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
550	12879_s_at	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
551	20017_at	gb AAC16079.1 (AC004521) unknown protein [Arabidopsis thaliana]
552	13177_at	emb CAB40989.1 (AL049640) growth factor like protein [Arabidopsis thaliana]
553	19946_at	gb AAF18611.1 AC005170_1 (AC005170) similar to senescence-associated protein [Arabidopsis thaliana]
554	17894_at	gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]
555	15855_at	gb AAD15572.1 (AC006340) unknown protein [Arabidopsis thaliana]
556	15558_r_at	emb CAB45807.1 (AL080253) putative protein [Arabidopsis thaliana]
557	15208_s_at	No hits found less than or equal to 1e-15.

558	16153_s_at	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]
559	14636_s_at	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]
560	19178_at	dbj BAA86999.1 (AB035137) blue copper binding protein [Arabidopsis thaliana]
561	17580_at	emb CAB56039.1 (AJ133786) gigantea protein [Arabidopsis thaliana]
562	14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
563	18946_at	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
564	13009_i_at	emb CAA17138.1 (AL021889) putative protein [Arabidopsis thaliana]
565	18508_s_at	gb AAA33709.1 (L16797) glutamate decarboxylase [Petunia x hybrida]
566	12556_at	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
567	13115_at	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]
568	15046_s_at	gb AAB87120.1 (AC003000) unknown protein [Arabidopsis thaliana]
339	17303_s_at	gb AAC67339.2 (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]
569	18597_at	emb CAB45881.1 (AL080282) berberine bridge enzyme-like protein [Arabidopsis thaliana]
570	13908_s_at	emb CAB42588.1 (A71590) unnamed protein product [Arabidopsis thaliana]
571	14553_at	emb CAB41103.1 (AL049655) putative protein [Arabidopsis thaliana]
572	18928_at	gb AAB64044.1 (AC002333) putative endochitinase [Arabidopsis thaliana]

		gb AAC72119.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from <i>Daucus carota</i> . ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470, gb R65072, gb N76373, gb F15470, gb Z35182, gb H76373, gb Z34678 and gb Z35387>
573	12772_at	emb CAA18124.1 (AL022141) putative receptor protein kinase [<i>Arabidopsis thaliana</i>]
574	16326_at	
575	20479_i_at	emb CAB38908.1 (AL035708) cytochrome P450-like protein [<i>Arabidopsis thaliana</i>] gb AAD28318.1 AC006436_9 (AC006436) putative receptor-like protein kinase
576	16393_s_at	[<i>Arabidopsis thaliana</i>]
577	17413_s_at	emb CAA67551.1 (X99097) peroxidase [<i>Arabidopsis thaliana</i>] gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase
578	14620_s_at	[<i>Arabidopsis thaliana</i>]
579	20480_s_at	emb CAB38908.1 (AL035708) cytochrome P450-like protein [<i>Arabidopsis thaliana</i>] gb AAC79625.1 (AC005770) unknown protein
580	15866_s_at	[<i>Arabidopsis thaliana</i>]
581	19182_at	emb CAA21214.1 (AL031804) putative protein [<i>Arabidopsis thaliana</i>] gb AAC79625.1 (AC005770) unknown protein
582	18255_at	[<i>Arabidopsis thaliana</i>]
583	16054_s_at	emb CAA74639.1 (Y14251) glutathione S-transferase [<i>Arabidopsis thaliana</i>]
584	14672_s_at	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [<i>Arabidopsis thaliana</i>]
585	20291_s_at	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [<i>Arabidopsis thaliana</i>] emb CAA74639.1 (Y14251) glutathione S-transferase
586	16053_i_at	[<i>Arabidopsis thaliana</i>]
587	17083_s_at	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [<i>Arabidopsis thaliana</i>]
588	12889_s_at	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [<i>Arabidopsis thaliana</i>] gb AAD22285.1 AC006920_9 (AC006920) unknown protein
589	12642_at	[<i>Arabidopsis thaliana</i>]

590	17487_s_at	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
591	14838_s_at	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
592	17104_s_at	dbj BAA13640.1 (D88541) phosphoserine aminotransferase [Arabidopsis thaliana]
593	19892_at	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
594	16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
664	13273_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
595	12892_g_at	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
596	15141_s_at	dbj BAA22096.1 (D85191) vegetative storage protein [Arabidopsis thaliana]
597	18231_at	emb CAA55322.1 (X78585) Di21 [Arabidopsis thaliana]
598	15629_s_at	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
599	15978_at	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
600	20269_at	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
601	14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
602	17930_s_at	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
603	16952_s_at	gb AAC78532.1 (AC005662) calmodulin-like protein [Arabidopsis thaliana]
604	12930_s_at 12842_s_at	gb AAC49679.1 (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana] No hits found less than or equal to 1e-15.
605	16063_s_at	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
228	12904_s_at	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
606	12908_s_at	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

607	15937_at	emb CAA17127.1 (AL021889) hypothetical protein [Arabidopsis thaliana]
608	17843_s_at	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
609	18966_at	gb AAC95196.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
610	20519_at	gb AAC80599.1 (AC005106) T25N20.20 [Arabidopsis thaliana]
611	19641_at	gb AAC95189.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
612	17408_at	gb AAD32297.1 AC006533_21 (AC006533) putative glucosyltransferase [Arabidopsis thaliana]
613	15646_s_at	gb AAC37474.1 (L42212) serine acetyltransferase [Arabidopsis thaliana]
614	14731_s_at	gb AAC49988.1 (AF014960) multidrug resistance-associated protein 2; AtMRP2 [Arabidopsis thaliana]
615	20685_at	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]
616	16968_at	emb CAA17559.1 (AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]
617	18253_s_at	gb AAC78440.1 (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis thaliana] thaliana]
618	15496_at	gb AAD20156.1 (AC006282) putative glucosyl transferase [Arabidopsis thaliana]
619	19137_at	emb CAA52771.1 (X74755) ATAF1 [Arabidopsis thaliana]
620	19132_s_at	emb CAA18722.1 (AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]
621	13656_at	gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function. [Arabidopsis thaliana]
622	17024_s_at	gb AAB67854.1 (U61231) cytochrome P450 [Arabidopsis thaliana]
623	14705_i_at	emb CAB69849.1 (AL137189) anthranilate N-benzoyltransferase-like protein [Arabidopsis thaliana]
624	17500_s_at	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]

625	13217_s_at	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
626	15196_s_at	gb AAC49573.1 (U43412) 3'-phosphoadenosine 5'-phosphosulfate reductase [Arabidopsis thaliana]
627	18590_at	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
628	14700_at	No hits found less than or equal to 1e-15.
629	14665_r_at	emb CAA69879.1 (Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
630	12630_at	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
631	18953_at	gb AAC69851.1 (AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
632	13514_s_at	emb CAA16793.1 (AL021713) putative protein [Arabidopsis thaliana]
633	12490_at	gb AAF02787.1 AF195115_7 (AF195115) weak similarity to receptor protein kinase [Arabidopsis thaliana]
634	12246_s_at	emb CAB10404.1 (Z97340) phytochrome D [Arabidopsis thaliana]
635	20536_s_at	emb CAB37488.1 (AL035539) putative protein [Arabidopsis thaliana]
636	18409_at	gb AAC72122.1 (AC005278) F15K9.14 [Arabidopsis thaliana]
637	19387_at	gb AAD21475.1 (AC007017) unknown protein [Arabidopsis thaliana]
638	16117_s_at	gb AAB70244.1 (AF016848) WD-40 repeat protein [Arabidopsis thaliana]
639	18347_s_at	emb CAA21480.1 (AL031986) putative protein [Arabidopsis thaliana]
640	15880_at	emb CAB38906.1 (AL035708) putative protein [Arabidopsis thaliana]
667	20471_at	gb AAC49767.1 (AF003094) AP2 domain containing protein RAP2.1 [Arabidopsis thaliana]
641	16603_s_at	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]
642	12049_at	gb AAC13598.1 (AF058914) F21E10.13 gene product [Arabidopsis thaliana]
643	12048_at	gb AAC78704.1 (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

		gb AAB61117.1 (AC002062) ESTs
644	14064_at	gb N38288,gb T43486,gb AA395242 come from this gene. [Arabidopsis thaliana]
645	12149_at	gb AAC04492.1 (AC003974) unknown protein [Arabidopsis thaliana]
646	14295_s_at	emb CAA91183.1 (Z54356) HD-ZIP [Arabidopsis thaliana]
647	19034_at	emb CAA16930.1 (AL021768) TMV resistance protein N-like [Arabidopsis thaliana]
648	18624_at	gb AAC27848.1 (AC004218) unknown protein [Arabidopsis thaliana]
649	13181_at	gb AAC97218.1 (AC005936) unknown protein [Arabidopsis thaliana]
650	18866_at	gb AAD10163.1 (AC005917) putative Tal1-like non-LTR retroelement protein [Arabidopsis thaliana]
651	19502_at	emb CAB44686.1 (AL078620) cytochrome P450-like protein [Arabidopsis thaliana]
652	16301_s_at	emb CAA19807.1 (AL031018) hypothetical protein [Arabidopsis thaliana]
653	19411_at	gb AAD32774.1 AC007661_11 (AC007661) unknown protein [Arabidopsis thaliana]
654	20300_g_at	emb CAA71588.1 (Y10556) CONSTANS [Arabidopsis thaliana]
655	20299_at	emb CAA71588.1 (Y10556) CONSTANS [Arabidopsis thaliana]
656	18696_s_at	gb AAB57688.1 (U96045) APS reductase [Arabidopsis thaliana]
657	15186_s_at	gb AAC26980.1 (AF016283) 5'-adenylylsulfate reductase [Arabidopsis thaliana] [Arabidopsis thaliana]
659	16609_s_at	AtERF2 (, BAA32419.1; AB008104)
660	12909_s_at	EREBP4-like, AtERF6 (, CAB10530.1; Z97343)
661	16536_s_at	AtERF5 (, BAA32422.1; AB008107)
301	15665_s_at	put. C2H2 zinc finger transcription factor (, AAB80922.1; AF022658)
668	13176_at	Myb-like (, emb CAA20567.1 (AL031394) putative protein
670	15778_at	X98676.2_at
671	20619_at	AC005896.161_at
672	12966_s_at	AL023094.197_s_at
673	20335_s_at	Y14208.2_s_at
674	18949_at	Z54136.1_at
675	13015_s_at	X98673.2 s at-emb CAB41311.1

		(AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
676	19646_s_at	AC005819.55_s_at
677	19855_at	AC007260.16_at
		AC007047.101_at gb AAC49767.1
		(AF003094) AP2 domain containing protein
678	18475_at	RAP2.1 [Arabidopsis thaliana]
		unspecified t-factor gb AAC49775.1
		(AF003102) AP2 domain containing protein
679	13001_at	RAP2.9 [Arabidopsis thaliana]
		AC004665.101_at emb CAA67234.1
		(X98676) zinc finger protein [Arabidopsis thaliana]
680	15219_at	ATTHIRED4_s_at gb AAC98070.1
		(AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
681	13189_s_at	hsp70_s_at emb CAA18838.1 (AL023094)
		bZIP transcription factor ATB2 [Arabidopsis thaliana]
684	13284_s_at	

Table 10

<u>Set</u>	<u>Content</u>	<u>Number of unique genes</u>
2	7 or 8 not edm1 not	55 genes
5	rps2 not pad4 or NahG	
3	edm1 not rps2 not pad4 or NahG	44 genes
4	rps2 not edm1 not pad4 or NahG	12 genes
5	pad4 or NahG not edm1 not rps2	20 genes
6	edm1 and rps2 not pad4 or NahG	17 genes
10	7	18 genes
	8	7 genes
	9	<u>11 genes</u>
	Total	184 genes

- 15 For engineering resistance to pathogens whose growth is restricted by RPP7 or RPP8 dependent responses, such as oomycete pathogens, all 184 genes are potentially useful. The 128 genes in sets 2, 3, 4, and 6 are more likely to be useful, as *pad4* and *NahG* do not interfere with resistance mediated by *RPP7* or *RPP8*, so genes under their control should not be important for this type of
- 20 resistance. The 99 genes in sets 2 and 3 are even more likely to be useful, because they not affected by *rps2*, and *RPP7* and *RPP8* trigger a different kind of resistance response than the one triggered by *RPS2*. The 44 genes in set 3 are

most likely to be useful, as they require *EDM1*, and *EDM1* is required for resistance.

Example 3

5 Transcriptional Responses Triggered by the RPP7 Defense Signaling Pathway

The *RPP7* defense-signaling pathway (Figure 1) mediates resistance of the *Arabidopsis* ecotype Col-0 against the *Peronospora* isolate Hiks1. In contrast to conventional *R*-gene dependent defense signaling pathways in *Arabidopsis*, such as the *RPP4* pathway, the *RPP7* pathway does not essentially
10 require salicylic acid accumulation or previously described defense regulators, such as *EDS1*, *NDR1*, *NPR1*, *PAD4* and others.

A comparative analysis of transcriptional responses triggered by the *RPP7* and *RPP8* pathways was performed by gene expression profiling using Affymetrix oligonucleotide chips with roughly 8,200 different *Arabidopsis*
15 genes, representing roughly a third of the genome. For the analysis, 2 week old seedlings were harvested 0, 12 or 48 hours post infection with a particular *Peronospora* isolate (Table 11). To examine *RPP8* triggered transcriptional responses, a transgenic line Col-0 line carrying the *RPP8* resistance gene from the *Arabidopsis* ecotype Landsberg erecta was infected with the *Peronospora*
20 isolate Emco5. This interaction is incompatible. The interaction between Emco5 and Col-0 wild type plants served as compatible control. Responses triggered by the *RPP7* pathway were analyzed using the incompatible interaction between the *Peronospora* isolate Hiks1 and Col-0 wild type plants, as well as compatible interactions between Hiks1 and the susceptible mutants *rpp7*, *edm1*,
25 *edm2* and *edm3*. To compare transcriptional responses triggered by the unconventional *RPP7* and *RPP8* pathways with those triggered by the more conventional *RPP4* pathway, Col-0 wild type plants were infected with the *Peronospora* isolate Emoy2, which is avirulent on this ecotype. The interactions between Emoy2 and NahG plants, as well as the mutants *pad4*, *ndr1* and *npr1*,
30 served as compatible controls. Whereas *pad4* and NahG plants are fully Emoy2 susceptible, *ndr1* and *npr1* plants are only partly compromised in Emoy2 resistance.

Table 11

	<u>Plant</u>	<u>Peronospora isolate</u>	<u>Interaction type</u>
	Col-0 (tgRPP8)	Emco5	incompatible
	Col-0 (rpp8)	Emco5	compatible
5	Col-0 (RPP7)	Hiks1	incompatible (2x)
	Col-0 (rpp7; 3929)	Hiks1	compatible
	Col-0 (edm1)	Hiks1	compatible
	Col-0 (edm2)	Hiks1	compatible
	Col-0 (edm3)	Hiks1	compatible
10	Col-0 (RPP4)	Emoy2	incompatible
	Col-0 (ndr-1-1)	Emoy2	intermediate
	Col-0 (pad4-1)	Emoy2	compatible
	Col-0 (NahG)	Emoy2	compatible
	Col-0 (npr1-1)	Emoy2	intermediate

15

ResultsIdentification of Genes Potentially Required for RPP7 Mediated Peronospora Resistance

Genes that play a role in the establishment of resistance may show differences in their regulation or their expression levels between compatible and incompatible interactions (e.g., genes may show lower expression levels in “loss of Hiks-resistance mutants” as compared to Col-0 wild type plants). Thus, for each gene expression, ratios were calculated between Col-0 and each of the four Hiks response mutants (*rpp7*, *edm1*, *edm2* or *edm3*) at each time point (0, 12 and 48 hours). The resulting data set, consisting of 12 expression ratios for each of the 8,775 probe sets on the chip, was first analyzed with “CLUSTER” and “TREE VIEW”, two commonly used programs for chip and micro-array data analysis (Eisen et al., 1998). Genes that demonstrated only minor or less significant expression differences between Col-0 wild type and the mutants were excluded from analysis. Genes that showed at least one 3-fold expression difference over all 12 calculated expression ratios were first considered for further analysis.

Table 12 shows 194 probe sets corresponding to genes having SEQ ID NOs: 301-494, the expression of which is altered after infection of *Arabidopsis* with *P. parasitica* (wild-type relative to *rpp7*, *edm1*, *edm2*, or *edm3*). Table 13

depicts about 100 genes (genes comprising SEQ ID NOs: 373, 385, 242, 369,
 306, 232, 346, 367, 212, 221, 307, 322, 240, 313, 270, 252, 383, 245, 377, 212,
 327, 297, 375, 263, 250, 282, 358, 257, 332, 560, 284, 220, 259, 355, 248, 281,
 215, 236, 309, 386, 253, 333, 336, 296, 319, 414, 354, 353, 293, 278, 324, 339,
 5 345, 225, 249, 264, 310, 228, 214, 311, 343, 298, 384, 277, 314, 372, 331, 338,
 370, 352, 365, 261, 374, 238, 344, 241, 380, 371, 262, 258, 256, 304, 275, 303,
 274, 254, 223, 348, 318, 251, 291, 289, 361, 285, 368, 342, 290, 351, 312, 286,
 287, 273, 239, 326, 226, 227, 350, 280, 317, 359, 294, 279, 382, 356, 234, 218,
 217, 347, 379, 401, 378, 363, 341, 208, 268, 267, 364, 266, 337, 269, 269, 325,
 10 793 and 224) represented by 137 probe sets that show at least one 3-fold-
 expression difference in comparisons between wild type *Arabidopsis* Col-0 and
 mutants *rrp7* or *edm1*, *edm2*, or *edm3* infected with *P. parasitica* Hiks1 (i.e.,
 probe sets that show at least one 3-fold difference in expression levels over all 12
 expression ratios calculated between Col-0 wild type and each of the 4 Hiks
 15 response mutants at each of the time points). Genes were grouped together
 according to similarities of their expression characteristics. Expression ratios
 were color encoded. Positive expression ratios were red and negative ratios were
 green. Black indicated no expression difference. Genes were represented in
 rows and infection treatments in columns. Red generally indicated that a gene at
 20 a given time point is more strongly expressed in Col-0 wild type plants as
 compared to the respective mutant. One cluster represented genes that are
 upregulated in response to Hiks1 infection by the *RPP7* pathway (Table 14;
 genes comprising SEQ ID NOs: 365, 261, 374, 238, 344, 241, 380, 371, 262,
 258, 256, 304, 275, 303, 274, 254, 310, 228, 214, 347 and 225, which are
 25 induced by Hiks1-infection and which are *RPP7*, *EDM1*, *EDM2*, *EDM3*-
 dependent genes and so may encode regulators acting downstream of those
 genes; see probe sets 12505, 13217 and 12904 which correspond to genes that
 encode potential regulators of Hiks response pathway). Genes in this cluster
 represent genes that are more strongly expressed in Col-0 wild type than in all
 30 four mutants predominantly at the 12 hour time-point in each comparison. The
 expression difference is less pronounced in the case of *edm2* and *edm3*, but it is
 consistent over all four comparisons.

Table 12

Affy ID (Probe Set)	Reference No.
12324_i_at	AC007212
12333_at	AJ286345
12345_at	L36246
12500_s_at	AF081067
12505_s_at	AC005309
12608_i_at	S70188
12642_at	AC006920
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843_s_at	AC007195
12845_s_at	AJ004810
12879_s_at	U40856
12891_at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12911_s_at	X84229
12916_s_at	AF021244
13138_at	AL096882
13177_at	AL049640
13178_at	U93215
13187_i_at	U35829
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13273_s_at	U68017
13284_s_at	AJ002551
13604_at	AC000104
13615_at	AC002332
13617_at	AC006592
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14028_at	AF075597
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309

14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14295_s_at	Z54356
14595_at	AL022580
14608_at	AC007357
14614_at	AC004165
14621_at	AC004747
14627_i_at	X76609
14628_r_at	X76609
14635_s_at	AC005398
14636_s_at	AC013258
14643_s_at	AC006836
14672_s_at	U18993
14675_s_at	D85191
14691_at	AP002046
14704_s_at	AC006067
14706_r_at	AL137189
14709_at	AP002046
14711_s_at	AF085279
14731_s_at	AF014960
14784_at	AC005310
14951_at	AL049481
14965_at	AC002329
15057_at	AL035440
15085_s_at	AL031018
15105_s_at	Z14987
15116_f_at	AF121356
15125_f_at	D85190
15141_s_at	D85191
15145_s_at	D64155
15154_s_at	AL096860
15161_s_at	U90522
15178_s_at	U43489
15216_s_at	U75198
15431_at	AL030978
15496_at	AC006282
15523_s_at	AL078637
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15622_s_at	U43945

15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15950_at	AC006429
15954_at	U72155
15969_s_a	AJ133036
15978_at	X68592
15982_s_a	X98190
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16412_s_at	AL022603
16442_s_at	AJ002551
16461_I_at	AC004683
16462_s_a	AC004683
16504_s_at	Z97335
16510_at	AL034567
16514_at	AL035538
16536_s_at	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16578_s_at	AL137080
16609_s_at	AB008104
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
16951_i_at	AC005662
16952_s_at	AC005662
16981_s_at	U35829
17014_s_at	U05206
17033_s_at	U83179
17054_s_at	AF134128
17073_s_at	AC006836
17119_s_at	AF132212
17123_s_at	AF106087
17128_s_at	AC005398
17187_at	AF128396
17303_s_at	AC005499
17379_at	AC018721
17386_at	AC006264
17413_s_at	X99097

17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17549_s_a	L37126
17567_at	AL162751
17886_at	AC004484
17899_at	Z97339
17917_s_at	AC004261
17961_at	AC007323
17963_at	AL049730
18003_at	AF188334
18064_r_at	
18069_at	
18070_r_at	
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18255_at	AC005770
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590_at	AJ222713
18591_at	X74756
18607_s_at	U78721
18635_at	AC004005
18706_s_a	X75782
18716_at	AC007396
18876_at	AF002109
18920_at	AC002338
18928_at	AC002338
19034_at	AL021768
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19594_i_at	X98321
19640_at	AC004561
19977_at	AL049659
20017_at	AC004521
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20297_at	AC007153
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336

20555_s_a	AL080318
20585_s_at	AC005309
20641_at	X91919

Table 13

Probe Set	Description
12324_i_at	AC007212
12345_at	L36246
12505_s_at	AC005309
12608_i_at	S70188
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843_s_at	AC007195
12845_s_at	AJ004810
12879_s_at	U40856
12891_at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12908_s_at	AB008107
12911_s_at	X84229
13138_at	AL096882
13178_at	U93215
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13604_at	AC000104
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309
14116_at	AF077407
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14248_at	AC007357
14250_r_at	AL050300
14595_at	AL022580

14608_at	AC007357
14621_at	AC004747
14627_i_at	X76609
14628_r_at	X76609
14635_s_at	AC005398
14636_s_at	AC013258
14675_s_at	D85191
14691_at	AP002046
14704_s_at	AC006067
14709_at	AP002046
14711_s_at	AF085279
14731_s_at	AF014960
14784_at	AC005310
14951_at	AL049481
15057_at	AL035440
15105_s_at	Z14987
15116_f_at	AF121356
15125_f_at	D85190
15141_s_at	D85191
15145_s_at	D64155
15154_s_at	AL096860
15161_s_at	U90522
15178_s_at	U43489
15431_at	AL030978
15496_at	AC006282
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15846_at	AC006067
15847_g_at	AC006067
15950_at	AC006429
15954_at	U72155
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16504_s_at	Z97335
16510_at	AL034567
16536_s_at	AB008107
16578_s_at	AL137080
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
17014_s_at	U05206
17033_s_at	U83179

17054_s_at	AF134128
17123_s_at	AF106087
17128_s_at	AC005398
17187_at	AF128396
17303_s_at	AC005499
17386_at	AC006264
17413_s_at	X99097
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17567_at	AL162751
17886_at	AC004484
17899_at	Z97339
17961_at	AC007323
17963_at	AL049730
18003_at	AF188334
18064_r_at	
18069_at	
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590_at	AJ222713
18607_s_at	U78721
18635_at	AC004005
18716_at	AC007396
18920_at	AC002338
18928_at	AC002338
19034_at	AL021768
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19640_at	AC004561
19977_at	AL049659
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336
20585_s_at	AC005309
20641_at	X91919

Table 14

Probe Set	Description
12505_s_at	AC005309
12879_s_at	U40856
12904_s_at	AB008103
13189_s_at	U35829
13217_s_at	AL049862
14116_at	AF077407
14148_at	AF224762
14201_at	AL163972
14248_at	AC007357
14250_r_at	AL050300
14691_at	AP002046
14704_s_at	AC006067
15846_at	AC006067
15847_g_at	AC006067
16063_s_at	AB008103
17500_s_at	AL049862
17544_s_at	U40856
18716_at	AC007396
19178_at	AB035137
19640_at	AC004561
20269_at	AC002387

Thus, Hiks1 induced upregulation is compromised in all four tested “loss of Hiks1 resistance mutants” and there is a correlation between breakdown of resistance and deregulation of these genes. This may indicate that these genes play important roles in mediating Hiks1 resistance. Furthermore, these genes appear to act downstream of all four genetically defined *RPP7* pathway components, *RPP7*, *EDM1*, *EDM2* and *EDM3*. Some genes of this set may encode important regulators; whereas others may indicate metabolic processes required for Hiks1 resistance.

Seventy-eight genes (Table 15; genes comprising SEQ ID NOs:330, 292, 311, 243, 237, 302, 315, 283, 300, 372, 308, 335, 272, 305, 357, 213, 362, 331, 254, 384, 277, 343, 298, 349, 314, 265, 262, 258, 256, 303, 321, 304, 275, 274, 323, 238, 374, 241, 344, 244, 365, 261, 380, 371, 295, 255, 316, 233, 345, 225, 260, 229, 324, 301, 235, 340, 278, 320, 231, 319, 230, 354, 353, 293, 376, 247, 246, 366, 216, 214, 276, 299, 310, 334, 271, 381 and 228) that show the same, but less pronounced, expression characteristics were selected using relaxed selection criterion (at least one 2-fold expression difference over all 12 calculated expression ratios). With a lower cutoff criterion of at least one 2-fold-expression difference across all twelve expression ratios, this cluster is larger

than that shown in Table 14. Genes that are part of this less stringently defined cluster were included in further analyses so as to not exclude potentially important genes. Potential regulators in this cluster are listed in Table 16 (genes comprising SEQ ID NOs: 220, 323, 231, 319, 214, 301, 340, 243, 227, 321, 235, 315, 298, 314, 328, 344 and 349). Four different ERF transcription factors genes are upregulated by the *RPP7*-pathway. Genes encoding ERFs are known to be upregulated in response to several stress-related stimuli, such as wounding, pathogens or ethylene. Moreover, ERF transcription factors bind to GCC boxes, which are ethylene, wounding and pathogen-responsive *cis*-elements. This cluster also contains a gene encoding an ACC synthase, a component of the ethylene biosynthetic pathway. Therefore, ethylene may play a role in the Hiks response pathway.

Table 15

Probe Set	Description
12500_s_at	AF081067
12505_s_at	AC005309
12642_at	AC006920
12879_s_at	U40856
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12916_s_at	AF021244
13177_at	AL049640
13187_i_at	U35829
13189_s_at	U35829
13217_s_at	AL049862
13273_s_at	U68017
13284_s_at	AJ002551
13615_at	AC002332
13617_at	AC006592
14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14201_at	AL163972
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14614_at	AC004165
14643_s_at	AC006836
14672_s_at	U18993

14691_at	AP002046
14704_s_at	AC006067
14706_r_at	AL137189
14709_at	AP002046
14711_s_at	AF085279
15085_s_at	AL031018
15216_s_at	U75198
15431_at	AL030978
15523_s_at	AL078637
15616_s_at	AL078637
15622_s_at	U43945
15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15978_at	X68592
16063_s_at	AB008103
16105_s_at	U68017
16393_s_at	AB008103
16412_s_at	U68017
16442_s_at	AJ002551
16536_s_at	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16609_s_at	AB008104
16620_s_at	AF051338
16952_s_at	AC005662
16981_s_at	U35829
17073_s_at	AC006836
17119_s_at	AF132212
17379_at	AC018721
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17917_s_at	AC004261
18070_r_at	
18216_at	AC012375
18217_g_at	AC012375
18255_at	AC005770
18591_at	X74756
18716_at	AC007396
18876_at	AF002109
19178_at	AB035137
19182_at	AL031804
19640_at	AC004561
20017_at	AC004521

20269_at	AC002387
20297_at	AC007153
20429_s_at	Z97336

Additionally, a gene encoding a lipoxygenase, a component of the jasmonic acid biosynthetic pathway, is upregulated. Other regulators potentially acting downstream of RPP7, EDM1, EDM2 and EDM3 include some putative
 5 zinc finger transcription factors and protein kinases as well as two calmodulin-like proteins and a calcium binding protein, which may point to a role of calcium in the *RPP7*-pathway.

Table 16

10 I. Transcriptional regulators:

- 1.) AtERF1 (12904_s_at, BAA32418.1; AB008103)
- 2.) AtERF2 (16609_s_at, BAA32419.1; AB008104)
- 3.) EREBP4-like (12909_s_at, CAB10530.1; Z97343)
- 4.) AtERF5 (16536_s_at, BAA32422.1; AB008107)
- 15 5.) putative CONSTANS-like zinc finger (12505_s_at, AAC63643.1; AC005309)
- 6.) putative C2H2 zinc finger transcription factor (15665_s_at, AAB80922.1; AF022658)
- 7.) putative C3H zinc finger protein (17379_at, AAF18728.1; AC018721)
- 20 8.) heat shock transcription factor 4 (13273_s_at, AAC31756.1; U68017)
- 9.) SigA binding protein (14148_s_at, AAF34713.1; AF224762)

II. Other signaling proteins

- 10.) AtACS-6 (12892_g_at, CAB51412.1, AL096882, 35400..37154)
- 11.) lipoxygenase (16569_s_at, AAA32749.1; L23968)
- 25 12.) growth factor like protein (13177_at, CAB40989.1; AL049640)
- 13.) serine/threonine protein kinase (16412_s_at, CAA18704.1; AL022603)
- 14.) wall associated kinase 1 (15616_s_at, CAB08794.1; AJ009696)
- 15.) putative receptor-like protein kinase (16393_s_at, AAD28318.1; AC006436)
- 30 16.) calmodulin-like (16951_i_at, AAC78532.1; AC005662)
- 17.) calmodulin-like (17500_s_at; CAB42906.1; AL049862)
- 18.) calcium binding protein (17917_s_at, AAD12002.1; AC004261)

Twenty-six genes (genes comprising SEQ ID NOs: 300, 308, 272, 213, 362, 265, 374, 241, 261, 380, 310, 228, 233, 330, 311, 243, 237, 254, 230, 244, 365, 216, 316, 345, 225, 301, 278, 354, 353, 293, 335, 271 and 321, also shown in Table 15), represented by 33 probe sets, were found to be commonly
 5 upregulated in response to both *Peronospora* isolates, Hiks1 and Emco5, in an *RPP7*- or *RPP8*-dependent (and *EDM1*, *EDM2* and *EDM3*-dependent) manner (Table 17). Elevated expression of these genes may be required for resistance against both *Peronospora* isolates or against *Peronospora parasitica* in general. Among these 26 genes are those encoding ERF1, putative zinc finger
 10 transcription factors, two proteins potentially involved in calcium signaling, a lipoxygenase, and a cysteine rich antifungal protein.

Table 17

15	26 <i>Peronospora</i> (Hiks1 and Emco5) induced RPP8, RPP7, EDM1,2,3-dependent genes	
	Transcription factors	
	AtERF1	
	Putative salt-tolerance zinc finger transcription factor (18217_g_at)	
20	(ZFPI) hypothetical Cys-3-His zinc finger protein	
	Putative C2H2 zinc finger transcription factor	
	Heat shock transcription factor 4	
	Other potential proteins	
25	Calmodulin-like protein	
	Similarity to centrin, <i>Marsilea vestita</i> contains EF-hand calcium-binding domain (15431_at)	
	Lipoxygenase	
30	Others	
	heat shock protein 70	
	putative steroid sulfotransferase	tryptophan synthase alpha chain
	putative glucosyltransferase	similar to xyloglucan fucosyltransferase (12642_at)
35	phosphoglycerate dehydrogenase	Pad3 (Cytochrome P450)
	ATAF2	putative pectinesterase
	OPDA-reductase homolog	AIG1
	coronatine-induced protein 1	putative glutathione S-transferase
	thioredoxin h	adenosine nucleotide translocator
40	IAA-amino acid hydrolase	contains similarity to sugar transporters
		CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 PRECURSOR (AFP1) (18716_at)

Thirteen of these 26 genes (genes comprising SEQ ID NOs: 308, 300, 272, 362, 265, 242, 261, 380, 228, 243, 254, 216 and 225, *Peronospora* (Hiks1, Emco5 and Emoy2) induced and *RPP4*, *RPP8* and *RPP7* dependent) were also found to be more strongly expressed during the incompatible interaction between the *Peronospora* isolate Emoy2 and Col-0 plants as compared to Emoy2 infections of the compatible or intermediate type (see Table 18). These 13 genes may play an important role in defense against *Peronospora parasitica* in general. Among these genes is PAD3, which was previously demonstrated to be required for pathogen-induced phytoalexin production. Strikingly, Hiks1 resistance is, partially compromised in the *pad1-1/pad3-1* double mutant, whereas Emoy2 resistance is reduced in the *pad3-1* single mutant (Glazebrook et al. 1997).

Table 18

15	13 <i>Peronospora</i> (Hiks1, Emco5 and Emoy2) induced RRP4-pathway, RPP7-pathway, and RPP8-dependent genes
	-adenosine nucleotide translocator (15978_at)
20	-phosphoglycerate dehydrogenase (15629_s_at)
	-tryptophan synthase alpha chain (14672_s_at)
	-ATAF2 (18591_at)
25	-putative glucosyltransferase (14614_at)
	-calmodulin-like protein (13217_s_at)
30	-pad3 (cytochrome P450)(14248_at)
	-putative pectinesterase (20269_at)
	-ethylene responsive element binding factor 1 (12904_s_at)
35	-heat shock transcription factor 4 (13273_s_at)
	-sugar transporter-like (14116_at)
40	-similar to xyloglucan fucosyltransferase (12642_at)
	-AIG1 (12879_s_at)

Identification of promoter motifs common to *RPP7* and *RPP8* controlled genes

Sequence motifs conserved in the promoters of genes co-regulated by the *RPP7* or *RPP8* pathways may lead to information about the types of transcription factors controlling expression of these genes and may serve as starting points for isolating and/or cloning of such factors. Sub-categorization of *RPP7*-
 5 upregulated genes by K-means clustering, based on the absolute expression levels of the genes, revealed the existence of only a few basic expression profiles. K-means clustering into five gene sets gave the most consistent and tight clusters. For each of the five gene sets (Table 19), the expression changes in two repetitions of the Col-0 wild type/Hiks1 interaction are shown as well as
 10 in the *rpp7* mutant and *edm1*, *edm2* and *edm3*.

The first set comprises genes (genes comprising SEQ ID NOs: 292, 302, 315, 300, 308, 213, 265, 374, 241, 344, 261, 299, 365 and 276) that show early and transient upregulation. The genes peak at 12 hours and return to their ground-states at approximately the 48 hours post infection. Genes of the second
 15 set (genes comprising SEQ ID NOs: 267, 305, 357, 362, 380, 310, 228, 295, 233, 329, 312, 243, 237, 283, 372, 254, 314, 323, 216, 260, 229 and 235) are also rapidly upregulated, but show a less pronounced or no decline after the peak. In both sets, the response is weaker in the mutants. Only a few genes in the first set respond almost as strongly in *edm2* and *edm3* plants as in wild type plants.
 20 Genes of the third (genes comprising SEQ ID NOs: 258, 256, 303, 304, 275, 244, 316, 354 and 225) and fifth (genes comprising SEQ ID NOs: 330, 384, 277, 343, 298, 349, 262, 274, 238 and 301) set show an almost linear increase of transcript level in wild type. In the mutants, this increase is delayed and in some cases less steep. In the fourth set (genes comprising SEQ ID NOs: 432, 347,
 25 370, 412, 323, 411, 322, 449, 448, 385, 471, and 339) the expression levels rise in the first repetition of the Col-0 wild type/Hiks interaction, but respond very little in the second one. In *edm3*, the transcript levels drop from a high ground state. The probe sets and genes corresponding to each of these K-means cluster sets are shown in Table 19.

30

Table 19

K-means set 1	Description	K-means set2	Description
12500_s_at	AF081067	12642_at	AC006920
13217_s_at	AL049862	12904_s_at	AB008103
14248_at	AC007357	12905_s_at	AB008104

14614_at	AC004165	12916_s_at	AF021244
14706_r_at	AL137189	13177_at	AL049640
15216_s_at	U75198	13187_i_at	U35829
15622_s_at	U43945	13273_s_at	U68017
15629_s_at	AB010407	14116_at	AF077407
15680_s_at	D42061	14223_at	AL024486
15978_at	X68592	14672_s_at	X76609
16412_s_at	U68017	15085_s_at	AL031018
17500_s_at	AL049862	15523_s_at	AL078637
18070_r_at		15866_s_at	AC005770
18716_at	AC007396	16063_s_at	AB008103
19640_at	AC004561	16105_s_at	AL049730

K-means set 3 Description

12879_s_at	U40856
13284_s_at	AJ002551
14148_at	AF224762
14201_at	AC068667
14704_s_at	AC006067
15846_at	AC006067
15847_g_at	AC006067
16442_s_at	AJ002551
17544_s_at	U40856

K-means set4 Description

12908_s_at	AB008107
12909_s_at	Z97343
13617_at	AC006592
14141_at	AC011437
14711_s_at	AF085279
15431_at	AL030978
16536_s_at	AB008107
16539_s_at	Z97343
17379_at	AC018721
18216_at	AC012375
18217_g_at	AC012375
20017_at	AC004521

16393_s_at	AC006436
16609_s_at	AB008104
16952_s_at	AC005662
18255_at	AC005770
18591_at	X74756
19182_at	AL031804
20269_at	AC002387

K-means set 5 Description

13189_s_at	U35829
14250_r_at	AL050300
14691_at	AP002046
14709_at	AP002046
15616_s_at	AJ009696
15665_s_at	AF022658
16981_s_at	U35829
17499_s_at	AF107726
17917_s_at	AC004261
20429_s_at	Z97336

Recently, the plant specific family of WRKY transcription factors has been implicated in the regulation of defense-associated genes. Promoters of genes upregulated during systemic acquired resistance were found to be strongly enriched in potential WRKY binding sites. WRKY factors comprise a large family of 72 different members in *Arabidopsis*. Generally these factors appear to bind to sequence motifs containing the core T G A C (W box). It has not yet

been determined whether individual WRKY family members differ in their preferences for distinct W box variations. However, it is probable that a given WRKY protein has a binding preference for a certain variation of the W box motif.

5 Using the program AlignACE, three variations of potential WRKY binding sites were found to be conserved in sub-sets of *RPP7* controlled genes. Two of these motifs are highly enriched in promoters of genes from K-means cluster 3, representing genes that show a linear increase in transcript level after *Peronospora* infection (Table 20; genes comprising SEQ ID NOs: 384, 298, 349, 10 262 and 238 for W box I and genes comprising SEQ ID NOs: 384, 349, 262, 238 and 301 for W box II). These motifs are also present in promoters of K-means cluster 5, which represents a similar expression profile. Focusing on sustained up-regulated genes, that show a particularly pronounced expression difference between Col-0 wild type plants and the Hiks1 response mutants, a third variation 15 of potential WRKY binding sites was found to be significantly enriched (Table 21; genes comprising SEQ ID NOs: 397, 371, 238, 262, 256, 275, 254, 214 and 225). In all three cases, sequence conservation clearly exceeds the core motif of WRKY binding sites that appears to be recognized by all members of this family. These additionally conserved positions may confer specificity for 20 certain WRKY family members. They may provide a highly defined binding site preferentially recognized by a distinct WRKY factor or may serve as binding sites for another transcription factor binding closely adjacent to and specifically interacting with a distinct WRKY factor. In any case, the high conservation of extended potential WRKY binding motifs strongly suggests that specific 25 members of this family participate in the regulation of certain sub-sets of *RPP7*-controlled genes.

Table 20

<u>W box I</u>		MAP Score: 8.98114		
30	GTCATCTTTTAATCTCTGG	0	638	1
	GTCATCTTTTAATCGCCGG	0	932	1
	GCCTTTGCTTATTTATAGG	0	1036	1
	GTCATTTGTTACAAAGAGG	1	318	1
	GTCATTGATCATAAACTGT	1	389	0
35	GCCACTGCTGAATTGTCGG	1	494	1
	GTCCATTGTCAATAAATGG	2	689	1
	GTCCATTGTAAATAAATGT	2	949	1

5
 GTCATCTTTTAATCTCTGT 3 475 0
 GTCACGTATGAATGGAAGG 4 73 1
 GTC AACGTTTAGTTCATGT 4 226 0
 GTC AAGTTTTAAATTGTGG 4 352 1
 GTC AACGTTTAGTTCATGT 4 401 0
 *** * * * * **

GTCANNTNTNANTNNNNGG

G A T

Expected frequency by chance: 0.02/1kb
 10 Observed frequency: 1.2/1kb
 Enrichment: ~60 fold

W box II MAP Score: 15.2966

15
 ATTAAAAGATGAC 0 638 0
 ATTAAAAGATGAC 0 932 0
 ATTAAATGCTGTC 2 752 0
 ATTAAATGCTGTC 2 1011 0
 AGCAAAAGCTGAC 2 1092 1
 ATTAAAAGATGAC 3 481 1
 ATCAAAAGTTGTC 3 829 1
 20 ACTAAACGTTGAC 4 232 1
 ACTAAACGTTGAC 4 407 1
 ACTAAAAAGTGAC 5 755 1
 * **** * ****

25 W II ANTAAANGNTGAC
 C A T

W I: CCNNNNANTNANCNNTGAC
 A T A

30 Expected frequency by chance: 0.04/1kb
 Observed frequency: 1.35/1kb
 Enrichment: ~30 fold
 Table 21

35 ATAGGTGGTCAAGT 1 106 0
 AATTGTGGTCATTT 1 823 0
 ACTTGTGGTCAATT 2 804 0
 AAAAGGGGTCATTT 2 970 1
 ATATGTCGTCTCTT 2 994 0
 AGTTGTGGTCTACC 3 502 0
 40 AAAAGTTGTCAATT 3 732 1
 AGACGTCGTAATTT 4 400 0
 ACGTGGCGTCATAT 5 179 0
 ATGTGGCGTCTCCT 6 249 1
 AGTTGGTGTCACGT 6 925 1
 45 ATTCGTGGTCAACT 7 582 1
 ATATGTCGTCACTT 7 875 1
 * **** * *

ANNNGTNGTCANNT

G

50

expected: 0.05/1kb;
 in random set: 0/1kb;
 this set: 1/1kb;
 enrichment: 10-20 fold;

5

Novel, conserved promoter motifs were also found. Genes of K-means set 1, which are early and transient *RPP7*-pathway specific genes, share two similar highly conserved promoter motifs, G G T/C C C A (SEQ ID NO:714; genes comprising SEQ ID NOs: 302, 315, 308, 265, 374, 241, 261, 299 and 365) and G N C C A A A (SEQ ID NO:715; genes comprising SEQ ID NOs: 292, 302, 308, 265, 374, 241, 261, 299, 365 and 276) (Table 22). Both motifs are almost perfectly conserved and are represented in nearly all promoters of this gene set. They are compact six- or seven-mers, which is typical for transcription factor binding sites. For the second motif, the permutations G A C C A A A and G T C C A A A are strongly represented. These permutations may constitute the preferred binding site of a so far unknown transcription factor.

15

Table 22

20

Two related novel motifs are highly enriched in all
 11 promoters of K-means set1

25

30

35

40

GGTCCA 1 232 0

GGCCCA 1 289 1

GGTCCA 1 597 1

GGTCCA 2 517 0

GGTCCA 3 211 1

GGCCCA 3 360 1

GGTCCA 4 597 1

GGCCCA 4 681 1

GGTCCA 5 352 0

GGTCCA 5 1060 1

GGTCCA 6 358 0

GGCCCA 7 776 0

GGCCCA 7 816 0

GGTCCA 8 285 0

GGTCCA 9 888 1

GGTCCA C

Expected frequency by chance: 0.22/1kb

Observed frequency: 1.2/1kb

Enrichment: 5.4 fold

GCCCAA 0 601 1

GTCCAAA 10 1186 1

GTCCAAA 9 562 1

5 GACCAAA 8 640 0
 GCCCAA 7 774 0
 GTCCAA 7 717 1
 GTCCAA 6 712 1
 5 GACCAAA 5 970 1
 GTCCAA 5 350 0
 GACCAAA 4 1164 1
 GACCAAA 4 1072 1
 GTCCAA 4 784 0
 10 GACCAAA 4 714 0
 GGCCAA 4 698 0
 GCCCAA 3 361 1
 GACCAAA 1 920 0
 GTCCAA 1 230 0
 15 *****
 GNCCAA
 Expected frequency by chance: 0.32/kb
 Observed frequency: 1.3/kb
 Enrichment: 4 fold

20

Following a similar approach as for the Hiks1-induced *RPP7* pathway controlled genes, a cluster of early and transiently Emco5-induced *RPP8*-dependent genes were defined (Table 23). In Col-0-*RPP8* plants these genes (genes comprising SEQ ID NOs: 364, 341, 288, 378, 363, 379 and 219) show a

25 very pronounced upregulation 12 hours post Emco5 infection, after which they return to expression ground states. Using AlignACE, two different motifs (see Example 2) were found to be strongly enriched in the promoters of this cluster. The first motif strongly resembles the type I consensus binding site of Myb transcription factors. This motif is also almost identical to a recently identified

30 *cis*-element conferring rapid elicitor responsive gene expression in parley cell culture (Kirsch et al., 2001). Interestingly, a gene encoding a Myb-like transcription factor (highlighted in yellow) is co-regulated with other genes of this cluster. The Myb-like transcription factor gene is the only gene of this cluster that does not contain this conserved motif in its promoter. This MYB-

35 like factor could be a regulator of this cluster. The second motif does not resemble any known stress responsive plant *cis* element or transcription factor binding site. However, the second motif was found to be strongly represented in promoters from other defense related genes, such as SAR genes. As is typical of many transcription factor binding sites, certain permutations of its consensus

sequence may constitute palindromes. This motif was also found to be conserved by the program MEME.

Table 23

5	Glutathione-conjugate transporter AtMRP4 putative GST putative cytochrome P450 (AC002340) PAD3 (similar to cytochrome P450) CTF2B (similarity to proteins involved in Hydroxylation and oxidation of aromatic rings)	
10	Ribonuclease RNS1 Putative Myb-like protein AlignACE Motif 1:	CAACTTTGAC AA TT CAACTG T G
15	type I Myb binding site:	
	Frequency by chance: 0.05/1kb Observed frequency in control cluster: 0.13/1kb	
20	Observed frequency in this cluster: 1.10/1kb AlignACE Motif2:	TTGGGNCNAA A A
	MEME motif:	GTCTNTTGGGNCAAAA TT A G C
25	Frequency by chance: 0.13/1kb Observed frequency in control cluster: 0/1kb Observed frequency in this cluster: 1.2/1kb	

Different types of transcription factors may participate in the control of distinct *RPP7*-pathway dependent expression profiles. Promoters of genes showing a linear sustained increase of transcript are enriched in different variations of WRKY binding sites. However, no *WRKY*-pathway gene was found to be upregulated by the *RPP7* pathway. Therefore, WRKY factors involved in *RPP7* mediated up-regulation of K-means cluster 3 and 5 genes may already be pre-formed when the pathogen signal is perceived. However, only 21 *WRKY* genes out of 72 members of this family in *Arabidopsis* are represented on the oligonucleotide chip. Upregulated WRKY factors participating in *RPP7* mediated gene regulation may not be present on the chip. A novel type of transcription factor may be involved in regulation of early and transient *RPP7*-controlled genes (K-means cluster 1). Promoter stretches containing this motif may be used in yeast one hybrid screenings for novel factors. In addition, transgenic plants carrying appropriate promoter-reporter constructs could be used

as a basis for mutant screenings with the aim of identifying regulators acting on this motif.

A Myb-like transcription factor appears to be involved in the regulation of early and transient *RPP8*-controlled genes. A gene showing a similar pattern of regulation may encode a candidate factor controlling this cluster. The potential role of this factor in regulating *RPP8*-controlled genes may be examined using T-DNA insertion mutants.

Potential constitutive effects of the *RPP7*-pathway

In order to focus on genes showing multiple expression differences between Col-0 wild type plants and Hiks response mutants, all genes that showed at least four 1.8-fold expression differences across all comparisons were selected. The resulting clustergram contains the majority of *RPP7* pathway-dependent Hiks1-induced genes. Two more clusters of genes behaving consistently in all four tested Hiks1-response mutants were found. The first cluster comprises genes that show at all tested time points (including the 0 hpi time point) elevated transcript levels in Col-0 wild type plants as compared to all four mutants (Table 24; genes comprising SEQ ID NOs: 364, 288, 378, 363, 379, 219, 399, 389 and 390). In most cases, expression levels are not affected by Hiks1 infection. These elevated expression levels may be directed by constitutive (non Hiks1-triggered) signal flow via the *RPP7* pathway. This signal flow is disrupted in the *rpp7*, *edm1*, *edm2* and *edm3* mutants. Constitutive expression of these genes may be required for effective disease resistance and may be a prerequisite for induction of subsequent defense responses. A HD-ZIP transcription factor, which is included in this cluster, may act as a pre-formed regulator controlling genes responding to Hiks1-recognition. Its potential role in regulating *RPP7* pathway-dependent genes may be examined using T-DNA insertion mutants.

Table 24

The *RPP7* pathway constitutively activates a cluster of genes including a HD-ZIP transcription factor

PROBE SET	DESCRIPTION
14965 at	AC002329
18635 at	AC004005
14295 s at	Z54356
17386 at	AC006264

15145 s at	D64155
20201 at	AL078470
18607 s at	U78721
20227 s at	AC007153
12761 s at	AC006577
20555 s a	AL080318

Genes of the second cluster show the opposite behavior (Table 25). Their transcript levels are elevated in all four Hiks1 response mutants as compared to Col-0 wild type plants. Hiks1-infection does also not affect their expression levels. Surprisingly, this cluster contains six genes encoding peroxidases. Since peroxidases are believed to play roles in conferring disease resistance, the biological significance of this phenomenon is obscure. Perhaps the mutant plants “realize” disruption of the *RPP7*-defense pathway and compensate for their reduced defense capacity by constitutively up-regulating some defense mechanisms. Alternatively, elevated expression of these peroxidases may be advantageous for invading *Peronospora* hyphae. Therefore, expression of these genes could be constitutively reduced by the *RPP7* pathway.

Table 25

Probe Set	Description
15982_s_at	X98190
15954_at	U72155
12333_at	AJ286345
19594_i_at	X98321
15969_s_at	AJ133036
16462_s_at	AC004683
16461_i_at	AC004683
12324_i_at	AC007212
12778_r_at	AC006577
16514_at	AL035538
17549_s_at	L37126
14028_at	AF075597
17054_s_at	AF134128

Predictions about *RPP7*-pathway hierarchy

Clustering of the Hiks1-infection data in the “treatment” dimension, instead of the “gene” dimension, revealed that at all three infection time points, gene expression profiles of the *rpp7* mutant resemble most those of the *edm1* mutant. Similarly, expression profiles of the *edm2* mutant resemble those of the

edm3 mutant. This may indicate that RPP7 and EDM1 closely act together at a certain level in the *RPP7* signalling cascade, whereas EDM2 and EDM3 may act closely together at a different level of the pathway. Close interaction of RPP7 and EDM1 is also suggested by a T-DNA tagged *rpp7* mutant that

5 phenotypically resembles the *edm1* mutant. In contrast to *rpp7*, *edm2* and *edm3*, which appear only to be compromised in resistance against the *Peronospora* isolate Hiks1, *edm1* is also compromised in resistance to other *Peronospora* isolates that are avirulent on Col-0 plants. Like *edm1*, the putatively T-DNA tagged *rpp7* mutant is also susceptible to a variety of normally Col-0

10 incompatible *Peronospora* isolates. This observation may indicate that the EDM1 protein requires a portion of the RPP7 protein for proper function, which is disrupted in the T- DNA tagged *rpp7* mutant. Assuming that RPP7, which appears to constitute an NBS-LRR receptor, acts at the top of the Hiks1 recognition pathway hierarchy, EDM1 could act at a high level as well and

15 EDM2 and EDM3 may act more downstream in the cascade.

Table 26



Table 27 shows the plant and fungal orthologs of the *Arabidopsis* sequences identified herein.

Table 27

Query= AIG1_s_at 12879_s_at/id_source genbank /description gb aac49282.1 (u40856) aig1 [arabidopsis thaliana] /blast_score 1.00e-150	
5	(1381 letters)
Database: plantfungal 661,018 sequences; 426,114,510 total letters	
10	Searching.....done
<div>Score E</div> <div>Sequences producing significant alignments: (bits) Value</div>	
15	gb U64925 NTU64925 Nicotiana tabacum geranylgeranylated protein ... 260 1e-68 emb AW625701 AW625701 EST319608 tomato radicle, 5 d post-imbibit... 228 6e-59 emb AW720227 AW720227 LjNEST17c4r Lotus japonicus nodule library... 219 4e-56 emb AW220184 AW220184 EST302667 tomato root during/after fruit s... 208 7e-53 emb AI774580 AI774580 EST255680 tomato resistant, Cornell Lycopersicon... 173 2e-42
20	emb AW685484 AW685484 NF030E02NR1F1000 Nodulated root Medicago t... 171 2e-41 emb AI443867 AI443867 sa44d09.y1 Gm-cl004 Glycine max cDNA clone... 170 3e-41 emb AW397252 AW397252 sg76f06.y1 Gm-cl007 Glycine max cDNA clone... 168 1e-40 emb AW033368 AW033368 EST276939 tomato callus, TAMU Lycopersicon... 162 5e-39 emb AV417858 AV417858 AV417858 Lotus japonicus young plants (two... 153 4e-36
25	emb AI780050 AI780050 EST260929 tomato susceptible, Cornell Lyco... 138 9e-32 emb AW039095 AW039095 EST281068 tomato mixed elicitor, BTI Lycopersicon... 111 2e-23 emb AI780139 AI780139 EST261018 tomato susceptible, Cornell Lyco... 86 7e-16 emb AW164180 AW164180 Ljirmp21-672-c8 Ljirmp Lambda HybriZap ... 84 2e-15 emb AI781596 AI781596 EST262475 tomato susceptible, Cornell Lyco... 75 1e-12
30	emb AW774764 AW774764 EST333915 KV3 Medicago truncatula cDNA clo... 62 7e-09 emb AW348781 AW348781 GM210003A22H11R Gm-r1021 Glycine max cDNA ... 54 2e-06 emb AI491210 AI491210 EST241919 tomato shoot, Cornell Lycopersicon... 29 0.010 emb AW651526 AW651526 EST329980 tomato germinating seedlings, TA... 29 0.011 emb AW220594 AW220594 EST296979 tomato fruit mature green, TAMU ... 29 0.011
35	emb AW926585 AW926585 HVSMEg0007J19 Hordeum vulgare pre-anthesis... 29 0.025 emb AW032321 AW032321 EST275775 tomato callus, TAMU Lycopersicon... 28 0.026 emb AW736598 AW736598 EST333090 KV3 Medicago truncatula cDNA clo... 37 0.39 emb AW736597 AW736597 EST333089 KV3 Medicago truncatula cDNA clo... 37 0.39 emb AW713727 AW713727 h1f12ne.fl Neurospora crassa evening cDNA ... 35 1.0
40	emb AW711542 AW711542 f3g07ne.fl Neurospora crassa evening cDNA ... 35 1.0 emb AB009972 AB009972 Aspergillus oryzae gene for beta-1,4-xylos... 35 1.0 emb AW713709 AW713709 h1e09ne.fl Neurospora crassa evening cDNA ... 35 1.0 emb AW712721 AW712721 g3a07ne.fl Neurospora crassa evening cDNA ... 35 1.0 emb AW709185 AW709185 d3e02ne.fl Neurospora crassa evening cDNA ... 35 1.0
45	emb Y09354 SPABC1 S.pombe ABC1 gene. 35 1.4 emb Z99262 SPAC9E9 S.pombe chromosome I cosmid c9E9. 35 1.4 emb AJ225108 STA225108 Solanum tuberosum (cultivar Bintje) mitoc... 35 1.4 emb AW933326 AW933326 EST359169 tomato fruit mature green, TAMU ... 26 1.5 emb Z25870 CACDC10G C.albicans CDC10 gene for cell division cycl... 31 1.5
50	emb AC008368 AC008368 Trypanosoma brucei chromosome II clone RPC... 35 1.9 emb AQ942780 AQ942780 Sheared DNA-42B15.TR Sheared DNA Trypanoso... 35 1.9 emb AQ953508 AQ953508 Sheared DNA-33G8.TR Sheared DNA Trypanosom... 35 1.9 emb AC009463 AC009463 Trypanosoma brucei chromosome II clone RPC... 35 1.9 emb AQ950237 AQ950237 Sheared DNA-39C11.TF Sheared DNA Trypanoso... 35 1.9
55	emb AQ643883 AQ643883 RPCI93-DpnII-26C13.TV RPCI93-DpnII Trypano... 35 1.9 emb AQ948491 AQ948491 Sheared DNA-49H2.TF Sheared DNA Trypanosom... 35 1.9 emb AW727289 AW727289 GA__Ea0011H24 Gossypium arboreum 7-10 dpa ... 35 1.9 emb AW729536 AW729536 GA__Ea0025E24 Gossypium arboreum 7-10 dpa ... 35 1.9 gb L36856 PEAIAP34A Pisum sativum GTP-binding protein (IAP34) mR... 28 2.1
60	emb Z28341 PSCLOEP P.sativum (miranda) mRNA for chloroplast oute... 28 2.1

emb|AW776020|AW776020 EST335085 DSIL Medicago truncatula cDNA cl... 28 2.2
 emb|AW685649|AW685649 NF032G04NR1F1000 Nodulated root Medicago t... 28 2.2
 emb|AW690755|AW690755 NF037H10ST1F1000 Developing stem Medicago ... 28 2.2
 emb|AW256896|AW256896 EST305033 KV2 Medicago truncatula cDNA clo... 28 2.3
 5 emb|AV422565|AV422565 AV422565 Lotus japonicus young plants (two... 28 2.3
 emb|AW832303|AW832303 sm07c04.y1 Gm-cl027 Glycine max cDNA clone... 27 2.3
 emb|AL136538|SPAC30 S.pombe chromosome I cosmid c30. 34 2.6
 emb|AI724721|AI724721 RHIZ1_26_C05.y2_A001 Rhizome1 Sorghum hale... 34 2.6
 emb|AW256609|AW256609 EST304746 KV2 Medicago truncatula cDNA clo... 34 2.6
 10 emb|AI775696|AI775696 EST256796 tomato resistant, Cornell Lycopen... 28 3.1
 emb|Z71682|SCYNR067C S.cerevisiae chromosome XIV reading frame O... 34 3.6
 emb|AI776315|AI776315 EST257415 tomato resistant, Cornell Lycopen... 34 3.6
 emb|AF230371|AF230371 Lycopersicon esculentum allene oxide synth... 34 3.6
 emb|AA741645|AA741645 LmLv39p3/255A Leishmania major promastigot... 34 3.6
 15 gb|U08843|PPU08843 Porphyra purpurea putative polysaccharide bin... 34 3.6
 emb|AF124792|AF124792 Sporothrix schenckii protein kinase C (PCK... 29 4.7
 emb|AQ399149|AQ399149 mgxb0019C01fCUGI Rice Blast BAC Library P... 33 5.0
 emb|AW615911|AW615911 EST325409 tomato flower buds 0-3 mm, Corne... 33 5.0
 emb|AW035453|AW035453 EST281191 tomato callus, TAMU Lycopersicon... 33 5.0
 20 emb|AF051695|AF051695 Trypanosoma cruzi sialidase homolog (P85.1... 33 5.0
 emb|Z37538|LTGRR4-L.tarentolae mRNA encoding putative NADH subun... 28 5.5
 emb|X85021|SCXLTORFS S.cerevisiae DNA from left arm of chromosom... 33 6.8
 gb|L25088|YSCMEF2MIT Saccharomyces cerevisiae nuclear-encoded mi... 33 6.8
 emb|AQ443826|AQ443826 GSSTc01287 Trypanosoma cruzi random genom... 33 6.8
 25 emb|AQ502942|AQ502942 V47H4 mTn-3xHA/lacZ Insertion Library Sacc... 33 6.8
 emb|Z85962|MSZ85962 Musa sp. DNA for sequence tagged microsatell... 33 6.8
 emb|Z49377|SCYJL102W S.cerevisiae chromosome X reading frame ORF... 33 6.8
 emb|AW224537|AW224537 EST302980 tomato root, plants pre-anthesis... 31 7.5
 emb|AW257183|AW257183 EST305320 KV2 Medicago truncatula cDNA clo... 32 9.4
 30 emb|AQ642922|AQ642922 RPCI93-DpnII-27E7.TV RPCI93-DpnII Trypanos... 32 9.4
 emb|AW738509|AW738509 EST339936 tomato flower buds, anthesis, Co... 32 9.4
 emb|AW217351|AW217351 EST296174 tomato flower buds 0-3 mm, Corne... 32 9.4
 emb|AW219255|AW219255 EST301737 tomato root during/after fruit s... 32 9.4
 emb|AC007865|AC007865 Trypanosoma brucei chromosome II clone RPC... 32 9.4
 35 emb|AW684118|AW684118 NF012F02NR1F1000 Nodulated root Medicago t... 32 9.4
 emb|AW622239|AW622239 EST313037 tomato root during/after fruit s... 32 9.4
 emb|AQ651543|AQ651543 Sheared DNA-7C22.TF Sheared DNA Trypanosom... 32 9.4
 emb|Y11565|NC11565 N.crassa acu-15 gene. 32 9.4
 emb|AW775944|AW775944 EST335009 DSIL Medicago truncatula cDNA cl... 32 9.4
 40 emb|AB014493|AB014493 Gibberella zeae gene for reductase, partia... 32 9.4

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 gb|aaa32738.1| (m92353) anthranilate synthase alpha subunit
 45 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link /ncgi
 (1788 letters)

Database: plantfungal
 50 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 55 Sequences producing significant alignments: (bits) Value
 gb|L34344|RTAANTSYNB Ruta graveolens anthranilate synthase alpha... 772 0.0
 gb|L34343|RTAANTSYNB Ruta graveolens anthranilate synthase alpha... 467 0.0
 emb|AF079168|AF079168 Nicotiana tabacum feedback-insensitive ant... 365 0.0
 60 emb|AW931942|AW931942 EST357785 tomato fruit mature green, TAMU ... 356 3e-97
 emb|AW218352|AW218352 EST303535 tomato radicle, 5 d post-imbibit... 210 1e-73

	emb AL031966 SPCC1442 <i>S.pombe</i> chromosome III cosmid c1442.	209	6e-69
	emb AW651095 AW651095 EST329549 tomato germinating seedlings, TA...	222	2e-64
	dbj D89256 D89256 <i>Schizosaccharomyces pombe</i> mRNA, partial cds, c...	205	5e-64
	emb AW982499 AW982499 HVSMEg0003G22f <i>Hordeum vulgare</i> pre-anthesi...	215	2e-58
5	emb AW460005 AW460005 si07d11.y1 <i>Gm-c1029</i> Glycine max cDNA clone...	116	1e-57
	gb U18839 SCE9747 <i>Saccharomyces cerevisiae</i> chromosome V cosmids ...	123	4e-48
	emb X68327 SCTRP2 <i>S.cerevisiae</i> TRP2 gene for anthranilate syntha...	123	4e-48
	emb AW719463 AW719463 LjNEST5b1r <i>Lotus japonicus</i> nodule library,...	184	1e-45
	emb AI736775 AI736775 sb33d01.y1 <i>Gm-c1012</i> Glycine max cDNA clone...	104	2e-40
10	gb K01388 YSCTRP2 Yeast (<i>S.cerevisiae</i>) TRP2 gene coding for anth...	122	4e-38
	emb AL032684 SPBP8B7 <i>S.pombe</i> chromosome II pl p8B7.	95	6e-25
	emb AW509018 AW509018 si39b01.y1 <i>Gm-r1030</i> Glycine max cDNA clone...	113	5e-24
	gb T14852 T14852 crs299 lambdaZAPST <i>Ricinus communis</i> cDNA clone ...	107	2e-22
	emb AW223881 AW223881 EST300692 tomato fruit red ripe, TAMU Lyco...	103	4e-21
15	emb AF119554 AF119554 <i>Plasmodium falciparum</i> para-aminobenzoic ac...	67	6e-10
	emb AL111470 CNS019CM <i>Botrytis cinerea</i> strain T4 cDNA library un...	45	2e-05
	emb AI329873 AI329873 b9g02ne.r1 <i>Neurospora crassa</i> evening cDNA ...	48	3e-04
	emb AW224247 AW224247 EST300974 tomato fruit red ripe, TAMU Lyco...	46	7e-04
	emb AF149719 AF149719 <i>Aspergillus fumigatus</i> para aminobenzoic ac...	42	0.012
20	emb AQ448372 AQ448372 mgxb0020C12f CUGI Rice Blast BAC Library P...	39	0.15
	emb AQ324360 AQ324360 mgxb0018K01r CUGI Rice Blast BAC Library P...	39	0.15
	emb AQ160089 AQ160089 mgxb0003G09r CUGI Rice Blast BAC Library P...	39	0.15
	emb AW599019 AW599019 gb01b03.y1 Moss EST library PPN Physcomitr...	37	0.38
	emb AW599000 AW599000 ga99h03.y1 Moss EST library PPN Physcomitr...	37	0.38
25	emb AW678847 AW678847 WS1_1_A04.g1_A002 Water-stressed 1 (WS1) S...	35	0.88
	emb AW680390 AW680390 WS1_52_D12.g1_A002 Water-stressed 1 (WS1) ...	35	0.89
	emb AW678385 AW678385 WS1_15_H06.g1_A002 Water-stressed 1 (WS1) ...	35	0.89
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35	emb AW744836 AW744836 LG1_384_E07.g1_A002 Light Grown 1 (LG1) So...	35	0.90
	emb AW746170 AW746170 WS1_39_B05.g1_A002 Water-stressed 1 (WS1) ...	35	0.90
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	emb AQ648582 AQ648582 RPCI93-EcoRI-1M22.TP RPCI93-EcoRI Trypanos...	36	0.99
	emb AQ643551 AQ643551 RPCI93-EcoRI-3I24.TJ RPCI93-EcoRI Trypanos...	36	0.99
40	emb AI443370 AI443370 sa31b05.x1 <i>Gm-c1004</i> Glycine max cDNA clone...	35	1.4
	emb AW101313 AW101313 sd77d08.y1 <i>Gm-c1009</i> Glycine max cDNA clone...	35	1.4
	emb AW678030 AW678030 WS1_12_B10.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
	emb AW349006 AW349006 GM210004A12H10R <i>Gm-r1021</i> Glycine max cDNA ...	35	1.4
	emb AW309961 AW309961 sf27b12.x1 <i>Gm-c1028</i> Glycine max cDNA clone...	35	1.4
45	emb AW678582 AW678582 WS1_16_E09.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
	emb AW317198 AW317198 sf38f03.x1 <i>Gm-c1028</i> Glycine max cDNA clone...	35	1.4
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	emb AW680905 AW680905 WS1_8_A08.b1_A002 Water-stressed 1 (WS1) S...	35	1.4
	emb AW679666 AW679666 WS1_30_B11.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
50	emb AL031746 PFMAL1P3 <i>Plasmodium falciparum</i> MAL1P3, complete seq...	35	1.9
	emb AI959816 AI959816 sc94f02.y1 <i>Gm-c1019</i> Glycine max cDNA clone...	35	1.9
	emb AW924277 AW924277 WS1_52_D12.b1_A002 Water-stressed 1 (WS1) ...	35	1.9
	gb J03998 PFAGAR <i>Plasmodium falciparum</i> glutamic acid-rich protei...	35	1.9
	emb AW696796 AW696796 NF109A07ST1F1052 Developing stem <i>Medicago</i> ...	35	1.9
55	emb AW396753 AW396753 sf37c11.x1 <i>Gm-c1028</i> Glycine max cDNA clone...	35	2.6
	gb M98871 SOYCHS7A Glycine max chalcone synthase (chs7) gene, co...	35	2.6
	emb AI460797 AI460797 sa69d02.y1 <i>Gm-c1004</i> Glycine max cDNA clone...	35	2.6
	emb AW348617 AW348617 GM210002B22G1R <i>Gm-r1021</i> Glycine max cDNA 3...	35	2.6
	emb AW310362 AW310362 sf35a09.x1 <i>Gm-c1028</i> Glycine max cDNA clone...	35	2.6
60	emb AI437832 AI437832 sa40c07.y1 <i>Gm-c1004</i> Glycine max cDNA clone...	35	2.6
	gb BE023927 BE023927 sm94c05.y1 <i>Gm-c1015</i> Glycine max cDNA clone ...	35	2.6

emb|AW424189|AW424189 sh62b04.y1 Gm-c1015 Glycine max cDNA clone... 35 2.6
 emb|AW101907|AW101907 sd72d01.y1 Gm-c1008 Glycine max cDNA clone... 35 2.6
 emb|AW102370|AW102370 sd86h01.y1 Gm-c1009 Glycine max cDNA clone... 35 2.6
 emb|AW309356|AW309356 sf16d02.x1 Gm-c1028 Glycine max cDNA clone... 35 2.6
 5 emb|AL355932|NCB5022 Neurospora crassa DNA linkage group II BAC ... 34 3.5
 emb|AQ652663|AQ652663 Sheared DNA-20A9.TR Sheared DNA Trypanosom... 34 3.5
 emb|Z98056|SPAC5D6 S.pombe chromosome I cosmid c5D6. 34 3.5
 emb|AW348286|AW348286 GM210001B23B6R Gm-r1021 Glycine max cDNA 3... 34 4.9
 emb|AB018422|AB018422 Pisum sativum mRNA for DNA binding zinc fi... 34 4.9
 10 emb|AW734949|AW734949 sk93b10.y1 Gm-c1035 Glycine max cDNA clone... 34 4.9
 emb|AW679089|AW679089 WS1_22_A07.g1_A002 Water-stressed 1 (WS1) ... 34 4.9
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 gb|M36941|BLYHORDCA Hordeum vulgare C-hordein gene, complete cds. 29 5.3
 gb|BE034677|BE034677 ML01H08 ML Mesembryanthemum crystallinum cD... 33 6.7
 15 emb|Z26877|SCDCHR11 S.cerevisiae (S288C) 36.2kb DNA fragment fro... 33 6.7
 emb|AW267708|AW267708 EST305836 DSIR Medicago truncatula cDNA cl... 33 6.7
 emb|Z28162|SCYKL162C S.cerevisiae chromosome XI reading frame OR... 33 6.7
 emb|AW980990|AW980990 EST392143 GVN Medicago truncatula cDNA clo... 33 6.7
 gb|BE037412|BE037412 MP20G03 MP Mesembryanthemum crystallinum cD... 33 6.7
 20 emb|Z28161|SCYKL161C S.cerevisiae chromosome XI reading frame OR... 33 6.7
 emb|AI726247|AI726247 BNLGHi5399 Six-day Cotton fiber Gossypium ... 33 6.7
 emb|AE001401|AE001401 Plasmodium falciparum chromosome 2, sectio... 33 6.7
 emb|AW573801|AW573801 EST316392 GVN Medicago truncatula cDNA clo... 33 6.7
 emb|Z98547|PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque... 33 9.2
 25 emb|AQ659747|AQ659747 Sheared DNA-16J5.TR Sheared DNA Trypanosom... 33 9.2
 gb|BE021269|BE021269 sm56h04.y1 Gm-c1028 Glycine max cDNA clone ... 33 9.2
 emb|AW222457|AW222457 EST299268 tomato fruit red ripe, TAMU Lyco... 33 9.2
 emb|AB012116|AB012116 Vigna mungo UFGlyT mRNA for UDP-glycose:fl... 33 9.2
 emb|AW725836|AW725836 GA__Ea0019N24 Gossypium arboreum 7-10 dpa ... 33 9.2
 30 emb|AQ324451|AQ324451 mgxb0018L23r CUGI Rice Blast BAC Library P... 33 9.2
 gb|M73492|LEIHSP90 Leishmania donovani heat shock protein 90 mRN... 33 9.2
 emb|AW132634|AW132634 se06h07.y1 Gm-c1013 Glycine max cDNA clone... 33 9.2
 emb|AI166186|AI166186 a032p32u Hybrid aspen plasmid library Popu... 33 9.2
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 gb|aac63850.1| (u73786) acc synthase [arabidopsis thaliana]
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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|atacs6|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|atacs6|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|atacs6|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?atacs6>
 (1567 letters)

45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

50

	Score	E	
Sequences producing significant alignments:		(bits)	Value
emb X82273 BOACCS B.oleracea mRNA for ACC synthase.	944	0.0	
55 emb X72676 BJMACC B. juncea mRNA for 1-Aminocyclopropane-1-carbo...	833	0.0	
emb AB034992 AB034992 Malus domestica MdACS-5A mRNA for 1-aminoc...	725	0.0	
emb AF057563 AF057563 Nicotiana glutinosa 1-aminocyclopropane-1-...	729	0.0	
emb AJ005002 NTAJ5002 Nicotiana tabacum mRNA for 1-aminocyclopro...	726	0.0	
emb AB034993 AB034993 Malus domestica MdACS-5B mRNA for 1-aminoc...	723	0.0	
60 gb U72389 LEU72389 Lycopersicon esculentum 1-aminocyclopropane-1...	724	0.0	
gb U72390 LEU72390 Lycopersicon esculentum 1-aminocyclopropane-1...	720	0.0	

	gb U68216 CPU68216	Carica papaya ACC synthase mRNA, complete cds.	435	0.0
	emb AB033503 AB033503	Populus euramericana peacs-2 mRNA for 1-am...	713	0.0
	emb AF061605 AF061605	Nicotiana glutinosa ACC synthase mRNA, com...	712	0.0
	emb AJ012551 CSI012551	Citrus sinensis mRNA for ACC synthase.	420	0.0
5	emb AB033502 AB033502	Populus euphratica peacs-1 mRNA for 1-amin...	591	0.0
	emb AB013100 AB013100	Lycopersicon esculentum LE-ACS6 mRNA for 1...	706	0.0
	emb AB013346 AB013346	Lycopersicon esculentum mRNA for 1-aminocy...	704	0.0
	gb U88971 PHU88971	Pelargonium hortorum 1-aminocyclopropane-1-ca...	423	0.0
	emb Z11613 VRACCSYNM	V.radiata mRNA for ACC synthase.	428	0.0
10	emb X98492 NTACCS	Nicotiana tabacum mRNA for ACC-synthase (clone...	425	0.0
	emb X67100 GMCACCS1	G.max mRNA for ACC synthase.	429	0.0
	emb AJ012696 CSI012696	Citrus sinensis mRNA for ACC synthase (AC...	422	0.0
	emb Z18953 PHAMCRBSY	P.hybrida mRNA for 1-aminocyclopropane 1-ca...	424	0.0
	emb AJ011095 CSI011095	Citrus sinensis mRNA for ACC synthase (ac...	424	0.0
15	emb Z18952 DCAMCRBSY	D.caryophyllus mRNA for 1-aminocyclopropane...	686	0.0
	emb AB006804 AB006804	Cucumis sativus CS-ACS2 mRNA for ACC synth...	423	0.0
	emb AF080258 AF080258	Musa acuminata 1-aminocyclopropane-1-carbo...	680	0.0
	emb AF016459 AF016459	Pisum sativum 1-aminocyclopropane-1-carbox...	415	0.0
	dbj D30805 CUS1A1CS	Melon mRNA for 1-aminocyclopropane-1-carboxy...	678	0.0
20	emb X65982 NTXACCSYN	N.tabacum mRNA for 1-aminocyclopropane-1-ca...	417	0.0
	emb AF109927 AF109927	Musa acuminata 1-aminocyclopropane-1-carbo...	676	0.0
	emb AB006803 AB006803	Cucumis sativus CS-ACS1 mRNA for ACC synth...	676	0.0
	gb U17231 PHU17231	Pelargonium hortorum clone pGAC-2 1-aminocycl...	423	0.0
	emb AB021906 AB021906	Musa acuminata MA-ACS1 mRNA for ACC syntha...	671	0.0
25	emb AF129508 AF129508	Musa acuminata 1-aminocyclopropane-1-carbo...	671	0.0
	emb AB015625 AB015625	Pyrus pyrifolia pPPACS3 mRNA for 1-aminocy...	393	0.0
	emb AB031026 AB031026	Prunus mume PM-ACS1 mRNA for ACC synthase,...	405	0.0
	emb Y11357 CP1A1CS	C.papaya mRNA for 1-aminocyclopropane-1-carbo...	404	0.0
	dbj D01032 CUCACCW	Cucurbita maxima mRNA for 1-aminocyclopropane...	666	0.0
30	dbj E03724 E03724	cDNA encoding detriment induced type 1-aminocy...	666	0.0
	emb X62536 LEACC	L.esculentum mRNA for ACC synthase.	327	0.0
	gb L20634 POTACCSYN	Solanum tuberosum 1-aminocyclopropane-1-carb...	403	0.0
	emb X59145 LEACC2MR	Lycopersicon esculentum LE-ASCC2 mRNA (ptACC...	326	0.0
	gb M58323 CUCACCSYN	Cucurbita pepo 1-aminocyclopropane-1-carboxy...	663	0.0
35	emb AF057562 AF057562	Nicotiana glutinosa 1-aminocyclopropane-1-...	412	0.0
	emb AF239987 AF239987	Prunus persica ACC synthase ACS1 mRNA, par...	662	0.0
	gb M34289 TOMACS	Tomato 1-aminocyclopropane-1-carboxylate syntha...	327	0.0
	gb M63490 TOMACCS	Tomato 1-aminocyclopropane-1-carboxylate synth...	657	0.0
	emb X59146 LEACC4MR	Lycopersicon esculentum LE-ACC4 mRNA (ptACC4...	656	0.0
40	emb Y15739 MAACSYNTH	Musa acuminata mRNA for 1-aminocyclopropane...	655	0.0
	gb U79999 MAU79999	Musa acuminata ACC synthase (acs3) mRNA, comp...	655	0.0
	emb AF178076 AF178076	Carica papaya 1-aminocyclopropane-1-carbox...	395	0.0
	gb U17229 PHU17229	Pelargonium hortorum clone pGAC-1 1-aminocycl...	407	0.0
	emb X82265 CAACC1	C.anuum mRNA for 1-aminocyclopropane-1-carboxyl...	639	0.0
45	gb U70842 STU70842	Solanum tuberosum 1-aminocyclopropane-1-carbo...	637	0.0
	emb AF144746 AF144746	Solanum melongena 1-aminocyclopropane-1-ca...	636	0.0
	emb AJ276295 CSI276295	Citrus sinensis partial mRNA for ACC synt...	418	0.0
	emb AJ012577 CPA012577	Carica papaya mRNA for 1-aminocyclopropan...	387	e-180
	emb AF038945 AF038945	Rumex palustris 1-aminocyclopropane-1-carb...	372	e-179
50	gb U73815 MDU73815	Malus domestica ACC synthase (MdACS-2) mRNA, ...	623	e-178
	dbj D37937 D37937	Cucumis melo mRNA for 1-aminocyclopropane-1-ca...	380	e-177
	emb Z11562 VRACCSYN	V.radiata mRNA for 1-aminocyclopropane-1-car...	375	e-176
	emb AF177769 AF177769	Carica papaya 1-aminocyclopropane-1-carbox...	369	e-175
	emb AF083814 AF083814	Antirrhinum majus ACC synthase 1 (ACS1) mR...	605	e-172
55	emb AF178077 AF178077	Carica papaya 1-aminocyclopropane-1-carbox...	316	e-171
	emb AF239989 AF239989	Prunus persica ACC synthase ACS25 mRNA, pa...	597	e-170
	gb U22523 MIU22523	Mangifera indica 1-aminocyclopropane-carboxyl...	359	e-169
	emb X66605 DCACCS	D.caryophyllus mRNA for 1-aminocyclopropane-1-...	396	e-168
	emb AF049137 AF049137	Dianthus caryophyllus 1-aminocyclopropane-...	338	e-167
60	emb AF170705 AF170705	Mangifera indica 1-aminocyclopropane-1-car...	290	e-167
	emb AJ277160 CPA277160	Carica papaya partial paccs1A gene for 1-...	266	e-165

emb|AB015624|AB015624 Pyrus pyrifolia mRNA for 1-aminocyclopropa... 359 e-163
 gb|U03294|MSU03294 Malus sylvestris 1-aminocyclopropane-1-carbox... 359 e-163
 gb|L31347|MAUACCSYN Malus domestica 1-aminocyclopropane-1-carbox... 357 e-162
 emb|AB015495|AB015495 Passiflora edulis PE-ACS2 mRNA for ACC syn... 368 e-162
 5 emb|Z77854|PSPACS1 Phalaenopsis species mRNA for 1-aminocyclopro... 514 e-161
 dbj|D01033|CUCACCA Cucurbita maxima mRNA for 1-aminocyclopropane... 349 e-159
 emb|X87112|PCPCACS1G P.communis mRNA for 1-aminocyclopropane-1-c... 346 e-159
 emb|AB007449|AB007449 Actinidia deliciosa mRNA for 1-aminocyclop... 336 e-159
 gb|U73816|MDU73816 Malus domestica ACC synthase (MdACS-3) mRNA, ... 504 e-158
 10 gb|U17972|LEU17972 Lycopersicon esculentum 1-aminocyclopropane-1... 343 e-157
 emb|AB007639|AB007639 Pyrus pyrifolia mRNA for 1-aminocyclopropa... 502 e-157
 gb|M66619|DINCARACC D.caryophyllus 1-aminocyclopropane-1-carboxy... 495 e-156
 emb|AB006805|AB006805 Cucumis sativus CS-ACS3 mRNA for ACC synth... 342 e-156
 gb|U34987|VRU34987 Vigna radiata 1-aminocyclopropane-1-carboxyli... 305 e-151
 15 emb|AB000679|AB000679 Vigna radiata mRNA for 1-aminocyclopropane... 340 e-151
 gb|U34986|VRU34986 Vigna radiata 1-aminocyclopropane-1-carboxyli... 340 e-149
 gb|U64031|DCU64031 Dendrobium crumenatum ACC synthase gene, comp... 259 e-149
 emb|AF016458|AF016458 Pisum sativum 1-aminocyclopropane-1-carbox... 336 e-148
 emb|Z27233|STACCAS1 S.tuberosum (STAC1) gene for amino cycloprop... 238 e-147
 20 emb|Z27234|STACCAS2 S.tuberosum STACS2 gene for 1-Aminocycloprop... 234 e-146
 gb|U37774|CMU37774 Cucurbita maxima 1-aminocyclopropane-1-carbox... 235 e-145
 emb|AF043122|AF043122 Lycopersicon esculentum ACC synthase (LE-A... 237 e-145
 emb|Z12135|VRACCSYN4 V.radiata gene for ACC synthase (pMAC-4). 376 e-145
 gb|L34171|TOMACS3A Lycopersicon esculentum 1-aminocyclopropane-1... 236 e-143
 25 gb|U18055|LEU18055 Lycopersicon esculentum 1-aminocyclopropane-1... 236 e-143
 emb|AF074927|AF074927 Sinapis arvensis 1-aminocyclopropane-1-car... 330 e-142
 emb|AF083815|AF083815 Antirrhinum majus ACC synthase 2 (ACS2) mR... 482 e-141
 emb|AF151961|AF151961 Vigna radiata 1-aminocyclopropane-1-carbox... 234 e-141
 emb|AB021907|AB021907 Musa acuminata MA-ACS2 mRNA for ACC syntha... 310 e-140
 30 gb|L07883|DORAMICARB Moth orchid 1-aminocyclopropane-1-carboxyla... 243 e-139
 emb|AB021908|AB021908 Musa acuminata MA-ACS3 mRNA for ACC syntha... 298 e-138

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40 Database: plantfungal
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Searching.....done

45 Score E
 Sequences producing significant alignments: (bits) Value

emb|X82273|BOACCS B.oleracea mRNA for ACC synthase. 944 0.0
 emb|X72676|BJMACC B. juncea mRNA for 1-Aminocyclopropane-1-carbo... 833 0.0
 50 emb|AB034992|AB034992 Malus domestica MdACS-5A mRNA for 1-aminoc... 725 0.0
 emb|AF057563|AF057563 Nicotiana glutinosa 1-aminocyclopropane-1-... 729 0.0
 emb|AJ005002|NTAJ5002 Nicotiana tabacum mRNA for 1-aminocyclopro... 726 0.0
 emb|AB034993|AB034993 Malus domestica MdACS-5B mRNA for 1-aminoc... 723 0.0
 gb|U72389|LEU72389 Lycopersicon esculentum 1-aminocyclopropane-1... 724 0.0
 55 gb|U72390|LEU72390 Lycopersicon esculentum 1-aminocyclopropane-1... 720 0.0
 gb|U68216|CPU68216 Carica papaya ACC synthase mRNA, complete cds. 435 0.0
 emb|AB033503|AB033503 Populus euramericana peacs-2 mRNA for 1-am... 713 0.0
 emb|AF061605|AF061605 Nicotiana glutinosa ACC synthase mRNA, com... 712 0.0
 emb|AJ012551|CSI012551 Citrus sinensis mRNA for ACC synthase. 420 0.0
 60 emb|AB033502|AB033502 Populus euphratica peacs-1 mRNA for 1-amin... 591 0.0
 emb|AB013100|AB013100 Lycopersicon esculentum LE-ACS6 mRNA for 1... 706 0.0

	emb AB013346 AB013346 <i>Lycopersicon esculentum</i> mRNA for 1-aminocy...	704	0.0
	gb U88971 PHU88971 <i>Pelargonium hortorum</i> 1-aminocyclopropane-1-ca...	423	0.0
	emb Z11613 VRACCSYNM <i>V.radiata</i> mRNA for ACC synthase.	428	0.0
	emb X98492 NTACCS <i>Nicotiana tabacum</i> mRNA for ACC-synthase (clone...	425	0.0
5	emb X67100 GMCACCS1 <i>G.max</i> mRNA for ACC synthase.	429	0.0
	emb AJ012696 CSI012696 <i>Citrus sinensis</i> mRNA for ACC synthase (AC...	422	0.0
	emb Z18953 PHAMCRBSY <i>P.hybrida</i> mRNA for 1-aminocyclopropane 1-ca...	424	0.0
	emb AJ011095 CSI011095 <i>Citrus sinensis</i> mRNA for ACC synthase (ac...	424	0.0
	emb Z18952 DCAMCRBSY <i>D.caryophyllus</i> mRNA for 1-aminocyclopropane...	686	0.0
10	emb AB006804 AB006804 <i>Cucumis sativus</i> CS-ACS2 mRNA for ACC synth...	423	0.0
	emb AF080258 AF080258 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	680	0.0
	emb AF016459 AF016459 <i>Pisum sativum</i> 1-aminocyclopropane-1-carbox...	415	0.0
	dbj D30805 CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy...	678	0.0
	emb X65982 NTXACCSYN <i>N.tabacum</i> mRNA for 1-aminocyclopropane-1-ca...	417	0.0
15	emb AF109927 AF109927 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	676	0.0
	emb AB006803 AB006803 <i>Cucumis sativus</i> CS-ACS1 mRNA for ACC synth...	676	0.0
	gb U17231 PHU17231 <i>Pelargonium hortorum</i> clone pGAC-2 1-aminocycl...	423	0.0
	emb AB021906 AB021906 <i>Musa acuminata</i> MA-ACS1 mRNA for ACC syntha...	671	0.0
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20	emb AB015625 AB015625 <i>Pyrus pyrifolia</i> pPPACS3 mRNA for 1-aminocy...	393	0.0
	emb AB031026 AB031026 <i>Prunus mume</i> PM-ACS1 mRNA for ACC synthase,...	405	0.0
	emb Y11357 CP1A1CS <i>C.papaya</i> mRNA for 1-aminocyclopropane-1-carbo...	404	0.0
	dbj D01032 CUCACCW <i>Cucurbita maxima</i> mRNA for 1-aminocyclopropane...	666	0.0
	dbj E03724 E03724 cDNA encoding detriment induced type 1-aminocy...	666	0.0
25	emb X62536 LEACC <i>L.esculentum</i> mRNA for ACC synthase.	327	0.0
	gb L20634 POTACCSYN <i>Solanum tuberosum</i> 1-aminocyclopropane-1-carb...	403	0.0
	emb X59145 LEACC2MR <i>Lycopersicon esculentum</i> LE-ASCC2 mRNA (ptACC...	326	0.0
	gb M58323 CUCACCSYN <i>Cucurbita pepo</i> 1-aminocyclopropane-1-carboxy...	663	0.0
	emb AF057562 AF057562 <i>Nicotiana glutinosa</i> 1-aminocyclopropane-1-...	412	0.0
30	emb AF239987 AF239987 <i>Prunus persica</i> ACC synthase ACS1 mRNA, par...	662	0.0
	gb M34289 TOMACS <i>Tomato</i> 1-aminocyclopropane-1-carboxylate syntha...	327	0.0
	gb M63490 TOMACCS <i>Tomato</i> 1-aminocyclopropane-1-carboxylate synth...	657	0.0
	emb X59146 LEACC4MR <i>Lycopersicon esculentum</i> LE-ACC4 mRNA (ptACC4...	656	0.0
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35	gb U79999 MAU79999 <i>Musa acuminata</i> ACC synthase (acs3) mRNA, comp...	655	0.0
	emb AF178076 AF178076 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	395	0.0
	gb U17229 PHU17229 <i>Pelargonium hortorum</i> clone pGAC-1 1-aminocycl...	407	0.0
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40	emb AF144746 AF144746 <i>Solanum melongena</i> 1-aminocyclopropane-1-ca...	636	0.0
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	emb AF038945 AF038945 <i>Rumex palustris</i> 1-aminocyclopropane-1-carb...	372	e-179
	gb U73815 MDU73815 <i>Malus domestica</i> ACC synthase (MdACS-2) mRNA, ...	623	e-178
45	dbj D37937 D37937 <i>Cucumis melo</i> mRNA for 1-aminocyclopropane-1-ca...	380	e-177
	emb Z11562 VRACCSYN <i>V.radiata</i> mRNA for 1-aminocyclopropane-1-car...	375	e-176
	emb AF177769 AF177769 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	369	e-175
	emb AF083814 AF083814 <i>Antirrhinum majus</i> ACC synthase 1 (ACS1) mR...	605	e-172
	emb AF178077 AF178077 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	316	e-171
50	emb AF239989 AF239989 <i>Prunus persica</i> ACC synthase ACS25 mRNA, pa...	597	e-170
	gb U22523 MIU22523 <i>Mangifera indica</i> 1-aminocyclopropane-carboxyl...	359	e-169
	emb X66605 DCACCS <i>D.caryophyllus</i> mRNA for 1-aminocyclopropane-1-...	396	e-168
	emb AF049137 AF049137 <i>Dianthus caryophyllus</i> 1-aminocyclopropane-...	338	e-167
	emb AF170705 AF170705 <i>Mangifera indica</i> 1-aminocyclopropane-1-car...	290	e-167
55	emb AJ277160 CPA277160 <i>Carica papaya</i> partial paccs1A gene for 1-...	266	e-165
	emb AB015624 AB015624 <i>Pyrus pyrifolia</i> mRNA for 1-aminocyclopropa...	359	e-163
	gb U03294 MSU03294 <i>Malus sylvestris</i> 1-aminocyclopropane-1-carbox...	359	e-163
	gb L31347 MAUACCSYN <i>Malus domestica</i> 1-aminocyclopropane-1-carbox...	357	e-162
	emb AB015495 AB015495 <i>Passiflora edulis</i> PE-ACS2 mRNA for ACC syn...	368	e-162
60	emb Z77854 PSPACS1 <i>Phalaenopsis species</i> mRNA for 1-aminocyclopro...	514	e-161
	dbj D01033 CUCACCA <i>Cucurbita maxima</i> mRNA for 1-aminocyclopropane...	349	e-159

- emb|X87112|PCPCACS1G *P.communis* mRNA for 1-aminocyclopropane-1-c... 346 e-159
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 5 emb|AB007639|AB007639 *Pyrus pyrifolia* mRNA for 1-aminocyclopropana... 502 e-157
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 10 gb|U34986|VRU34986 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 340 e-149
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 emb|Z27234|STACCAS2 *S.tuberosum* STACS2 gene for 1-Aminocycloprop... 234 e-146
 15 gb|U37774|CMU37774 *Cucurbita maxima* 1-aminocyclopropane-1-carbox... 235 e-145
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 emb|Z12135|VRACCSYN4 *V.radiata* gene for ACC synthase (pMAC-4). 376 e-145
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 20 emb|AF074927|AF074927 *Sinapis arvensis* 1-aminocyclopropane-1-car... 330 e-142
 emb|AF083815|AF083815 *Antirrhinum majus* ACC synthase 2 (ACS2) mR... 482 e-141
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 (921 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

40 Score E
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dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 144 7e-44
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 45 dbj|D38123|TOBBY4A *Nicotiana tabacum* mRNA for ERF1, complete cds. 134 6e-41
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 emb|AB035270|AB035270 *Matricaria chamomilla* McEREBP1 mRNA for et... 155 5e-37
 gb|U89255|LEU89255 *Lycopersicon esculentum* DNA-binding protein P... 138 3e-32
 50 emb|AI771213|AI771213 EST252409 tomato ovary, TAMU *Lycopersicon* ... 135 1e-31
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- emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 111 6e-24
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emb|AI894873|AI894873 EST264316 tomato callus, TAMU Lycopersicon... 103 2e-21
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emb|AW030009|AW030009 EST273264 tomato callus, TAMU Lycopersicon... 103 2e-21
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30 emb|AI782381|AI782381 EST263260 tomato susceptible, Cornell Lyco... 100 1e-20
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35 emb|AW443265|AW443265 EST308195 tomato mixed elicitor, BTI Lycop... 100 3e-20
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30	Database: plantfungal 661,018 sequences; 426,114,510 total letters		
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Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

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	emb AF160869 AF160869	Citrus sinensis chlorophyllase mRNA, compl...	84 4e-54
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	emb AW616099 AW616099	EST296862 L. hirsutum trichome, Cornell Un...	67 1e-29
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	emb AW596770 AW596770	sj16e05.y1 Gm-c1032 Glycine max cDNA clone...	89 9e-17
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 (2616 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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20 Database: plantfungal
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 (528 letters)

Database: plantfungal
 20 661,018 sequences; 426,114,510 total letters

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	emb AW011327 AW011327 ST19E02 Pine TriplEx shoot tip library Pin...	160 5e-39
	emb AW011046 AW011046 ST16A08 Pine TriplEx shoot tip library Pin...	160 7e-39
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	emb AW290231 AW290231 NXNV015E05F Nsf Xylem Normal wood Vertical...	159 2e-38
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60	emb AW684766 AW684766 NF021G12NR1F1000 Nodulated root Medicago t...	124 1e-37
	emb AW706540 AW706540 sj57g11.y1 Gm-cl033 Glycine max cDNA clone...	156 1e-37

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 5 emb|AW754729|AW754729 PC07B04 Pine TriplEx pollen cone library P... 154 4e-37
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 (528 letters)

15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb X89759 BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen...	194	4e-49
	emb AB010434 AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ...	192	2e-48
25	emb AW255457 AW255457 ML480 peppermint glandular trichome Mentha...	191	4e-48
	emb AW569018 AW569018 si74e02.y1 Gm-c1031 Glycine max cDNA clone...	186	1e-46
	emb AI988470 AI988470 sd02f07.y1 Gm-c1020 Glycine max cDNA clone...	186	1e-46
	emb AI161830 AI161830 A007P52U Hybrid aspen plasmid library Popu...	184	3e-46
	emb Z70677 RCTHIORXN R.communis mRNA for thioredoxin.	183	9e-46
30	gb BE053835 BE053835 GA_Ea0009P21f Gossypium arboreum 7-10 dpa ...	182	2e-45
	emb AW565750 AW565750 LG1_349_G02.g1_A002 Light Grown 1 (LG1) So...	181	3e-45
	emb AW677651 AW677651 WS1_10_F03.b1_A002 Water-stressed 1 (WS1) ...	181	3e-45
	emb AW671668 AW671668 LG1_349_G02.b1_A002 Light Grown 1 (LG1) So...	181	3e-45
	emb AW924685 AW924685 WS1_71_B11.b1_A002 Water-stressed 1 (WS1) ...	181	3e-45
35	emb AW677726 AW677726 WS1_10_F03.g1_A002 Water-stressed 1 (WS1) ...	181	3e-45
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	emb AI461219 AI461219 sa76f11.y1 Gm-c1004 Glycine max cDNA clone...	180	6e-45
	emb AI938238 AI938238 sc41e05.y1 Gm-c1014 Glycine max cDNA clone...	180	6e-45
40	emb AW164730 AW164730 se77a02.y1 Gm-c1023 Glycine max cDNA clone...	180	8e-45
	emb AJ009762 TAE9762 Triticum aestivum mRNA for thioredoxin H.	179	2e-44
	emb AW255195 AW255195 ML185 peppermint glandular trichome Mentha...	178	2e-44
	emb AI165128 AI165128 A076P57U Hybrid aspen plasmid library Popu...	177	5e-44
	gb T24347 T24347 crs1466 lambdaZAPST Ricinus communis cDNA clone...	177	5e-44
45	dbj D87984 D87984 Fagopyrum esculentum mRNA for thioredoxin, com...	177	8e-44
	gb BE054543 BE054543 GA_Ea0026K15f Gossypium arboreum 7-10 dpa ...	177	8e-44
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50	emb AW217307 AW217307 EST296026 tomato flower buds 0-3 mm, Corne...	175	2e-43
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10 emb|AI441505|AI441505 sa87c03.y1 Gm-c1004 Glycine max cDNA clone... 171 2e-42
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15 emb|AW041395|AW041395 EST284259 tomato mixed elicitor, BTI Lycop... 171 5e-42
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20 emb|AI773303|AI773303 EST254403 tomato resistant, Cornell Lycop... 171 5e-42
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(433 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

Searching.....done

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	emb X62120 BNCRU1 B.napus cru1 gene for cruciferin subunit.	169	4e-48
	gb J05233 BNACRUCA B.napus cruciferin mRNA, 3' end.	169	9e-48
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	emb X59802 RSCRUI R.sativus pAF7 mRNA for cruciferin.	165	1e-42
25	emb X59804 RSCRUI R.sativus pAC2 mRNA for cruciferin.	123	1e-41
	emb X57850 BNCRU4RN B.napus cru4 mRNA for cruciferin cru4 subunit.	138	2e-32
	emb X57848 BNCRU4RNA B.napus cru4 mRNA for cruciferin cru4 subunit.	137	6e-32
	gb M16860 BNACRUC Rapeseed cruciferin mRNA, complete cds.	132	1e-30
	emb X59294 BNC1G B.napus BnCl gene for cruciferin storage protein.	132	1e-30
30	emb X14555 BNCRUA Brassica napus cruA gene for cruciferin.	132	1e-30
	emb X57849 BNCRU23 B.napus cru2/3 mRNA for cruciferin cru2/3 sub...	132	1e-30
	emb X59807 RSCRUI R.sativus pAE10 mRNA for cruciferin.	131	3e-30
	emb X59806 RSCRUI R.sativus pBB6 mRNA for cruciferin.	131	3e-30
	emb X59295 BNC2G B.napus BnCl gene for cruciferin storage protein.	130	5e-30
35	emb X82121 AHGLOBLN A.hypochondriacus mRNA for globulin.	118	3e-26
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	emb X59803 RSCRUI R.sativus pAG4 mRNA for cruciferin.	81	3e-22
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	emb X78119 PABTPRU1 P.amygdalus, Batsch (Texas) prul mRNA.	99	2e-20
	gb T23274 T23274 crs1128 lambdaZAPST Ricinus communis cDNA clone...	98	3e-20
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	gb U43727 GHU43727 Gossypium hirsutum legumin B (LegB-C134) gene...	92	2e-18
	gb M16936 COTSPB G.hirsutum (cotton) storage protein (beta-globu...	92	2e-18
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55	emb Y16976 CAR16976 Coffea arabica mRNA for 11S storage protein.	92	3e-18
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10	emb X68648 AS12S A.sativa pseudogene for 12S seed globulin.	86 1e-16
	gb M69188 COTDGALA Cotton legumin A D-genome alloallele gene, co...	86 1e-16
	gb M16905 COTSPD G.hirsutum (cotton) storage protein (beta-globu...	86 1e-16
	emb X74741 ASGLAV3G A.sativa GLAV 3 gene for 11S globulin.	86 1e-16
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	emb AW318204 AW318204 sg62d03.y1 Gm-c1007 Glycine max cDNA clone...	84 4e-16
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	emb X02985 GMGLY1A Soybean mRNA for glycinin A1aBx precursor.	84 4e-16
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	emb AW036121 AW036121 EST274497 tomato seed, TAMU Lycopersicon e...	83 1e-15
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	emb AF180392 AF180392 Perilla frutescens legumin-like protein mR...	80 7e-15
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 (965 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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gb U20736 MSU20736 Medicago sativa S-adenosyl-L-methionine:trans...	142	2e-68
emb AW624860 AW624860 EST313689 tomato radicle, 5 d post-imbibit...	139	2e-67
emb AF022775 AF022775 Nicotiana tabacum caffeoyl-CoA 3-O-methylt...	138	2e-67
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gb M69184 PUMCCOAMT Petroselinum crispum caffeoyl-CoA 3-O-methyl...	133	2e-66
gb U27116 PTU27116 Populus tremuloides caffeoyl-CoA 3-O-methyltr...	135	3e-66
emb AJ224894 PBTAJ4894 Populus balsamifera subsp. trichocarpa mR...	135	3e-66
gb U13151 ZEU13151 Zinnia elegans S-adenosyl-L-methionine:trans-...	136	4e-66
25 emb AI489305 AI489305 EST247644 tomato ovary, TAMU Lycopersicon ...	139	4e-66
emb AJ224895 PBTAJ4895 Populus balsamifera subsp. trichocarpa mR...	136	6e-66
emb AJ224896 PBTAJ4896 Populus balsamifera subsp. trichocarpa mR...	136	6e-66
emb AF168780 AF168780 Eucalyptus globulus caffeoyl-CoA O-methylt...	133	8e-66
emb AF053553 AF053553 Mesembryanthemum crystallinum caffeoyl-CoA...	132	1e-65
30 emb AF240466 AF240466 Populus tomentosa caffeoyl-CoA O-methyltra...	135	1e-65
emb A22706 A22706 Caffeoyl-CoA-3-O-Methyltransferase gene.	129	3e-65
gb U62734 NTU62734 Nicotiana tabacum caffeoyl-CoA O-methyltransf...	134	5e-65
emb Z56282 NTCCOAOMT N.tabacum mRNA for caffeoyl-CoA O-methyltra...	132	5e-65
gb U62736 NTU62736 Nicotiana tabacum caffeoyl-CoA O-methyltransf...	136	5e-65
35 gb U38612 NTU38612 Nicotiana tabacum caffeoyl-coenzymeA O-methyl...	136	5e-65
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gb L22203 SLASADEN Stellaria longipes S-adenosyl-L-methionine:tr...	124	8e-65
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40 emb AF036095 AF036095 Pinus taeda caffeoyl-CoA O-methyltransfera...	130	6e-64
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50 emb AI486500 AI486500 EST244821 tomato ovary, TAMU Lycopersicon ...	139	2e-55
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55 emb AW278810 AW278810 sf98g06.y1 Gm-c1019 Glycine max cDNA clone...	135	3e-54
emb AI939180 AI939180 sc67h02.y1 Gm-c1016 Glycine max cDNA clone...	125	3e-54
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 10 emb|AW424002|AW424002 sh59c10.y1 Gm-c1015 Glycine max cDNA clone... 115 2e-51
 emb|AW707192|AW707192 sk22a02.y1 Gm-c1028 Glycine max cDNA clone... 132 3e-50
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 emb|AW648499|AW648499 EST326953 tomato germinating seedlings, TA... 99 7e-50
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 20 emb|AA660318|AA660318 00189 MtrHE Medicago truncatula cDNA 5' si... 144 2e-47
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 25 emb|AI775483|AI775483 EST256583 tomato resistant, Cornell Lycope... 139 2e-46
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 30 emb|AW625126|AW625126 EST313943 tomato radicle, 5 d post-imbibit... 133 6e-45
 emb|AI974778|AI974778 T113251e KV2 Medicago truncatula cDNA clon... 142 6e-45
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 35 emb|AI166314|AI166314 xylem.est.159 Poplar xylem Lambda ZAPII li... 136 4e-44
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 40 emb|AW831448|AW831448 sm23c03.y1 Gm-c1028 Glycine max cDNA clone... 140 6e-43
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 emb|AW695899|AW695899 NF100E02ST1F1017 Developing stem Medicago ... 125 5e-42
 emb|AW774697|AW774697 EST333848 KV3 Medicago truncatula cDNA clo... 84 8e-42
 45 emb|AW683492|AW683492 NF012H09LF1F1079 Developing leaf Medicago ... 134 2e-41
 emb|AW152892|AW152892 se32d04.y1 Gm-c1015 Glycine max cDNA clone... 82 2e-41
 gb|BE125749|BE125749 DG1_55_H11.b1_A002 Dark Grown 1 (DG1) Sorgh... 127 2e-41
 gb|BE022002|BE022002 sm65c10.y1 Gm-c1028 Glycine max cDNA clone ... 137 3e-41
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 50 emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40
 emb|AW625461|AW625461 EST319368 tomato radicle, 5 d post-imbibit... 99 1e-40
 emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40
 emb|AI960196|AI960196 sc80a08.y1 Gm-c1018 Glycine max cDNA clone... 132 5e-40
 emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39
 55 emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39

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(827 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5

Searching.....done

Score E

Sequences producing significant alignments:

(bits) Value

10

emb|AI489346|AI489346 EST247685 tomato ovary, TAMU Lycopersicon ... 79 2e-28
 emb|AW350323|AW350323 GM210007B20E12R Gm-r1021 Glycine max cDNA ... 80 2e-27
 emb|AW509006|AW509006 si38h07.y1 Gm-r1030 Glycine max cDNA clone... 79 2e-26
 emb|AW685404|AW685404 NF028H10NR1F1000 Nodulated root Medicago t... 74 2e-24
 15 emb|AW781320|AW781320 sk68d07.y1 Gm-cl016 Glycine max cDNA clone... 86 2e-24
 emb|AI897832|AI897832 EST267275 tomato ovary, TAMU Lycopersicon ... 78 1e-23
 emb|AW102460|AW102460 sd88d10.y1 Gm-cl009 Glycine max cDNA clone... 70 2e-22
 emb|AI490284|AI490284 EST248610 tomato ovary, TAMU Lycopersicon ... 103 2e-22
 emb|AI487362|AI487362 EST245684 tomato ovary, TAMU Lycopersicon ... 72 3e-20
 20 gb|BE125690|BE125690 DG1_54_A02.g1_A002 Dark Grown 1 (DG1) Sorgh... 96 3e-19
 emb|X80231|LTCAMA L.tarentolae CAM A gene for calmodulin. 73 1e-18
 emb|AL115248|CNS01C9K Botrytis cinerea strain T4 cDNA library un... 65 4e-18
 dbj|D10521|TETCALW T.pyrififormis mRNA for calmodulin. 73 7e-18
 gb|M76407|SLECALMODU Stylonychia lemnae calmodulin gene, complet... 74 9e-18
 25 emb|AF007889|AF007889 Symbiodinium microadriaticum calmodulin (S... 74 1e-17
 emb|AF078679|AF078679 Olea europaea calcium-binding protein (PCA... 57 2e-17
 emb|X56511|TBCALUBG T. brucei genes for calmodulin, EFH5 and ubi... 77 2e-17
 emb|X52096|TCCALB2 Trypanosoma cruzi CalA2 calmodulin gene. 77 2e-17
 emb|AF030033|AF030033 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 75 2e-17
 30 emb|X90560|PPCAMPROT Physcomitrella patens mRNA for calmodulin. 71 2e-17
 gb|U91642|POU91642 Pleurotus ostreatus calmodulin mRNA, complete... 75 2e-17
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 emb|X85091|MPCAM M.pyrifera mRNA for calmodulin. 74 2e-17
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 35 emb|Y08373|TGCM T.gondii mRNA for calmodulin. 74 2e-17
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 gb|J05116|ACKCAL A.klebsiana calmodulin gene, complete cds. 75 4e-17
 emb|X70923|NCCALMOE N.crassa mRNA for calmodulin. 74 6e-17
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 45 gb|U12505|HCCMD Histoplasma capsulatum 186AS calmodulin mRNA, co... 74 8e-17
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 55 gb|K02944|TRBCMRSG Trypanosoma brucei gambiense calmodulin genes... 73 2e-16
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 emb|X89890|BPCALMGEM B.pilosa mRNA for calmodulin. 73 2e-16
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 5 emb|AL116760|CNS01DFK Botrytis cinerea strain T4 cDNA library un... 73 2e-16
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 20 gb|BE036340|BE036340 MO23E04 MO Mesembryanthemum crystallinum cD... 73 4e-16
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 25 gb|U49104|TAU49104 Triticum aestivum calmodulin TaCaM3-3 mRNA, c... 73 4e-16
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 30 gb|U48242|TAU48242 Triticum aestivum calmodulin TaCaM1-1 mRNA, c... 73 4e-16
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 35 gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16
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 (1408 letters)

55

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

60

Score E

Sequences producing significant alignments:

(bits) Value

	emb AB014483 AB014483 Nicotiana tabacum NtHSF1 mRNA for heat sho...	213	2e-62
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	emb AI055366 AI055366 coau0003M17 Cotton Boll Abscission Zone cD...	191	1e-47
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	emb AW931781 AW931781 EST357624 tomato fruit mature green, TAMU ...	189	3e-47
	emb AW686121 AW686121 NF033H01NR1F1000 Nodulated root Medicago t...	188	1e-46
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	emb AW109013 AW109013 gate0002O16f Gossypium arboreum 7-10 dpa f...	179	4e-44
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	emb AW906840 AW906840 EST342963 potato stolon, Cornell Universit...	140	2e-32
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	emb AW596493 AW596493 sj13a09.y1 Gm-cl032 Glycine max cDNA clone...	138	1e-31
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55	emb AW979619 AW979619 EST341218 tomato root deficiency, Cornell ...	137	2e-31
	emb AW932142 AW932142 EST357985 tomato fruit mature green, TAMU ...	136	3e-31
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gb|M94683|YSPHSF Schizosaccharomyces pombe heat shock transcript... 93 6e-18
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25 emb|AW933448|AW933448 EST359387 tomato fruit mature green, TAMU ... 89 8e-17
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30 gb|U00029|YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm... 83 5e-15
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gb|M22040|YSCHSF1A S.cerevisiae heat shock transcription factor ... 81 2e-14
emb|Z72596|SCYGL074C S.cerevisiae chromosome VII reading frame O... 81 2e-14
gb|J03139|YSCHSF S.cerevisiae heat shock factor gene (HSF), comp... 81 2e-14
35 emb|AI212342|AI212342 x3c12a1.rl Aspergillus nidulans 24hr asexu... 73 8e-14
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40 emb|AW307441|AW307441 sf57a06.y1 Gm-c1009 Glycine max cDNA clone... 70 5e-11
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post/entrez/query?db=n&form=6&dopt=g&uid=gb|hsp176a /ncgi
http://www.ncgr.org/cgi-bin/ff?hsp176a
50 (613 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

60 gb|M33901|PEAHSP177A Pisum sativum 17.7 kDa heat shock protein (... 126 3e-44
gb|M99429|PHNSHSPA Ipomoea nil small heat shock protein, complet... 171 4e-42

- emb|X98617|MSSHSP17KD M.sativa mRNA for 17kD heat shock protein. 171 6e-42
emb|AF159562|AF159562 Prunus dulcis cytosolic class II low molec... 105 7e-42
gb|L47740|PIAEMB29R Picea glauca class II cytoplasmic small mole... 169 2e-41
emb|AW569703|AW569703 si79c12.y1 Gm-c1031 Glycine max cDNA clone... 107 6e-41
5 emb|X99346|PASHSP P.abies mRNA for small heat shock protein. 166 1e-40
emb|AW667877|AW667877 GA_Ea0011C02 Gossypium arboreum 7-10 dpa ... 110 2e-40
emb|AW725392|AW725392 GA_Ea0017J18 Gossypium arboreum 7-10 dpa ... 110 2e-40
emb|AW569553|AW569553 si88e08.y1 Gm-c1031 Glycine max cDNA clone... 107 1e-39
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10 gb|BE053976|BE053976 GA_Ea0002N06f Gossypium arboreum 7-10 dpa ... 110 3e-39
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20 emb|AI812703|AI812703 18B10 Pine Lambda Zap Xylem library Pinus ... 145 3e-34
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25 emb|AJ225049|LPAJ5049 Lycopersicon peruvianum mRNA for Hsp20.2 p... 105 8e-26
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emb|X92983|PMLMWHSPA P.menziesii mRNA for low molecular weight h... 104 6e-22
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60 emb|AF123255|AF123255 Lycopersicon esculentum 17.7 kD class I sm... 61 3e-20
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 35 emb|AF089845|AF089845 Funaria hygrometrica cytosolic II small he... 94 1e-18
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45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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50 Score E
 Sequences producing significant alignments: (bits) Value

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 60 emb|AF042329|AF042329 Eimeria tenella heat shock protein 90-(hsp... 514 0.0
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20	emb Z49808 SC8010 S.cerevisiae chromosome XIII cosmid 8010.	447	e-158
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	emb AW982497 AW982497 HVSMEg0003G20f Hordeum vulgare pre-anthesi...	439	e-126
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35	emb AW731352 AW731352 GA__Ea0030E22 Gossypium arboreum 7-10 dpa ...	449	e-125
	emb AW621485 AW621485 EST312283 tomato root during/after fruit s...	445	e-124
	emb AW905909 AW905909 EST342082 potato stolon, Cornell Universit...	331	e-124
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40	emb AW931002 AW931002 EST356845 tomato fruit mature green, TAMU ...	436	e-121
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45	emb AW217696 AW217696 EST296410 tomato flower buds 8 mm to pre-a...	422	e-117
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	emb AW693965 AW693965 NF071A06ST1F1040 Developing stem Medicago ...	408	e-113
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 15 emb|AI781620|AI781620 EST262499 tomato susceptible, Cornell Lyco... 389 e-107
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 emb|AW092845|AW092845 EST286025 tomato mixed elicitor, BTI Lycop... 386 e-106
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 20 emb|AW651194|AW651194 EST329648 tomato germinating seedlings, TA... 266 e-106
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 emb|AW334905|AW334905 S40F8 AGS-1 Pneumocystis carinii f. sp. ca... 381 e-104
 30 emb|AW035244|AW035244 EST280506 tomato callus, TAMU Lycopersicon... 380 e-104

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Database: plantfungal
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emb AJ005341 LUAJ5341	Linum usitatissimum mRNA for MLO-like prot...	287 2e-76	
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emb AW132264 AW132264	sd98f11.y1 Gm-cl013 Glycine max cDNA clone...	128 2e-60	
55 emb AI779924 AI779924	EST260803 tomato susceptible, Cornell Lyco...	228 8e-59	
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emb AW132268 AW132268	sd98g11.y1 Gm-c1013 Glycine max cDNA clone...	124 5e-58	
emb AI729603 AI729603	BNLGH13760 Six-day Cotton fiber Gossypium...	202 8e-51	
emb AI054629 AI054629	coau0001J02 Cotton Boll Abscission Zone cD...	133 2e-44	
60 emb AV426381 AV426381	AV426381 Lotus japonicus young plants (two...	145 3e-43	
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20	emb A92832 A92832 Sequence 6 from Patent WO9804586.	98 2e-19
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50	emb X05498 SCSNR17B Yeast SNR17B gene for U3 small nuclear RNA.	35 1.8
	emb Z73500 SCYPL144W S.cerevisiae chromosome XVI reading frame O...	35 1.8
	gb U43703 SCU43703 Saccharomyces cerevisiae chromosome XVI cosmi...	35 1.8
	emb Z73499 SCYPL143W S.cerevisiae chromosome XVI reading frame O...	35 1.8
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 5 emb|AC005927|AC005927 *Leishmania major* chromosome 3 clone L3561 ... 34 3.5
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 emb|AL031263|SPBC17F3 *S.pombe* chromosome II cosmid c17F3. 34 4.7
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35 Database: plantfungal
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 emb|X70810|CLEGCGA Euglena gracilis chloroplast complete genome. 31 7.1
 10 emb|AW923451|AW923451 DG1_52_H09.b1_A002 Dark Grown 1 (DG1) Sorg... 31 7.1
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Database: plantfungal
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emb AF057379 AF057379 Nicotiana tabacum clone G8-1 unknown mRNA.	31	6.5
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60 emb AI460510 AI460510 sa80h11.y1 Gm-cl004 Glycine max cDNA clone...	31	7.3
emb AI026500 AI026500 TENU0712 T. cruzi epimastigote normalized ...	31	7.3

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 5 gb|L38011|L38011 BNAF0228E Mustard flower buds Brassica rapa cDN... 30 10.0

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Database: plantfungal
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40	emb AW775746 AW775746 EST334811 DSIL Medicago truncatula cDNA cl...	46	1e-04
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	emb AW278224 AW278224 sf41c11.y1 Gm-cl009 Glycine max cDNA clone...	45	3e-04
	gb BE059759 BE059759 sn36g02.y1 Gm-cl016 Glycine max cDNA clone ...	45	3e-04
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55	emb X02873 DCEXTG Carrot gene for extensin.	37	0.062
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	emb AW091576 AW091576 EST284852 tomato mixed elicitor, BTI Lycop...	35	0.22
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	gb M34311 YSCSDNAB S.cerevisiae telomeric sequence DNA, clone Y...	27	0.25
10	emb AF163953 AF163953 Saccharomyces cerevisiae isolate wt-2 telo...	29	0.26
	emb X59720 SCCHRIII S.cerevisiae chromosome III complete DNA seq...	28	0.30
	gb M15317 PFAHRPA P.lophurae histidine-rich protein mRNA, 3' end.	35	0.30
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	emb AF163955 AF163955 Saccharomyces cerevisiae isolate wt-8 telo...	33	0.34
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	gb BE034443 BE034443 MH05A01 MH Mesembryanthemum crystallinum cD...	34	0.42
	gb M12922 YSCARSX Yeast (S.cerevisiae) chromosome III L terminal...	28	0.44
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	emb Y15372 MTY15372 Medicago truncatula mRNA for MtN4 gene, part...	33	0.79
	emb AV393340 AV393340 AV393340 Chlamydomonas reinhardtii C9 Chla...	33	0.79
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45	emb AW725658 AW725658 GA_Ea0019C15 Gossypium arboreum 7-10 dpa ...	27	1.5
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	gb BE034655 BE034655 ML01E08 ML Mesembryanthemum crystallinum cD...	32	1.5
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55	emb AF163952 AF163952 Saccharomyces cerevisiae isolate wt-1 telo...	27	1.5
	emb Z98532 SPAC1B1 S.pombe chromosome I cosmid c1B1.	28	1.6
	emb X01469 PLHRP1 Plasmodium gene fragment for histidine-rich pr...	32	2.0
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AW217278 AW217278 EST295992 tomato callus, TAMU Lycopersicon...	50	6e-10
	emb AF179222 AF179222 Brassica rapa subsp. pekinensis floral nec...	43	2e-08
20	emb AW737522 AW737522 EST338949 tomato flower buds, anthesis, Co...	52	5e-06
	emb AW650581 AW650581 EST329035 tomato germinating seedlings, TA...	49	6e-06
	emb AW200887 AW200887 se94g08.y1 Gm-cl027 Glycine max cDNA clone...	50	3e-05
	emb AW774361 AW774361 EST333512 KV3 Medicago truncatula cDNA clo...	48	1e-04
	emb AW033701 AW033701 EST277272 tomato callus, TAMU Lycopersicon...	47	2e-04
25	emb AW738253 AW738253 EST339680 tomato flower buds, anthesis, Co...	46	5e-04
	emb AW285102 AW285102 LG1_300_F04.g1_A002 Light Grown 1 (LG1) So...	40	6e-04
	emb AI896626 AI896626 EST266069 tomato callus, TAMU Lycopersicon...	46	6e-04
	emb AW563740 AW563740 LG1_248_A08.g1_A002 Light Grown 1 (LG1) So...	43	0.004
	emb AW256640 AW256640 EST304777 KV2 Medicago truncatula cDNA clo...	42	0.006
30	emb AF133053 AF133053 Clarkia breweri S-adenosyl-L-methionine:sa...	42	0.006
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35	emb AW595921 AW595921 si95b09.y1 Gm-cl032 Glycine max cDNA clone...	35	0.94
	emb AW567624 AW567624 si65f05.y1 Gm-r1030 Glycine max cDNA clone...	35	1.3
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40	gb T02585 T02585 0228C3 cbsPfHB3.1, Debopam Chakrabarti Plasmodi...	34	2.4
	emb AC005507 AC005507 Plasmodium falciparum chromosome 12 clone ...	34	2.4
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45	emb AL109814 PFMAL13PB Plasmodium falciparum chromosome 13 strai...	34	2.4
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	gb U60200 STU60200 Solanum tuberosum lipoxxygenase (POTLX-1) mRNA...	33	4.6
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5	emb AF019613 AF019613 Solanum tuberosum lipoxxygenase (plox1) mRN...	33	4.6
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	emb AA495648 AA495648 c078 Zhou and Ragan 1993 Gracilaria gracil...	32	8.6
	emb AL049182 PFMAL13P5 Plasmodium falciparum chromosome 13 strai...	32	8.6
	emb X56775 HVGLB1 H.vulgare Glb 1 gene for 1-3,1-4-beta-D-glucan...	32	8.6
20	emb Z72916 SCYGR131W S.cerevisiae chromosome VII reading frame O...	32	8.6
	emb Z72915 SCYGR130C S.cerevisiae chromosome VII reading frame O...	32	8.6
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	emb AB026835 AB026835 Toxoplasma gondii mRNA for hypoxanthine-gu...	32	8.6
	gb U09219 TGU09219 Toxoplasma gondii RH hypoxanthine-guanine pho...	32	8.6
25	gb U10247 TGU10247 Toxoplasma gondii RH hypoxanthine-xanthine-gu...	32	8.6
	emb AB012774 AB012774 AB012774 Toxoplasma gondii mRNA (T.Koyama)...	32	8.6
	gb S73865 S73865 linoleate:oxygen oxidoreductase [Solanum tubero...	32	8.6
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40 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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50	emb AW687516 AW687516 NF010D12RT1F1101 Developing root Medicago ...	32	1.3
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55	emb AF030694 AF030694 Plasmodium falciparum strain Dd2 heat shoc...	31	3.3
	emb X12493 SCADR6 Yeast ADR6 gene for transcription factor.	30	4.5
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	emb Z46861 SC9905 S.cerevisiae chromosome IX cosmid 9905 and lam...	30	4.5
	gb L29456 TOBHIC12X Nicotiana tabacum histone H1 (H1C12) mRNA, c...	30	4.5
60	gb U33335 U33335 Saccharomyces cerevisiae chromosome XVI, left a...	30	4.5
	emb AJ290663 PAB290663 Picea abies copia like retroelement parti...	30	6.2

emb|AL115708|CNS01CMC Botrytis cinerea strain T4 cDNA library un... 30 6.2
 emb|Z71630|SCYNR015W S.cerevisiae chromosome XIV reading frame O... 29 8.5
 emb|Z71629|SCYNR014W S.cerevisiae chromosome XIV reading frame O... 29 8.5
 emb|AQ875584|AQ875584 V127B11 mTn-3xHA/lacZ Insertion Library, s... 29 8.5
 5 gb|L16451|YSAAPRP Candida albicans acid proteinase-related prote... 29 8.5
 emb|AW981797|AW981797 PC18H02 Pine TriplEx pollen cone library P... 29 8.5
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 emb|AW672524|AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So... 29 8.5
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 10 emb|AI895394|AI895394 EST264837 tomato callus, TAMU Lycopersicon... 27 9.6

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AI489151 AI489151 EST247490 tomato ovary, TAMU Lycopersicon ...	152	4e-54
30	emb AI483907 AI483907 EST249778 tomato ovary, TAMU Lycopersicon ...	152	1e-52
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	emb AI771546 AI771546 EST252646 tomato ovary, TAMU Lycopersicon ...	144	2e-49
	emb AW736637 AW736637 EST333129 KV3 Medicago truncatula cDNA clo...	142	6e-48
	emb AI166286 AI166286 xylem.est.133 Poplar xylem Lambda ZAPII li...	151	6e-40
35	emb AW693272 AW693272 NF064A05ST1F1000 Developing stem Medicago ...	143	3e-39
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	emb AW559446 AW559446 EST314494 DSIR Medicago truncatula cDNA cl...	143	1e-38
	emb AW730900 AW730900 GA__Ea0029G11 Gossypium arboreum 7-10 dpa ...	146	2e-37
	emb AW692307 AW692307 NF049H04ST1F1043 Developing stem Medicago ...	143	1e-36
40	emb AW737187 AW737187 EST338614 tomato flower buds, anthesis, Co...	149	3e-36
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45	emb AW688941 AW688941 NF013E03ST1F1000 Developing stem Medicago ...	121	4e-30
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	emb AW932074 AW932074 EST357917 tomato fruit mature green, TAMU ...	116	3e-26
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	emb AW307535 AW307535 sf58b08.y1 Gm-cl009 Glycine max cDNA clone...	63	2e-21
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55	emb AI772366 AI772366 EST253466 tomato resistant, Cornell Lycope...	63	7e-21
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5 emb|AW398635|AW398635 EST309135 *L. pennellii* trichome, Cornell U... 48 1e-18
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emb|AW266728|AW266728 L48-63T3 Ice plant Lambda Uni-Zap XR expre... 89 4e-17
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10 emb|AI726953|AI726953 BNLGHi6948 Six-day Cotton fiber *Gossypium* ... 66 5e-17
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15 emb|AW686542|AW686542 NF039C04NR1F1000 Nodulated root *Medicago* t... 60 4e-16
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emb|AW693273|AW693273 NF064A06ST1F1000 Developing stem *Medicago* ... 60 7e-15
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30 emb|AW691254|AW691254 NF042G01ST1F1000 Developing stem *Medicago* ... 71 6e-13
emb|AI771903|AI771903 EST253003 tomato ovary, TAMU *Lycopersicon* ... 58 2e-12
emb|AW755537|AW755537 sl05b09.y1 Gm-cl036 *Glycine max* cDNA clone... 43 2e-12
emb|AW690391|AW690391 NF030B07ST1F1000 Developing stem *Medicago* ... 49 3e-12
gb|BE125956|BE125956 DG1_60_B12.b1_A002 Dark Grown 1 (DG1) *Sorgh*... 56 2e-11
35 emb|AW933549|AW933549 EST359308 tomato fruit mature green, TAMU ... 46 3e-11
emb|AW573921|AW573921 EST316512 GVN *Medicago truncatula* cDNA clo... 59 6e-11
emb|AV425214|AV425214 AV425214 *Lotus japonicus* young plants (two... 54 6e-11
emb|AW621185|AW621185 EST311983 tomato root during/after fruit s... 62 1e-10
40 emb|AW720132|AW720132 LjNEST14h12r *Lotus japonicus* nodule librar... 57 1e-10
emb|AW697024|AW697024 NF111E05ST1F1038 Developing stem *Medicago* ... 43 1e-10
emb|AI727398|AI727398 BNLGHi7916 Six-day Cotton fiber *Gossypium* ... 66 2e-10
emb|AW317889|AW317889 sg58e01.y1 Gm-cl007 *Glycine max* cDNA clone... 64 2e-10
emb|AI773497|AI773497 EST254597 tomato resistant, Cornell Lycope... 66 6e-10
emb|AI779047|AI779047 EST259926 tomato susceptible, Cornell Lyco... 66 6e-10
45 emb|AW160290|AW160290 EST290148 *L. pennellii* trichome, Cornell U... 66 6e-10
emb|AW690159|AW690159 NF028E04ST1F1000 Developing stem *Medicago* ... 40 9e-10
emb|AW697130|AW697130 NF112E12ST1F1098 Developing stem *Medicago* ... 40 9e-10
emb|AA739537|AA739537 302 PtIFG2 *Pinus taeda* cDNA clone 8497M 3'... 57 9e-10
50 emb|AW934683|AW934683 EST353575 tomato flower buds 0-3 mm, Corne... 44 1e-09
emb|AW217676|AW217676 EST296390 tomato flower buds 8 mm to pre-a... 44 1e-09
gb|L47871|L47871 BNAF1521 Mustard flower buds *Brassica rapa* cDNA... 47 1e-09
emb|AI163871|AI163871 A050p31u Hybrid aspen plasmid library Popu... 59 1e-09
emb|AW728602|AW728602 GA__Ea0017E06 *Gossypium arboreum* 7-10 dpa ... 64 1e-09
emb|AW617945|AW617945 EST314019 *L. pennellii* trichome, Cornell U... 46 2e-09
55 emb|AW647996|AW647996 EST326450 tomato germinating seedlings, TA... 64 2e-09
emb|AW218271|AW218271 EST303452 tomato radicle, 5 d post-imbibit... 64 2e-09
emb|AI776062|AI776062 EST257162 tomato resistant, Cornell Lycope... 64 2e-09
emb|AW036254|AW036254 EST278333 tomato seed, TAMU *Lycopersicon* e... 64 2e-09
emb|AW650814|AW650814 EST329268 tomato germinating seedlings, TA... 64 2e-09
60 emb|AI443133|AI443133 sa84g05.y1 Gm-cl004 *Glycine max* cDNA clone... 63 3e-09
emb|AW906997|AW906997 EST343224 potato stolon, Cornell Universit... 63 3e-09

emb|AI495275|AI495275 sb02h04.y1 Gm-c1004 Glycine max cDNA clone... 50 3e-09
 gb|BE053949|BE053949 GA__Ea0031D21f Gossypium arboreum 7-10 dpa ... 48 4e-09
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 (507 letters)

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

15 Searching.....done

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 Sequences producing significant alignments: (bits) Value

20 emb|AV427887|AV427887 AV427887 Lotus japonicus young plants (two... 61 6e-17
 emb|AV419761|AV419761 AV419761 Lotus japonicus young plants (two... 56 1e-15
 emb|AI967590|AI967590 Ljimpest06-480-c9 Ljimp Lambda HybriZap ... 68 2e-14
 emb|AW684644|AW684644 NF019C10NR1F1000 Nodulated root Medicago t... 62 9e-12
 gb|BE036389|BE036389 MO24B03 MO Mesembryanthemum crystallinum cD... 44 2e-06
 25 gb|BE034652|BE034652 ML01E04 ML Mesembryanthemum crystallinum cD... 35 0.57
 emb|AC005308|AC005308 Plasmodium falciparum chromosome 12 clone ... 35 0.57
 gb|N60116|N60116 TgESTzy01b10.r1 TgRH Tachyzoite cDNA Toxoplasma... 34 0.78
 emb|AF161334|AF161334 Raphanus raphanistrum subsp. raphanistrum ... 33 1.5
 gb|L37356|PUMPAL3A Petroselinum crispum phenylalanine ammonia-ly... 33 2.0
 30 emb|AI974840|AI974840 T113322e KV2 Medicago truncatula cDNA clon... 32 2.8
 gb|U36470|NCU36470 Neurospora crassa vacuolar ATPase 41 kDa subu... 32 2.8
 emb|AI938788|AI938788 sc60a05.y1 Gm-c1016 Glycine max cDNA clone... 32 2.8
 emb|AF114794|AF114794 Porphyra purpurea mitochondrion, complete ... 32 3.8
 emb|AI374339|AI374339 T6652 MVAT4 bloodstream form of serodeme W... 32 3.8
 35 emb|AI374387|AI374387 T6725 MVAT4 bloodstream form of serodeme W... 32 3.8
 emb|AI374381|AI374381 T6716 MVAT4 bloodstream form of serodeme W... 32 3.8
 emb|AI894927|AI894927 EST264370 tomato callus, TAMU Lycopersicon... 31 5.2
 emb|AA550548|AA550548 1711m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 31 5.2
 emb|AJ223459|ANAJ3459 Aspergillus nidulans prnA gene. 31 5.2
 40 emb|AJ390536|CAL390536 Candida albicans DNA, clone 222g9. 31 5.2
 emb|AW119888|AW119888 sd54b09.y1 Gm-c1016 Glycine max cDNA clone... 31 5.2
 emb|AI431203|AI431203 sa22f12.y2 Gm-c1006 Glycine max cDNA clone... 31 5.2
 emb|AF161331|AF161331 Sinapis arvensis S-locus related 1 (SLR1) ... 31 7.2
 emb|AF137311|AF137311 Miscanthus sinensis phytochrome B (PHYB) g... 31 7.2
 45 gb|T36711|T36711 EST101701 S. cerevisiae strain X2180-1A Sacchar... 31 7.2
 emb|AW781868|AW781868 sl97g02.y1 Gm-c1027 Glycine max cDNA clone... 31 7.2
 emb|AW755482|AW755482 sl04e07.y1 Gm-c1036 Glycine max cDNA clone... 30 9.9
 emb|AW694935|AW694935 NF081F05ST1F1046 Developing stem Medicago ... 30 9.9
 emb|AZ215370|AZ215370 Sheared DNA-56C1.TF Sheared DNA Trypanosom... 30 9.9
 50 emb|AQ945786|AQ945786 Sheared DNA-30C5.TR Sheared DNA Trypanosom... 30 9.9
 emb|AA739646|AA739646 411 PtIFG2 Pinus taeda cDNA clone 8694M 3'... 30 9.9
 emb|AL034353|SPBC1271 S.pombe chromosome II cosmid c1271. 30 9.9
 gb|N69599|N69599 TgESTzy41b11.r1 TgRH Tachyzoite cDNA Toxoplasma... 30 9.9

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments: (bits) Value

10 emb|AW266797|AW266797 L48-136T3 Ice plant Lambda Uni-Zap XR expr... 59 5e-08
 emb|AI776331|AI776331 EST257431 tomato resistant, Cornell Lycope... 51 8e-06
 emb|AI938454|AI938454 sc45e10.y1 Gm-c1015 Glycine max cDNA clone... 44 0.001
 emb|AF086822|AF086822 Candida boidinii dihydroxyacetone synthase... 36 0.38
 emb|AV406828|AV406828 AV406828 Lotus japonicus young plants (two... 31 0.49
 15 emb|AI731942|AI731942 BNLGHi11450 Six-day Cotton fiber Gossypium... 35 0.71
 emb|AQ255443|AQ255443 mgxb0014I21r CUGI Rice Blast BAC Library P... 35 0.71
 emb|AQ940346|AQ940346 Sheared DNA-33M2.TF Sheared DNA Trypanosom... 34 1.3
 emb|AI210373|AI210373 i0e05a1.r1 Aspergillus nidulans 24hr asexu... 34 1.8
 emb|AQ935542|AQ935542 CpG2525A CpIOWAgDNA1 Cryptosporidium parvu... 33 2.5
 gb|T18147|T18147 0722c3 czapPFDd2.1, Debopam Chakrabarti Plasmod... 33 2.5
 20 emb|AW651276|AW651276 EST329730 tomato germinating seedlings, TA... 33 3.5
 emb|AI392128|AI392128 NCSM1B1T7 Subtracted Mycelial Neurospora c... 32 4.8
 emb|AW330094|AW330094 TENU4840 T.cruzi epimastigote normalized c... 32 4.8
 emb|AF055296|AF055296 Zantedeschia aethiopica geranylgeranyl red... 32 4.8
 emb|AI725804|AI725804 BNLGHi13200 Six-day Cotton fiber Gossypium... 32 4.8
 25 emb|AW686984|AW686984 NF004F11RT1F1094 Developing root Medicago ... 32 6.6
 emb|AJ273808|AJ273808 AJ273808 Metarhizium anisopliae ARSEF 2575... 32 6.6
 emb|AQ943530|AQ943530 Sheared DNA-42D24.TR Sheared DNA Trypanoso... 31 9.0
 emb|AQ941987|AQ941987 Sheared DNA-42F7.TR Sheared DNA Trypanosom... 31 9.0
 emb|AW620371|AW620371 sj04d01.y1 Gm-c1032 Glycine max cDNA clone... 31 9.0
 30 emb|AI973930|AI973930 sd13g08.y1 Gm-c1020 Glycine max cDNA clone... 31 9.0
 emb|AF069470|AF069470 Phleum pratense group V allergen Phl p 5.0... 31 9.0
 emb|AL160716|P406R Leishmania major Friedlin PAC P406 right end-... 31 9.0
 emb|AQ851400|AQ851400 LMAJFV1_lm40b04.y1 Leishmania major FV1 ra... 31 9.0
 emb|AF061068|AF061068 Phleum pratense clone 10029 major allergen... 31 9.0
 35 emb|AQ953188|AQ953188 Sheared DNA-50B12.TF Sheared DNA Trypanoso... 31 9.0
 emb|AW719942|AW719942 LjNEST12c6r Lotus japonicus nodule library... 31 9.0
 emb|X74735|PPHLP5 P. pratense mRNA for PhlpV. 31 9.0
 emb|AW396374|AW396374 sh27d05.y1 Gm-c1016 Glycine max cDNA clone... 31 9.0
 gb|N60997|N60997 TgESTzy23f10.r1 TgRH Tachyzoite cDNA Toxoplasma... 31 9.0
 40 emb|AI164737|AI164737 A068P10U Hybrid aspen plasmid library Popu... 31 9.0
 emb|AW348348|AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3... 26 9.5
 emb|AW309665|AW309665 sf22g06.x1 Gm-c1028 Glycine max cDNA clone... 26 9.5
 emb|AW310247|AW310247 sf33d01.x1 Gm-c1028 Glycine max cDNA clone... 26 9.5
 emb|AW508196|AW508196 si50d10.y1 Gm-r1030 Glycine max cDNA clone... 27 9.6
 45 emb|AW102012|AW102012 sd81h10.y1 Gm-c1009 Glycine max cDNA clone... 26 9.8
 emb|AW309166|AW309166 sg05b01.y1 Gm-c1019 Glycine max cDNA clone... 26 9.8
 emb|AW598779|AW598779 sj46h06.y1 Gm-c1033 Glycine max cDNA clone... 26 9.8
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(430 letters)

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

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	emb AW698685 AW698685 R125 non-glandular-haired subtracted cDNA ...	32	1.4
5	emb AF061282 AF061282 Sorghum bicolor 22 kDa kafirin cluster.	31	5.6
	emb AL031854 SPBC337 S.pombe chromosome II cosmid c337.	31	5.6
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S...	31	5.6
	emb AC006280 AC006280 Plasmodium falciparum chromosome 12 clone ...	31	5.6
	gb M74062 YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl...	31	5.6
10	emb AQ947500 AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso...	31	5.6
	gb M83307 YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl...	31	5.6
	emb AL031856 SPBC1734 S.pombe chromosome II cosmid c1734.	31	5.6
	emb AC073246 AC073246 Trypanosoma brucei chromosome II clone RPC...	30	7.7
	emb AL031535 SPCC16C4 S.pombe chromosome III cosmid c16C4.	30	7.7
15	emb AC012647 AC012647 Trypanosoma brucei chromosome II clone RPC...	30	7.7
	gb L28038 TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc...	30	7.7
	emb AB004322 AB004322 Nicotiana sylvestris NsPMT1 gene for putre...	30	7.7
	emb AQ941496 AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso...	30	7.7
	emb AQ946940 AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom...	30	7.7
20	emb AQ942433 AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom...	30	7.7
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25 Query= Novartis73_RC_at 14202_at /id_source
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(430 letters)

30 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

	Score E	
35	Sequences producing significant alignments:	(bits) Value
	emb AQ952678 AQ952678 Sheared DNA-48H20.TF Sheared DNA Trypanoso...	35 0.32
	emb AW698685 AW698685 R125 non-glandular-haired subtracted cDNA ...	32 1.4
	emb AF061282 AF061282 Sorghum bicolor 22 kDa kafirin cluster.	31 5.6
40	emb AL031854 SPBC337 S.pombe chromosome II cosmid c337.	31 5.6
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S...	31 5.6
	emb AC006280 AC006280 Plasmodium falciparum chromosome 12 clone ...	31 5.6
	gb M74062 YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl...	31 5.6
	emb AQ947500 AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso...	31 5.6
45	gb M83307 YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl...	31 5.6
	emb AL031856 SPBC1734 S.pombe chromosome II cosmid c1734.	31 5.6
	emb AC073246 AC073246 Trypanosoma brucei chromosome II clone RPC...	30 7.7
	emb AL031535 SPCC16C4 S.pombe chromosome III cosmid c16C4.	30 7.7
	emb AC012647 AC012647 Trypanosoma brucei chromosome II clone RPC...	30 7.7
50	gb L28038 TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc...	30 7.7
	emb AB004322 AB004322 Nicotiana sylvestris NsPMT1 gene for putre...	30 7.7
	emb AQ941496 AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso...	30 7.7
	emb AQ946940 AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom...	30 7.7
	emb AQ942433 AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom...	30 7.7
55	emb AF133529 AF133529 Candida albicans mRNA cap methyltransferas...	30 7.7

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(1761 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5 Searching.....done

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10	emb AW745943 AW745943 WS1_38_H06.b1_A002 Water-stressed I (WS1) ...	240	3e-62
	gb BE023215 BE023215 sm70a04.y1 Gm-c1028 Glycine max cDNA clone ...	236	5e-61
	emb AW399343 AW399343 EST309843 L. pennellii trichome, Cornell U...	234	2e-60
	emb AW618318 AW618318 EST320304 L. pennellii trichome, Cornell U...	177	1e-53
	emb AW310982 AW310982 sg31b02.x1 Gm-c1024 Glycine max cDNA clone...	97	1e-51
15	emb AI442277 AI442277 sa66a04.y1 Gm-c1004 Glycine max cDNA clone...	200	2e-50
	emb AW687759 AW687759 NF013B05RT1F1044 Developing root Medicago ...	160	1e-46
	emb AW684122 AW684122 NF012F06NR1F1000 Nodulated root Medicago t...	83	2e-44
	emb AW309867 AW309867 sf25g10.x1 Gm-c1028 Glycine max cDNA clone...	89	5e-43
	gb BE020423 BE020423 sm40e08.y1 Gm-c1028 Glycine max cDNA clone ...	88	2e-39
20	emb AW691118 AW691118 NF041D08ST1F1000 Developing stem Medicago ...	78	2e-35
	emb AW160235 AW160235 EST290093 L. pennellii trichome, Cornell U...	120	6e-32
	emb AI960862 AI960862 sc91f07.y1 Gm-c1019 Glycine max cDNA clone...	74	5e-30
	emb AW349633 AW349633 GM210006A11B3R Gm-r1021 Glycine max cDNA 3...	89	8e-29
	emb AW775076 AW775076 EST334227 KV3 Medicago truncatula cDNA clo...	81	6e-26
25	gb BE020331 BE020331 sm40d08.y1 Gm-c1028 Glycine max cDNA clone ...	69	4e-23
	emb AW746031 AW746031 WS1_39_A03.b1_A002 Water-stressed I (WS1) ...	74	8e-23
	emb AW621546 AW621546 EST312344 tomato root during/after fruit s...	64	1e-13
	emb AW622846 AW622846 EST306916 tomato flower buds 3-8 mm, Corne...	54	2e-12
	gb L43984 BLYBD Hordeum vulgare (clone ABG377) chromosome 3H STS...	69	8e-11
30	emb AW774216 AW774216 EST333367 KV3 Medicago truncatula cDNA clo...	69	1e-10
	emb AW774324 AW774324 EST333475 KV3 Medicago truncatula cDNA clo...	69	1e-10
	emb AW686169 AW686169 NF038H07NR1F1000 Nodulated root Medicago t...	68	2e-10
	emb AW160234 AW160234 EST290092 L. pennellii trichome, Cornell U...	46	2e-08
	emb AW685496 AW685496 NF030G02NR1F1000 Nodulated root Medicago t...	45	2e-07
35	emb AW684082 AW684082 NF011H08NR1F1000 Nodulated root Medicago t...	55	2e-06
	emb AW693839 AW693839 NF069F08ST1F1074 Developing stem Medicago ...	53	6e-06
	emb AI163659 AI163659 A046p04u Hybrid aspen plasmid library Popu...	53	6e-06
	emb AW033404 AW033404 EST276975 tomato callus, TAMU Lycopersicon...	49	1e-04
	emb AI054662 AI054662 coau0001K11 Cotton Boll Abcission Zone cD...	37	2e-04
40	emb AW758414 AW758414 874008A01.y1 C. reinhardtii CC-1690, Lambd...	41	0.022
	emb AW746188 AW746188 WS1_39_A03.g1_A002 Water-stressed I (WS1) ...	41	0.022
	emb Z99126 SPAC26H5 S.pombe chromosome I cosmid c26H5.	41	0.022
	emb AJ225805 EDKCHALPH Egeria densa mRNA for inward potassium ch...	39	0.14
	emb AI488725 AI488725 EST247064 tomato ovary, TAMU Lycopersicon ...	38	0.20
45	emb Z69731 SPAC6C3 S.pombe chromosome I cosmid c6C3.	36	0.71
	emb Z38061 SC9168 S.cerevisiae chromosome IX cosmid 9168.	36	0.71
	emb AW925349 AW925349 HVSMEg0001B12 Hordeum vulgare pre-anthesis...	36	0.71
	emb AW671585 AW671585 LG1_348_H11.b1_A002 Light Grown I (LG1) So...	36	0.97
	gb BE024935 BE024935 894007A03.x1 C. reinhardtii CC-1690, normal...	36	0.97
50	emb AW216501 AW216501 EST295215 tomato callus, TAMU Lycopersicon...	36	0.97
	emb AW680841 AW680841 WS1_7_E11.g1_A002 Water-stressed I (WS1) S...	35	1.3
	emb AQ911629 AQ911629 LMAJFV1_lm96c04.y1 Leishmania major FV1 ra...	35	1.3
	emb AW100578 AW100578 sd57b08.y1 Gm-c1008 Glycine max cDNA clone...	35	1.3
	emb AW010724 AW010724 ST11E02 Pine TriplEx shoot tip library Pin...	35	1.8
55	emb AL138854 SPAC23G3 S.pombe chromosome I cosmid c23G3.	35	2.5
	emb AW934681 AW934681 EST353573 tomato flower buds 0-3 mm, Corne...	34	3.5
	emb Z98975 SPAC19E9 S.pombe chromosome I cosmid c19E9.	34	3.5
	emb AW690479 AW690479 NF035A03ST1F1000 Developing stem Medicago ...	34	3.5
	emb Z50142 SPAC2F7 S.pombe chromosome I cosmid c2F7.	34	3.5
60	emb AA728334 AA728334 LmLv39p7/70M Leishmania major promastigote...	34	4.8
	emb AI779448 AI779448 EST260327 tomato susceptible, Cornell Lyco...	34	4.8

emb|AQ639314|AQ639314 927P1-2A10.TV 927P1 Trypanosoma brucei gen... 34 4.8
emb|AW725460|AW725460 GA__Ea0018B02 Gossypium arboreum 7-10 dpa ... 34 4.8
emb|AW256577|AW256577 EST304714 KV2 Medicago truncatula cDNA clo... 34 4.8
emb|AW234006|AW234006 sF3a07.y1 Gm-cl028 Glycine max cDNA clone... 34 4.8
5 emb|AW727061|AW727061 GA__Ea0011B08 Gossypium arboreum 7-10 dpa ... 34 4.8
emb|AZ221057|AZ221057 Sheared DNA-64F1.TR Sheared DNA Trypanosom... 34 4.8
emb|AI781303|AI781303 EST262182 tomato susceptible, Cornell Lyco... 34 4.8
emb|AA898817|AA898817 NCP3G4T7 Perithecial Neurospora crassa cDN... 34 4.8
emb|AI329539|AI329539 b6b04ne.fl Neurospora crassa evening cDNA ... 33 6.6
10 emb|AW754602|AW754602 PC04B10 Pine TriplEx pollen cone library P... 33 6.6
emb|AL049181|PFMAL13P4 Plasmodium falciparum chromosome 13 strai... 33 6.6
emb|AW756307|AW756307 sl19a02.y1 Gm-cl036 Glycine max cDNA clone... 33 6.6
emb|AC004145|AC004145 Leishmania major chromosome 3 clone L5801 ... 33 6.6
emb|AI778201|AI778201 EST259080 tomato susceptible, Cornell Lyco... 33 9.0
15 emb|AZ215585|AZ215585 Sheared DNA-74E7.TR Sheared DNA Trypanosom... 33 9.0
emb|AF216960|AF216960 Pichia pastoris strain GS115 Sec12 (SEC12)... 33 9.0
emb|AI896488|AI896488 EST265931 tomato callus, TAMU Lycopersicon... 33 9.0
emb|AW670919|AW670919 LG1_266_B11.b1_A002 Light Grown 1 (LG1) So... 33 9.0
emb|AQ842680|AQ842680 CpG1185B CpIOWAgDNA1 Cryptosporidium parvu... 33 9.0
20 emb|AW982007|AW982007 PC23H10 Pine TriplEx pollen cone library P... 33 9.0
gb|U51030|YSCD9954 Saccharomyces cerevisiae chromosome IV cosmid... 33 9.0
emb|AQ988815|AQ988815 11E1D03NE.R1 C. parvum Lambda Zap Express ... 33 9.0
emb|AV419655|AV419655 AV419655 Lotus japonicus young plants (two... 33 9.0
emb|AQ023613|AQ023613 CpGR0073A Cryptosporidium parvum genomic r... 33 9.0
25 gb|BE024936|BE024936 894007A03.y1 C. reinhardtii CC-1690, normal... 33 9.0
gb|L31407|YSCAKR Saccharomyces cerevisiae ankyrin repeat-contain... 33 9.0
emb|AQ648055|AQ648055 RPCI93-DpnII-30G1.TJ RPCI93-DpnII Trypanos... 33 9.0
emb|AQ641411|AQ641411 RPCI93-DpnII-28C15.TJ RPCI93-DpnII Trypano... 33 9.0
emb|AZ215288|AZ215288 Sheared DNA-83F7.TR Sheared DNA Trypanosom... 33 9.0
30 emb|AW282605|AW282605 LG1_310_E08.g1_A002 Light Grown 1 (LG1) So... 29 9.8

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Database: plantfungal

40 661,018 sequences; 426,114,510 total letters

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50 emb AV422547 AV422547 AV422547 Lotus japonicus young plants (two...	28	0.006
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emb AW508852 AW508852 si41b07.y1 Gm-r1030 Glycine max cDNA clone...	28	0.015
emb AW432586 AW432586 sh76d11.y1 Gm-cl015 Glycine max cDNA clone...	28	0.016
emb AI965714 AI965714 sc77f01.y1 Gm-cl018 Glycine max cDNA clone...	28	0.021
55 emb AI930916 AI930916 sb44d12.y1 Gm-cl015 Glycine max cDNA clone...	28	0.031
emb AW100187 AW100187 sd26g01.y1 Gm-cl012 Glycine max cDNA clone...	26	0.031
emb AW153030 AW153030 se34a10.y1 Gm-cl015 Glycine max cDNA clone...	30	0.13
gb BE055645 BE055645 GA__Ea0021E15f Gossypium arboreum 7-10 dpa ...	33	0.19
gb U91857 SHU91857 Stylosanthes hamata ethylene-responsive eleme...	28	0.29
60 emb AW329270 AW329270 N200490e rootphos(-) Medicago truncatula c...	29	0.33
emb X02873 DCEXTG Carrot gene for extensin.	35	0.34

	gb M11221 DAREXTA Carrot (<i>D.carota</i>) extensin mRNA, partial cds.	35	0.47
	emb AW306694 AW306694 sf47b08.y1 Gm-c1009 Glycine max cDNA clone...	27	0.54
	emb AW035648 AW035648 EST281480 tomato callus, TAMU Lycopersicon...	28	0.57
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5	emb AV411578 AV411578 AV411578 Lotus japonicus young plants (two...	26	0.68
	emb AW618112 AW618112 EST314162 L. pennellii trichome, Cornell U...	28	0.72
	emb AW164515 AW164515 se74g06.y1 Gm-c1023 Glycine max cDNA clone...	27	0.74
	emb AI900852 AI900852 sb95c05.y1 Gm-c1012 Glycine max cDNA clone...	27	0.75
	emb AW328989 AW328989 N200181e rootphos(-) Medicago truncatula c...	27	0.81
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	emb AW647824 AW647824 EST326278 tomato germinating seedlings, TA...	28	1.2
	emb AI486798 AI486798 EST245120 tomato ovary, TAMU Lycopersicon ...	28	1.3
15	emb AW568194 AW568194 si57g03.y1 Gm-r1030 Glycine max cDNA clone...	29	1.3
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	emb AW622531 AW622531 EST313331 tomato root during/after fruit s...	28	1.3
	dbj D38124 TOBBY4B Tobacco mRNA for EREBP-3, complete cds.	28	1.4
	emb AW695699 AW695699 NF097F03ST1F1029 Developing stem Medicago ...	31	1.4
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	dbj D86853 D86853 Catharanthus roseus cycl5 mRNA for extensin, c...	33	1.7
	emb AW650803 AW650803 EST329257 tomato germinating seedlings, TA...	33	1.7
	emb X63339 SRENOD2 S.rostrata Enod2 gene for nodulin.	32	2.3
25	gb C95684 C95684 C95684 Marchantia polymorpha immature sex organ...	32	2.3
	gb M12865 YSCRSCATC Yeast (<i>S.cerevisiae</i>) CAT repetitive element,...	27	2.7
	emb AW040234 AW040234 EST282740 tomato mixed elicitor, BTI Lycop...	28	3.0
	emb AW720424 AW720424 LjNEST22g2r Lotus japonicus nodule library...	32	3.2
	emb AW686730 AW686730 NF041H01NR1F1000 Nodulated root Medicago t...	32	3.2
30	emb AV412432 AV412432 AV412432 Lotus japonicus young plants (two...	26	3.2
	emb AV407890 AV407890 AV407890 Lotus japonicus young plants (two...	26	3.4
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	emb AV413265 AV413265 AV413265 Lotus japonicus young plants (two...	26	3.6
	gb U10398 YSCH9315 Saccharomyces cerevisiae chromosome VIII cosm...	27	3.6
35	emb AV412856 AV412856 AV412856 Lotus japonicus young plants (two...	26	3.7
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	emb AV419065 AV419065 AV419065 Lotus japonicus young plants (two...	26	4.0
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	emb AV413154 AV413154 AV413154 Lotus japonicus young plants (two...	28	4.3
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45	emb AW278410 AW278410 sf43g05.y1 Gm-c1009 Glycine max cDNA clone...	25	5.0
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emb|AF056182|AF056182 Emericella nidulans G-protein beta subunit... 30 8.2
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5 emb|AW686992|AW686992 NF004G07RT1F1055 Developing root Medicago ... 30 8.2
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emb|AQ910557|AQ910557 GSSTc05793 Trypanosome cruzi random genomi... 28 8.5
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10 emb|AW932239|AW932239 EST358082 tomato fruit mature green, TAMU ... 26 8.7
emb|AW933044|AW933044 EST358887 tomato fruit mature green, TAMU ... 26 8.7
emb|AW030545|AW030545 EST273800 tomato callus, TAMU Lycopersicon... 26 8.8
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20 gb|t76255, gb|t20906 and gb|ai100027 come from this gene."
/blast_score 0 /ec_number /family /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
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25 (1635 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

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gb|L24438|THLCYP450A Thlaspi arvense germline cytochrome P450 mR... 144 2e-48
emb|Z22545|PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA. 77 9e-47
40 dbj|D14588|PETHF1 Petunia hybrida Hfl mRNA for flavonoid-3',5'-h... 77 9e-47
emb|Z22544|PHFLAHYDA P.hybrida flavonoid 3',5'-hydroxylase mRNA. 71 2e-44
dbj|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 85 8e-44
emb|AW234222|AW234222 sf22f08.y1 Gm-c1028 Glycine max cDNA clone... 147 5e-43
emb|Y09423|NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... 126 8e-40
45 emb|AF122821|AF122821 Capsicum annuum cytochrome P450 (PepCYP) m... 127 2e-39
gb|U48435|SCU48435 Solanum chacoense putative cytochrome P450 ge... 136 3e-39
emb|AJ238612|CRO238612 Catharanthus roseus mRNA for cytochrome P... 135 3e-39
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emb|AW053855|AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... 130 9e-39
50 gb|U48434|SCU48434 Solanum chacoense cytochrome P450 mRNA, compl... 124 2e-38
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55 emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. 130 2e-36
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emb|AW668053|AW668053 GA_Ea0012G23 Gossypium arboreum 7-10 dpa ... 129 3e-36
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- 5 emb|X70981|SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase. 119 7e-34
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- emb|X71130|PHPET1 P.hybrida mRNA for P450 hydroxylase. 77 2e-33
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- emb|X71654|SMCYP71B3 S.melongena CYP71A2 mRNA for hydroxylase. 115 3e-32
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- 20 emb|AW310655|AW310655 sg22h01.x1 Gm-c1024 Glycine max cDNA clone... 140 3e-32
- emb|AF022459|AF022459 Glycine max cytochrome P450 monooxygenase ... 139 4e-32
- emb|AB028151|AB028151 Antirrhinum majus AFNS2 mRNA for cytochrom... 66 7e-32
- emb|AF150881|AF150881 Lycopersicon esculentum x Lycopersicon per... 78 3e-31
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- 25 emb|AW569661|AW569661 si89h01.y1 Gm-c1031 Glycine max cDNA clone... 137 3e-31
- emb|AW569417|AW569417 si86h05.y1 Gm-c1031 Glycine max cDNA clone... 137 3e-31
- emb|AW676782|AW676782 DG1_14_D06.g1_A002 Dark Grown 1 (DG1) Sorg... 135 4e-31
- emb|AW677294|AW677294 DG1_5_H08.g1_A002 Dark Grown 1 (DG1) Sorgh... 136 4e-31
- emb|AW623139|AW623139 EST321084 tomato flower buds 3-8 mm, Corne... 117 5e-31
- 30 emb|AW256491|AW256491 EST304628 KV2 Medicago truncatula cDNA clo... 136 6e-31
- dbj|D86351|D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,... 66 6e-31
- emb|AW922446|AW922446 DG1_19_F10.g1_A002 Dark Grown 1 (DG1) Sorg... 135 1e-30
- gb|U09610|U09610 Berberis stolonifera cytochrome P-450 CYP80 mRN... 125 2e-30
- emb|AW031613|AW031613 EST275067 tomato callus, TAMU Lycopersicon... 73 2e-30
- 35 emb|Y10490|GMC450CP3 G.max mRNA for putative cytochrome P450, cl... 133 3e-30
- emb|AF156976|AF156976 Gerbera hybrida flavone synthase II (CYP93... 63 3e-30
- emb|AW218579|AW218579 EST303762 tomato radicle, 5 d post-imbibit... 133 4e-30
- emb|AB028152|AB028152 Torenia hybrida TFNS5 mRNA for cytochrome ... 64 4e-30
- emb|AI489371|AI489371 EST247722 tomato ovary, TAMU Lycopersicon ... 111 6e-30
- 40 emb|AF000403|AF000403 Lotus japonicus putative cytochorome P450 ... 131 2e-29
- emb|AW394303|AW394303 sh31c01.y1 Gm-c1017 Glycine max cDNA clone... 130 3e-29
- emb|AW560246|AW560246 EST315294 DSIR Medicago truncatula cDNA cl... 130 3e-29
- emb|AW458764|AW458764 sh82d02.y1 Gm-c1016 Glycine max cDNA clone... 130 3e-29
- emb|AF135485|AF135485 Glycine max cytochrome P450 monooxygenaseC... 73 4e-29
- 45 emb|AF014800|AF014800 Eschscholzia californica (S)-N-methylcocla... 105 5e-29
- emb|AW923050|AW923050 DG1_48_G09.g1_A002 Dark Grown 1 (DG1) Sorg... 129 7e-29
- emb|AJ249799|CAR249799 Cicer arietinum partial mRNA for cytochro... 115 8e-29
- emb|AI938505|AI938505 sb46e03.y1 Gm-c1015 Glycine max cDNA clone... 128 9e-29
- emb|AW728587|AW728587 GA_Ea0017C12.Gossypium arboreum 7-10 dpa ... 101 1e-28
- 50 emb|AW922486|AW922486 DG1_19_B12.g1_A002 Dark Grown 1 (DG1) Sorg... 128 1e-28
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- 55 emb|AI776223|AI776223 EST257323 tomato resistant, Cornell Lycop... 126 6e-28
- emb|AW255421|AW255421 ML442 peppermint glandular trichome Mentha... 125 8e-28
- emb|AW256010|AW256010 MW364 peppermint glandular trichome Mentha... 125 8e-28
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10 emb|AW038144|AW038144 EST279801 tomato mixed elicitor, BTI Lycop... 123 3e-27
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emb|AF139532|AF139532 Liquidambar styraciflua aldehyde 5-hydroxy... 78 5e-27

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http://www3.ncbi.nlm.nih.gov/htbin-
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20 http://www.ncgr.org/cgi-bin/ff?pad4
(1732 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

30 emb|AW981483|AW981483 EST392636 DSIL Medicago truncatula cDNA cl... 126 8e-59
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emb|AI781175|AI781175 EST262054 tomato susceptible, Cornell Lyco... 62 4e-24
35 emb|AW011208|AW011208 ST18A05 Pine TriplEx shoot tip library Pin... 107 2e-23
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emb|AV423915|AV423915 AV423915 Lotus japonicus young plants (two... 98 6e-20
emb|AI778594|AI778594 EST259473 tomato susceptible, Cornell Lyco... 95 2e-19
emb|AW032676|AW032676 EST276235 tomato callus, TAMU Lycopersicon... 95 2e-19
40 emb|AW559251|AW559251 EST306087 DSIR Medicago truncatula cDNA cl... 97 4e-19
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emb|AW560897|AW560897 EST315945 DSIR Medicago truncatula cDNA cl... 73 1e-16
emb|AW257406|AW257406 EST305543 KV2 Medicago truncatula cDNA clo... 73 1e-16
45 emb|AW685948|AW685948 NF036G07NR1F1000 Nodulated root Medicago t... 73 1e-16
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60 emb|AW870069|AW870069 NXNV_123_G03_F Nsf Xylem Normal wood Verti... 58 2e-10
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5 emb|AZ212769|AZ212769 Sheared DNA-66C3.TR Sheared DNA Trypanosom... 34 3.4
emb|X82612|SCATM1 S.cerevisiae ATM1 gene. 34 3.4
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emb|AA649446|AA649446 T4369 MVAT4 bloodstream form of serodeme W... 34 4.7

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(1732 letters)

Database: plantfungal
20 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
25 Sequences producing significant alignments: (bits) Value

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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20	emb AW694081 AW694081 NF072E06ST1F1050 Developing stem Medicago ...	225	1e-57
	emb AW684895 AW684895 NF022G07NR1F1000 Nodulated root Medicago t...	222	9e-57
	emb AI899906 AI899906 sb96a02.y1 Gm-c1012 Glycine max cDNA clone...	220	5e-56
	emb AF036948 AF036948 Prunus avium phenylalanine ammonia-lyase (...)	220	6e-56
	emb AF237955 AF237955 Rubus idaeus phenylalanine ammonia-lyase 2...	220	6e-56
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661,018 sequences; 426,114,510 total letters

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 30 (400 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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emb X53375 HASF18 Sunflower anther-specific mRNA SF18.	75	3e-13
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	emb AW622923 AW622923 EST306993 tomato flower buds 3-8 mm, Corne...	40	0.007
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20	emb AW929939 AW929939 EST354209 tomato flower buds 8 mm to pre-a...	40	0.007
	emb AI897392 AI897392 EST266835 tomato ovary, TAMU Lycopersicon ...	40	0.008
	emb AI490243 AI490243 EST248569 tomato ovary, TAMU Lycopersicon ...	40	0.008
	emb AI487859 AI487859 EST246181 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AW217552 AW217552 EST296266 tomato flower buds 3-8 mm, Corne...	40	0.009
25	emb AI489818 AI489818 EST248157 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AI487398 AI487398 EST245720 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AW217379 AW217379 EST296063 tomato flower buds 0-3 mm, Corne...	40	0.010
	emb AI898009 AI898009 EST267452 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI897456 AI897456 EST266899 tomato ovary, TAMU Lycopersicon ...	40	0.010
30	emb AI483612 AI483612 EST249462 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI485550 AI485550 EST243871 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI484887 AI484887 EST243150 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI484497 AI484497 EST242507 tomato ovary, TAMU Lycopersicon ...	40	0.012
	emb AI490062 AI490062 EST248401 tomato ovary, TAMU Lycopersicon ...	40	0.012
35	emb AW775186 AW775186 EST331908 GVN Medicago truncatula cDNA clo...	39	0.016
	emb AI486656 AI486656 EST244977 tomato ovary, TAMU Lycopersicon ...	38	0.024
	emb AI485044 AI485044 EST243324 tomato ovary, TAMU Lycopersicon ...	37	0.041
	emb AW399651 AW399651 EST310151 L. pennellii trichome, Cornell U...	38	0.042
	emb A26964 A26964 D.merkii AMP2 sequence.	37	0.080
40	emb X77993 HASF18A H.annuus SF18 gene.	31	0.14
	emb A27063 A27063 L.cicera AFP sequence.	34	0.74
	emb AI757757 AI757757 EtESTea34d02.y1 Eimeria S5-2 Sporozoite st...	34	0.74
	emb AW217119 AW217119 EST295833 tomato callus, TAMU Lycopersicon...	27	0.90
	emb X95363 CAGT C.annuum gamma thionin gene.	33	1.0
45	emb X95730 CAGTHIOGN Capsicum annuum defensin gene.	33	1.0
	emb AL035477 PFMAL4P4 Plasmodium falciparum chromosome 4 strain ...	33	1.0
	emb AL117384 LMFL5883 Leishmania major Friedlin chromosome 23 co...	29	1.3
	emb Z74387 SCYDR262W S.cerevisiae chromosome IV reading frame OR...	33	1.4
	emb Z68329 SC9320A S.cerevisiae chromosome IV cosmid 9320A.	33	1.4
50	emb Z70202 SC9320X S.cerevisiae chromosome IV cosmid 9320X.	33	1.4
	emb AQ846121 AQ846121 LMAJFV1_lml4f01.y1 Leishmania major FV1 ra...	29	1.7
	emb AW725876 AW725876 GA_Ea0020A08 Gossypium arboreum 7-10 dpa ...	32	1.9
	emb AV387503 AV387503 AV387503 Chlamydomonas reinhardtii C9 Chla...	32	2.6
	emb AQ947439 AQ947439 Sheared DNA-50L12.TF Sheared DNA Trypanoso...	31	3.6
55	emb AA836739 AA836739 L30-187T3 Ice plant Lambda Uni-Zap XR expr...	31	3.6
	gb M65164 PAR51C P.tetraulera 51C surface protein gene, complet...	31	3.6
	emb X16877 VUSTORED Vigna unguiculata cDNA for stored cotyledon ...	31	3.6
	emb AW736134 AW736134 EST332130 KV3 Medicago truncatula cDNA clo...	25	4.8
	emb AL034381 SPCC61 S.pombe chromosome III cosmid c61.	31	5.0
60	emb AQ642382 AQ642382 RPCI93-DpnII-29C10.TV RPCI93-DpnII Trypano...	31	5.0
	gb L01579 PEADRR230B Pea (pi39) disease resistance response prot...	31	5.0

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emb|AI728914|AI728914 BNLGHi12020 Six-day Cotton fiber Gossypium... 31 5.0
gb|B07260|B07260 G236T7 MVAT4 sheared genomic library Trypanosom... 31 5.0
5 emb|AI728815|AI728815 BNLGHi11757 Six-day Cotton fiber Gossypium... 31 5.0
emb|AI726605|AI726605 BNLGHi6250 Six-day Cotton fiber Gossypium ... 31 5.0
gb|BE033595|BE033595 MF04D10 MF Mesembryanthemum crystallinum cD... 30 6.8
emb|AW508408|AW508408 si40e08.y1 Gm-r1030 Glycine max cDNA clone... 30 6.8
emb|AW830659|AW830659 sm05b06.y1 Gm-c1027 Glycine max cDNA clone... 30 6.8
10 emb|AW266371|AW266371 L30-3125T3 Ice plant Lambda Uni-Zap XR exp... 30 6.8
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emb|AW093819|AW093819 EST286999 tomato mixed elicitor, BTI Lycop... 30 6.8
emb|AI774224|AI774224 EST255419 tomato resistant, Cornell Lycop... 30 6.8
emb|AA962873|AA962873 L30-403T3 Ice plant Lambda Uni-Zap XR expr... 30 6.8
15 emb|AL034557|PFMAL4P1 Plasmodium falciparum chromosome 4 strain ... 30 6.8
emb|AQ905826|AQ905826 GSSTc010408 Trypanosome cruzi random genom... 30 6.8
emb|AW053406|AW053406 L30-1317T3 Ice plant Lambda Uni-Zap XR exp... 30 6.8

20 Query= PR.1_s_at 14635_s_at /id_source genbank /description
gb|aac69381.1| (ac005398) pathogenesis-related pr-1-like protein
[arabidopsis thaliana] /blast_score 1.00e-94 /ec_number /family
/chip nova /gb_link /ncgi
(738 letters)

25 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

30

	Score	E
Sequences producing significant alignments:	(bits)	Value
gb U70666 BNU70666 Brassica napus pathogenesis-related protein P...	323	3e-88
35 gb U21849 BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds.	323	3e-88
gb U64806 BNU64806 Brassica napus pathogenesis-related protein P...	209	4e-85
emb AI352851 AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl...	311	4e-84
emb AI352893 AI352893 MB72-6D PZ204.BNlib Brassica napus cDNA cl...	165	3e-62
emb AW217013 AW217013 EST295727 tomato callus, TAMU Lycopersicon...	152	4e-60
40 emb AW219671 AW219671 EST302153 tomato root during/after fruit s...	151	1e-59
emb AW092403 AW092403 EST285583 tomato mixed elicitor, BTI Lycop...	151	1e-59
emb AI895090 AI895090 EST264533 tomato callus, TAMU Lycopersicon...	151	1e-59
emb AW625930 AW625930 EST319825 tomato radicle, 5 d post-imbibit...	151	1e-59
emb AW032514 AW032514 EST276073 tomato callus, TAMU Lycopersicon...	151	1e-59
45 emb AW034260 AW034260 EST277831 tomato callus, TAMU Lycopersicon...	151	1e-59
emb AW040983 AW040983 EST283847 tomato mixed elicitor, BTI Lycop...	151	1e-59
emb AW034206 AW034206 EST277777 tomato callus, TAMU Lycopersicon...	151	1e-59
emb AW219480 AW219480 EST301878 tomato root during/after fruit s...	151	1e-59
emb AW092623 AW092623 EST285803 tomato mixed elicitor, BTI Lycop...	151	1e-59
50 emb AW040954 AW040954 EST283818 tomato mixed elicitor, BTI Lycop...	151	1e-59
emb AW034454 AW034454 EST278025 tomato callus, TAMU Lycopersicon...	151	1e-59
emb AW032723 AW032723 EST276282 tomato callus, TAMU Lycopersicon...	151	1e-59
emb AW033873 AW033873 EST277444 tomato callus, TAMU Lycopersicon...	151	1e-59
emb AI894650 AI894650 EST264093 tomato callus, TAMU Lycopersicon...	151	1e-59
55 emb AW033593 AW033593 EST277164 tomato callus, TAMU Lycopersicon...	151	3e-59
emb AW034724 AW034724 EST278526 tomato callus, TAMU Lycopersicon...	148	7e-59
emb AW041033 AW041033 EST283897 tomato mixed elicitor, BTI Lycop...	148	7e-59
emb X66942 NTPRB1B N.tabacum prb-1b gene.	146	9e-59
emb AW559895 AW559895 EST314943 DSIR Medicago truncatula cDNA cl...	160	1e-58
60 emb AW329241 AW329241 N200453e rootphos(-) Medicago truncatula c...	160	1e-58
emb AW559894 AW559894 EST314942 DSIR Medicago truncatula cDNA cl...	159	5e-58

- emb|AW035820|AW035820 EST281974 tomato callus, TAMU Lycopersicon... 145 6e-58
 emb|AW032139|AW032139 EST275593 tomato callus, TAMU Lycopersicon... 145 6e-58
 emb|AW034330|AW034330 EST277901 tomato callus, TAMU Lycopersicon... 144 2e-57
 emb|AW622143|AW622143 EST312941 tomato root during/after fruit s... 149 2e-57
 5 emb|AI352771|AI352771 MB58-5G PZ204.BNlib Brassica napus cDNA cl... 220 2e-57
 emb|AW032749|AW032749 EST276308 tomato callus, TAMU Lycopersicon... 149 3e-57
 emb|AI894391|AI894391 EST263846 tomato callus, TAMU Lycopersicon... 142 4e-57
 emb|AI896249|AI896249 EST265692 tomato callus, TAMU Lycopersicon... 142 5e-57
 emb|AI782621|AI782621 EST263500 tomato susceptible, Cornell Lyco... 144 7e-57
 10 emb|AW126362|AW126362 N100469e rootphos(-) Medicago truncatula c... 160 3e-56
 emb|AW981257|AW981257 EST392410 DSIL Medicago truncatula cDNA cl... 128 9e-56
 emb|AW033687|AW033687 EST277258 tomato callus, TAMU Lycopersicon... 149 2e-55
 emb|AI352783|AI352783 MB59-12D PZ204.BNlib Brassica napus cDNA c... 198 3e-55
 emb|X14065|NTPRP1 Nicotiana tabacum gene for basic form of patho... 140 4e-55
 15 emb|AW625666|AW625666 EST319573 tomato radicle, 5 d post-imbibit... 135 6e-55
 emb|AW032727|AW032727 EST276286 tomato callus, TAMU Lycopersicon... 147 1e-53
 emb|X52555|NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat... 116 1e-52
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 20 emb|AW559969|AW559969 EST315017 DSIR Medicago truncatula cDNA cl... 81 4e-52
 emb|AI352801|AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl... 194 1e-51
 emb|X17681|NTPR1CA Tobacco gene for pathogenesis-related protein... 111 2e-51
 emb|X05454|NTPR1CR Nicotiana tabacum mRNA for PR-1c protein. 111 2e-51
 emb|X12487|NTPR1C Tobacco mRNA fragment for pathogenesis-related... 111 2e-51
 25 emb|AJ011520|LES011520 Lycopersicon esculentum pr1a (P4) gene. 98 1e-50
 gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50
 emb|A22634|LEPI4GENE L.esculentum P14 gene. 98 1e-50
 emb|AJ250136|STU250136 Solanum tuberosum mRNA for pathogenesis r... 99 2e-50
 emb|AW218808|AW218808 EST301288 tomato root during/after fruit s... 116 3e-50
 30 emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50
 emb|AW094536|AW094536 EST287716 tomato mixed elicitor, BTI Lycop... 116 3e-50
 emb|AW038553|AW038553 EST280236 tomato mixed elicitor, BTI Lycop... 116 3e-50
 dbj|D90196|TOBPR1A Nicotiana tabacum mRNA for PR1a protein precu... 104 3e-50
 emb|X05959|NTPRIAG Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
 35 emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
 emb|X06361|NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela... 104 4e-50
 emb|X12485|NTPR1A Tobacco mRNA fragment for pathogenesis-related... 104 4e-50
 emb|AW033469|AW033469 EST277040 tomato callus, TAMU Lycopersicon... 116 5e-50
 emb|X06930|NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related ... 104 7e-50
 40 emb|AI352858|AI352858 MB70-10D PZ204.BNlib Brassica napus cDNA c... 197 7e-50
 emb|AI782416|AI782416 EST263295 tomato susceptible, Cornell Lyco... 95 7e-50
 emb|AW034882|AW034882 EST279111 tomato callus, TAMU Lycopersicon... 95 1e-49
 emb|AW031086|AW031086 EST274393 tomato callus, TAMU Lycopersicon... 116 1e-49
 emb|X74939|HVPR1AR H.vulgare HvPR-1a mRNA for a basic PR-1-type... 114 2e-49
 45 emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49
 emb|AW034167|AW034167 EST277738 tomato callus, TAMU Lycopersicon... 94 2e-49
 emb|X17680|NTPR1BA Tobacco gene for pathogenesis-related protein... 103 3e-49
 emb|X03465|NTPRPR Nicotiana tabacum mRNA for pathogenesis-relate... 103 3e-49
 dbj|D90197|TOBPR1B1 Nicotiana tabacum mRNA for PR1b protein. 103 3e-49
 50 emb|Y08804|LEPR1B1 L.esculentum mRNA for PR protein. 92 6e-49
 gb|M69248|TOMPRP6 Lycopersicon esculentum PR (pathogenesis relat... 92 6e-49
 emb|X68738|LEP1P14A L.esculentum mRNA for ethylene-induced P1(pl... 92 6e-49
 emb|AI781499|AI781499 EST262378 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI779424|AI779424 EST260303 tomato susceptible, Cornell Lyco... 92 6e-49
 55 emb|AW031093|AW031093 EST274400 tomato callus, TAMU Lycopersicon... 92 6e-49
 emb|AI779425|AI779425 EST260304 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI782545|AI782545 EST263424 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI782822|AI782822 EST263701 tomato susceptible, Cornell Lyco... 92 6e-49
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 60 emb|AI778680|AI778680 EST259559 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI899514|AI899514 EST268957 tomato susceptible, Cornell Lyco... 92 6e-49

emb|AI779287|AI779287 EST260166 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI773130|AI773130 EST254230 tomato resistant, Cornell Lycope... 92 6e-49
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 5 emb|AI778985|AI778985 EST259864 tomato susceptible, Cornell Lyco... 92 6e-49
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 emb|AI782288|AI782288 EST263167 tomato susceptible, Cornell Lyco... 92 6e-49
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 emb|AI781431|AI781431 EST262298 tomato susceptible, Cornell Lyco... 92 6e-49
 10 emb|AI780973|AI780973 EST261852 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI895236|AI895236 EST264679 tomato callus, TAMU Lycopersicon... 92 6e-49

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 (1236 letters)

20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E
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	gb M60729 HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge...	744	0.0
	emb A00741 A00741 A.rusticana synthetic gene (reverse complement...	692	0.0
	emb A00740 A00740 A.rusticana synthetic gene for peroxidase.	692	0.0
30	dbj E01651 E01651 cDNA encoding horseradish peroxidase.	692	0.0
	gb M37157 HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge...	371	e-133
	emb X97349 PTXP2PER P.trichocarpa mRNA for anionic peroxidase P...	473	e-132
	emb X97350 PTXP3PER P.trichocarpa mRNA for anionic peroxidase P...	469	e-131
	dbj D83224 POPP01 Populus nigra mRNA for peroxidase, complete cds.	468	e-131
35	gb M37156 HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge...	363	e-130
	emb X97348 PTXP1PER P.trichocarpa mRNA for anionic peroxidase P...	463	e-129
	dbj D30652 POPPA Populus kitakamiensis mRNA for peroxidase, part...	441	e-123
	emb X97351 PTXP4PER P.trichocarpa mRNA for anionic peroxidase P...	383	e-120
40	dbj D30653 POPPB Populus kitakamiensis mRNA for peroxidase, part...	356	e-112
	emb AF149277 AF149277 Phaseolus vulgaris peroxidase I precursor ...	227	e-107
	gb L36157 ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple...	229	e-107
	emb AF007211 AF007211 Glycine max peroxidase precursor (GMIPER1)...	229	e-106
	gb L07554 LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA...	381	e-105
	emb X90692 MSRNAPE1A M.sativa mRNA for peroxidase 1A.	211	e-105
45	dbj D90115 HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i...	296	e-103
	emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod ...	138	2e-97
	emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor ...	142	4e-97
	emb X90693 MSRNAPE1B M.sativa mRNA for peroxidase 1B.	231	1e-95
	emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C.	226	7e-94
50	gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA.	210	2e-89
	emb AI959837 AI959837 sc94h07.y1 Gm-cl019 Glycine max cDNA clone...	228	6e-89
	emb AF244924 AF244924 Spinacia oleracea peroxidase prx15 precurs...	208	9e-88
	emb AW559660 AW559660 EST314772 DSIR Medicago truncatula cDNA cl...	236	1e-87
	emb AW774581 AW774581 EST333732 KV3 Medicago truncatula cDNA clo...	236	7e-87
55	emb AF155124 AF155124 Gossypium hirsutum bacterial-induced perox...	215	2e-86
	emb AW981426 AW981426 EST392579 DSIL Medicago truncatula cDNA cl...	236	2e-85
	emb AB042103 AB042103 Asparagus officinalis AspPOX1 mRNA for per...	209	2e-85
	emb AF244923 AF244923 Spinacia oleracea peroxidase prx14 precurs...	205	9e-85
	emb AJ250121 PAB250121 Picea abies mRNA for SPI2 protein (spi2 g...	253	1e-83
60	emb AW775762 AW775762 EST334827 DSIL Medicago truncatula cDNA cl...	236	6e-83
	emb Y10466 SOPR XR5 S.oleracea mRNA for peroxidase, clone PC18.	218	3e-82

- emb|AW775425|AW775425 EST334490 DSIL Medicago truncatula cDNA cl... 208 1e-81
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emb|AF244922|AF244922 Spinacia oleracea peroxidase prx13 precurs... 212 3e-79
5 emb|X57564|ARNEUPERO A.rusticana mRNA for neutral peroxidase. 115 6e-78
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emb|AW267813|AW267813 EST305941 DSIR Medicago truncatula cDNA cl... 200 1e-76
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10 emb|AW256487|AW256487 EST304624 KV2 Medicago truncatula cDNA clo... 200 9e-76
emb|AW775890|AW775890 EST334955 DSIL Medicago truncatula cDNA cl... 200 3e-74
emb|AW257195|AW257195 EST305332 KV2 Medicago truncatula cDNA clo... 214 5e-74
gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 86 2e-73
gb|U41657|GMU41657 Glycine max seed coat peroxidase isozyme (SPO... 159 3e-73
15 emb|AB027752|AB027752 Nicotiana tabacum mRNA for peroxidase, com... 197 5e-73
gb|L36110|SSNPEROXIA Stylosanthes humilis peroxidase mRNA. 199 5e-73
gb|M37636|ARCPNC1 Arachis hypogaea cationic peroxidase (PNC1) mR... 204 7e-73
emb|AW685235|AW685235 NF027H10NR1F1000 Nodulated root Medicago t... 236 9e-73
emb|AW278775|AW278775 sf97d02.y1 Gm-cl019 Glycine max cDNA clone... 155 1e-72
20 emb|X71593|LECEV11A L.esculentum CEVI-1 mRNA. 99 2e-72
gb|J02979|TOBPXDLF Nicotiana tabacum lignin-forming peroxidase m... 100 2e-72
emb|AW559945|AW559945 EST314993 DSIR Medicago truncatula cDNA cl... 233 2e-72
emb|AW980744|AW980744 EST391897 GVN Medicago truncatula cDNA clo... 235 5e-70
emb|Y10467|SOPR XR6 S.oleracea mRNA for peroxidase, clone PC23. 105 1e-69
25 dbj|D83225|POPP02 Populus nigra peroxidase gene, complete cds. 196 2e-69
gb|M74103|TOBANPER Nicotiana sylvestris anionic peroxidase mRNA,... 205 6e-69
emb|AF043234|AF043234 Striga asiatica ferriprotein porphyrin-con... 211 1e-68
gb|BE034991|BE034991 MM01A12 MM Mesembryanthemum crystallinum cD... 202 6e-68
emb|AW574244|AW574244 EST316835 GVN Medicago truncatula cDNA clo... 202 1e-67
30 emb|Y10465|SOPR XR4 S.oleracea mRNA for peroxidase, clone PC44. 98 3e-67
emb|AW686084|AW686084 NF038B07NR1F1000 Nodulated root Medicago t... 236 5e-67
emb|AW561032|AW561032 EST316080 DSIR Medicago truncatula cDNA cl... 203 7e-67
emb|X56011|TAPERO Wheat mRNA for peroxidase. 111 2e-66
emb|AW185769|AW185769 se59d08.y1 Gm-cl019 Glycine max cDNA clone... 219 4e-65
35 emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase. 96 2e-64
gb|BE033422|BE033422 ME01E09 ME Mesembryanthemum crystallinum cD... 184 4e-64
emb|AB024438|AB024438 Scutellaria baicalensis mRNA for peroxidas... 205 7e-64
gb|M91374|CUSPREPERA Cucumis sativus peroxidase mRNA, complete cds. 76 2e-63
gb|L24120|LINFLXP Linum usitatissimum peroxidase precursor (FLXP... 167 2e-63
40 gb|M91372|CUSPREPERB Cucumis sativus peroxidase mRNA, complete cds. 134 2e-63
emb|AF043235|AF043235 Striga asiatica ferriprotein porphyrin-con... 199 3e-63
emb|AW288002|AW288002 N100846e rootphos(-) Medicago truncatula c... 182 7e-63
emb|AW126121|AW126121 N100318e rootphos(-) Medicago truncatula c... 216 1e-62
gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 133 5e-62
45 emb|AW687443|AW687443 NF009F07RT1F1062 Developing root Medicago ... 235 1e-61
emb|AW687957|AW687957 NF001D11ST1F1000 Developing stem Medicago ... 236 3e-61
emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidas... 163 3e-61
emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 133 5e-61
emb|AI496388|AI496388 sb04a11.y1 Gm-cl004 Glycine max cDNA clone... 224 6e-61
50 emb|AW686765|AW686765 NF042E07NR1F1000 Nodulated root Medicago t... 222 8e-61
dbj|D38050|POPP1 Aspen prxA3a gene for peroxidase, complete cds. 121 9e-61
emb|AW704659|AW704659 sk54h10.y1 Gm-cl019 Glycine max cDNA clone... 149 9e-61
emb|Y10464|SOPR XR3 S.oleracea mRNA for peroxidase, clone PC42. 80 3e-60
emb|AW705730|AW705730 sk51b02.y1 Gm-cl019 Glycine max cDNA clone... 149 8e-60
55 gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 100 9e-60
gb|U12314|CCU12314 Cenchrus ciliaris clone PX7 peroxidase mRNA, ... 105 9e-60
emb|AI938533|AI938533 sb46h09.y1 Gm-cl015 Glycine max cDNA clone... 145 1e-59
emb|AW705617|AW705617 sk50d03.y1 Gm-cl019 Glycine max cDNA clone... 149 2e-59
emb|AI781859|AI781859 EST262738 tomato susceptible, Cornell Lyco... 102 2e-59
60 emb|AF149278|AF149278 Phaseolus vulgaris peroxidase 3 precursor ... 90 3e-59
gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 102 4e-59

emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59
 emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 156 8e-59
 gb|M32742|CUSCUPER C.sativus peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58
 emb|AW705946|AW705946 sk52h07.y1 Gm-c1019 Glycine max cDNA clone... 224 6e-58

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 thaliana] /blast_score 1.00e-158 /ec_number /family /chip nova
 10 /gb_link /ncgi
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

20

emb|AW730233|AW730233 GA_Ea0014B16 Gossypium arboreum 7-10 dpa ... 352 5e-98
 emb|AW649960|AW649960 EST328414 tomato germinating seedlings, TA... 308 4e-83
 emb|AW621664|AW621664 EST312462 tomato root during/after fruit s... 290 1e-77
 emb|AW031327|AW031327 EST274781 tomato callus, TAMU Lycopersicon... 282 3e-75
 25 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 271 4e-72
 emb|AW775853|AW775853 EST334918 DSIL Medicago truncatula cDNA cl... 264 9e-70
 emb|Z21642|CHASTRNA Antithamnion sp. Chloroplast trnK, trnE, trpA... 255 4e-67
 gb|BE124387|BE124387 EST393422 GVN Medicago truncatula cDNA clon... 227 9e-59
 gb|BE121873|BE121873 894015F07.y1 C. reinhardtii CC-1690, normal... 227 1e-58
 30 emb|AF022186|AF022186 Cyanidium caldarium strain RK1 chloroplast... 220 1e-56
 emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53
 emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49
 dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49
 emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49
 35 emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47
 dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46
 emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46
 dbj|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45
 gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43
 40 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42
 emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42
 emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38
 emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38
 emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32
 45 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycops... 138 5e-32
 emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 74 3e-30
 emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26
 emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21
 emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19
 50 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17
 emb|AF084886|AF084886 Neurospora crassa 314-448A mutant tryptoph... 68 9e-11
 emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptop... 53 4e-10
 emb|AF084880|AF084880 Neurospora crassa EMSG9-9A mutant tryptoph... 66 5e-10
 emb|AF084885|AF084885 Neurospora crassa NG61-6A mutant tryptoph... 64 1e-09
 55 emb|AF084884|AF084884 Neurospora crassa 314-722A mutant tryptoph... 64 1e-09
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 emb|AF084881|AF084881 Neurospora crassa 314-693A mutant tryptoph... 64 2e-09
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 60 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08
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	emb AV390244 AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla...	49	4e-05
	emb AW616467 AW616467 EST322878 L. hirsutum trichome, Cornell Un...	48	7e-05
	emb AL354022 P761R Leishmania major Friedlin PAC P761 right end-...	44	0.002
5	gb M91656 CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1...	43	0.005
	emb AQ903789 AQ903789 GSSTc04230 Trypanosome cruzi random genom...	35	0.24
	emb AW727215 AW727215 GA__Ea0023N23 Gossypium arboreum 7-10 dpa ...	36	0.52
	gb M91654 CCITRP03 Coprinus cinereus tryptophan synthetase (TRP1...	36	0.52
	emb AW728975 AW728975 GA__Ea0018P19 Gossypium arboreum 7-10 dpa ...	35	0.64
10	emb AL139794 LMFP1105 Leishmania major Friedlin chromosome 4 PAC...	35	0.87
	emb AW926438 AW926438 HVSMEg0007D14 Hordeum vulgare pre-anthesis...	34	1.2
	emb AA965348 AA965348 e9d04a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
	gb U12630 ENU12630 Emericella nidulans R153 core histone H3 (H3)...	34	1.3
	emb AI007494 AI007494 e9c09a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
15	emb AA787433 AA787433 n3d04a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
	emb X55548 ANH3GENE A.nidulans gene for core histone for H3.	34	1.3
	emb AQ396426 AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P...	34	1.6
	emb AF262997 AF262997 Ricinus communis NADP-dependent malic prot...	34	1.6
	gb M19025 CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c...	34	1.6
20	emb AF084888 AF084888 Neurospora crassa 656-2A mutant tryptophan...	31	1.7
	emb AF084887 AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta...	31	1.7
	emb AW694774 AW694774 NF080A05ST1F1036 Developing stem Medicago ...	34	1.8
	emb Y18012 TVE18012 Trametes versicolor mRNA for laccase.	33	2.3
	emb AQ500614 AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc...	33	2.5
25	emb AW187498 AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW187530 AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW694072 AW694072 NF072B12ST1F1096 Developing stem Medicago ...	33	3.1
	emb AW186883 AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW187537 AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ...	33	3.1
30	emb AW187474 AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AA167859 AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor...	33	3.5
	emb AV421993 AV421993 AV421993 Lotus japonicus young plants (two...	33	4.3
	emb AF129874 AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp...	33	4.3
	emb AL112679 CNS01AA7 Botrytis cinerea strain T4 cDNA library un...	33	4.7
35	gb BE028433 BE028433 EtESTea78d07.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI166784 AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li...	32	5.9
	emb AQ941624 AQ941624 Sheared DNA-53E1.TF Sheared DNA Trypanosom...	32	5.9
	emb AW728623 AW728623 GA__Ea0017G06 Gossypium arboreum 7-10 dpa ...	32	5.9
	gb BE027723 BE027723 EtESTea86c08.y1 Eimeria M5-6 Merozoite stag...	32	5.9
40	emb AI757375 AI757375 EtESTea32d03.y1 Eimeria S5-2 Sporozoite st...	32	5.9
	gb BE027843 BE027843 EtESTea88c05.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI973878 AI973878 sd13a09.y1 Gm-c1020 Glycine max cDNA clone...	32	5.9
	dbj D85261 D85261 Plasmodium vivax clone TD439B DNA for merozoit...	32	5.9
	dbj D85251 D85251 Plasmodium vivax clone TD207B DNA for merozoit...	32	5.9
45	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom...	32	6.5
	emb Z71509 SCYNL233W S.cerevisiae chromosome XIV reading frame O...	32	6.5
	emb AW707662 AW707662 832011E08.y1 C. reinhardtii CC-125 nutrien...	28	7.3
	emb AF083075 AF083075 Fusarium oxysporum f. sp. lycopersici exop...	32	8.1
	emb AV411934 AV411934 AV411934 Lotus japonicus young plants (two...	32	8.1
50	emb AW703740 AW703740 sk23g09.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
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	emb AV420652 AV420652 AV420652 Lotus japonicus young plants (two...	32	8.1
55	emb AV408860 AV408860 AV408860 Lotus japonicus young plants (two...	32	8.1
	emb AV420989 AV420989 AV420989 Lotus japonicus young plants (two...	32	8.1
	emb AV419314 AV419314 AV419314 Lotus japonicus young plants (two...	32	8.1
	emb AW720540 AW720540 LjNEST18h4r Lotus japonicus nodule library...	32	8.1
60	emb X77895 CPGPRNL28 G.pyrenaica chloroplast trnL gene intron.	32	8.1

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 thaliana] thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link /ncgi
 5 (1526 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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15	emb AF042320 AF042320 <i>Camptotheca acuminata</i> tryptophan synthase ...	858	0.0
	emb AF047024 AF047024 <i>Chlamydomonas reinhardtii</i> tryptophan synth...	712	0.0
	gb J04594 NEUTRP3A <i>N.crassa</i> tryptophan synthetase (trp3) alpha-2...	473	e-140
	emb Z98974 SPAC19A8 <i>S.pombe</i> chromosome I cosmid c19A8.	462	e-135
	emb AW031813 AW031813 EST275267 tomato callus, TAMU <i>Lycopersicon</i> ...	429	e-119
20	emb AF121272 AF121272 <i>Gracilaria gracilis</i> putative NAD-myo-inosi...	426	e-118
	dbj D89113 D89113 <i>Schizosaccharomyces pombe</i> mRNA, partial cds, c...	310	e-114
	emb AI055312 AI055312 coau0003K07 Cotton Boll Abscission Zone cD...	404	e-112
	emb AF042321 AF042321 <i>Camptotheca acuminata</i> tryptophan synthase ...	346	e-109
	gb BE126222 BE126222 DG1_68_D09.b1_A002 Dark Grown 1 (DG1) Sorgh...	379	e-104
25	emb AW650635 AW650635 EST329089 tomato germinating seedlings, TA...	372	e-102
	emb AI487343 AI487343 EST245665 tomato ovary, TAMU <i>Lycopersicon</i> ...	354	8e-97
	emb AI488733 AI488733 EST247072 tomato ovary, TAMU <i>Lycopersicon</i> ...	353	2e-96
	emb AA495663 AA495663 c313 Zhou and Ragan 1993 <i>Gracilaria gracil</i> ...	350	1e-95
	emb AW160221 AW160221 EST290079 <i>L. pennellii</i> trichome, Cornell U...	327	1e-88
30	emb V01342 SCTRP5A Yeast gene (trp5) for tryptophan synthetase.	270	6e-88
	emb Z72548 SCYGL026C <i>S.cerevisiae</i> chromosome VII reading frame O...	270	6e-88
	emb AI485149 AI485149 EST243453 tomato ovary, TAMU <i>Lycopersicon</i> ...	319	3e-86
	emb AI966766 AI966766 sc57f10.y1 Gm-c1016 Glycine max cDNA clone...	306	3e-82
	gb M91659 CCITRP08 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	302	4e-81
35	gb BE058277 BE058277 sn13h12.y1 Gm-c1016 Glycine max cDNA clone ...	259	6e-68
	emb AI488512 AI488512 EST246851 tomato ovary, TAMU <i>Lycopersicon</i> ...	237	2e-63
	emb AI487792 AI487792 EST246114 tomato ovary, TAMU <i>Lycopersicon</i> ...	232	8e-62
	emb AW696637 AW696637 NF109C11ST1F1085 Developing stem <i>Medicago</i> ...	213	2e-59
	emb AI898827 AI898827 EST268270 tomato ovary, TAMU <i>Lycopersicon</i> ...	228	7e-59
40	emb AQ450225 AQ450225 500009D01.x1 CpIOWAM13mp18gDNA1 <i>Cryptospor</i> ...	175	3e-58
	emb AW160220 AW160220 EST290078 <i>L. pennellii</i> trichome, Cornell U...	223	3e-57
	emb AF084902 AF084902 <i>Neurospora crassa</i> TD2(4A-4A)2A mutant trypt...	214	2e-54
	emb AF084903 AF084903 <i>Neurospora crassa</i> TD71-19A mutant tryptoph...	213	3e-54
45	emb AF084904 AF084904 <i>Neurospora crassa</i> TD54-6A mutant tryptopha...	210	3e-53
	emb AI779245 AI779245 EST260124 tomato susceptible, Cornell Lyco...	208	8e-53
	emb AI487088 AI487088 EST245410 tomato ovary, TAMU <i>Lycopersicon</i> ...	149	3e-51
	emb AQ876415 AQ876415 V99F5 mTn-3xHA/lacZ Insertion Library, str...	183	4e-50
	emb AL116518 CNS01D8U <i>Botrytis cinerea</i> strain T4 cDNA library un...	160	2e-47
50	emb AW745773 AW745773 WS1_37_G06.b1_A002 Water-stressed 1 (WS1) ...	167	2e-40
	emb AF084893 AF084893 <i>Neurospora crassa</i> TD24-2A-28A mutant trypt...	130	8e-38
	emb AF084892 AF084892 <i>Neurospora crassa</i> 314-567-9A mutant trypto...	132	1e-37
	emb AF084891 AF084891 <i>Neurospora crassa</i> 314-616-2A mutant trypto...	132	1e-37
	emb AF084895 AF084895 <i>Neurospora crassa</i> TD10-8A mutant tryptopha...	130	1e-37
55	emb AF084894 AF084894 <i>Neurospora crassa</i> TD7(13A-11A)13A mutant t...	130	1e-37
	emb AF084901 AF084901 <i>Neurospora crassa</i> TD72-1-25A mutant trypto...	129	1e-37
	emb AF084900 AF084900 <i>Neurospora crassa</i> TD85-1-24A mutant trypto...	129	1e-37
	emb AF084899 AF084899 <i>Neurospora crassa</i> TD86-1-22A mutant trypto...	129	1e-37
	emb AF084898 AF084898 <i>Neurospora crassa</i> TD6(1-8A)22A mutant trypt...	129	1e-37
60	emb AF084896 AF084896 <i>Neurospora crassa</i> NG29-3A mutant tryptopha...	129	1e-37
	emb AW745836 AW745836 WS1_37_G06.g1_A002 Water-stressed 1 (WS1) ...	157	2e-37

	emb AF084897 AF084897 <i>Neurospora crassa</i> TD3-32-16A mutant trypto...	128	3e-37
	emb AI399300 AI399300 NCW07F11T3 Westergaards <i>Neurospora crassa</i> ...	145	3e-37
	emb AF084906 AF084906 <i>Neurospora crassa</i> NG40-5A mutant tryptopha...	152	8e-36
	emb AF084905 AF084905 <i>Neurospora crassa</i> NG25-4A mutant tryptopha...	152	8e-36
5	gb BE024522 BE024522 894003E01.y1 <i>C. reinhardtii</i> CC-1690, normal...	142	6e-33
	emb AJ229567 KLAJ9567 <i>Khuyveromyces lactis</i> DNA fragment for sequ...	137	3e-31
	emb AQ449630 AQ449630 500002F12.x2 CplOWAM13mp18gDNA1 <i>Cryptospor...</i>	116	1e-27
	emb AW695848 AW695848 NF099D01ST1F1012 Developing stem <i>Medicago</i> ...	116	9e-27
10	emb AW098758 AW098758 ga01a03.y1 Moss EST library CPU <i>Ceratodon</i> ...	118	1e-25
	gb M91658 CCITRP07 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	115	8e-25
	emb AW086510 AW086510 ga01a03.x1 Moss EST library CPU <i>Ceratodon</i> ...	103	4e-21
	emb AW221168 AW221168 EST297637 tomato fruit mature green, TAMU ...	96	5e-19
	emb AW650217 AW650217 EST328671 tomato germinating seedlings, TA...	95	1e-18
15	emb AV408265 AV408265 AV408265 <i>Lotus japonicus</i> young plants (two...	77	4e-13
	emb AW688230 AW688230 NF005A01ST1F1000 Developing stem <i>Medicago</i> ...	72	1e-11
	emb AI488384 AI488384 EST246706 tomato ovary, TAMU <i>Lycopersicon</i> ...	70	4e-11
	emb AW032971 AW032971 EST276530 tomato callus, TAMU <i>Lycopersicon</i> ...	60	6e-08
	emb AW755317 AW755317 sl01e06.y1 <i>Gm-c1036</i> Glycine max cDNA clone...	57	4e-07
20	emb AW153250 AW153250 se37h08.y1 <i>Gm-c1015</i> Glycine max cDNA clone...	56	1e-06
	emb AQ450041 AQ450041 500007C05.x1 CplOWAM13mp18gDNA1 <i>Cryptospor...</i>	37	2e-04
	emb AW625162 AW625162 EST319069 tomato radicle, 5 d post-imbibit...	45	0.001
	gb M91656 CCITRP05 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	45	0.002
	emb AW926725 AW926725 HVSMEg0007P16 <i>Hordeum vulgare</i> pre-anthesis...	42	0.013
25	emb X99652 ANG3PDEHY <i>A.niger</i> gpd gene.	35	0.084
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	emb AV417838 AV417838 AV417838 <i>Lotus japonicus</i> young plants (two...	38	0.17
	emb AV414417 AV414417 AV414417 <i>Lotus japonicus</i> young plants (two...	38	0.17
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	gb BE060085 BE060085 HVSMEg0011G11f <i>Hordeum vulgare</i> pre-anthesis...	38	0.23
	gb U30626 SCU30626 <i>Saccharomyces cerevisiae</i> var. diastaticus glu...	37	0.32
	emb AJ010201 GMA010201 Glycine max mRNA for inosine monophosphat...	37	0.32
35	emb AW185330 AW185330 se90b04.y1 <i>Gm-c1027</i> Glycine max cDNA clone...	37	0.32
	emb Z38061 SC9168 <i>S.cerevisiae</i> chromosome IX cosmid 9168.	37	0.32
	emb AF160799 AF160799 <i>Sporidiobolus salmonicolor</i> aldehyde reduct...	37	0.44
	emb AC016161 AC016161 <i>Leishmania major</i> chromosome 35 clone L8149...	37	0.44
	emb AW185636 AW185636 se80e06.y1 <i>Gm-c1023</i> Glycine max cDNA clone...	37	0.44
40	emb AB030490 AB030490 Glycine max SG-05 gene for thiamin biosynt...	36	0.60
	emb AW278827 AW278827 sf99b01.y1 <i>Gm-c1019</i> Glycine max cDNA clone...	36	0.60
	emb Z93048 SLZ93048 <i>S.latifolia</i> mRNA, clone CCLS 37.1.	30	0.72
	emb AV393412 AV393412 AV393412 <i>Chlamydomonas reinhardtii</i> C9 Chla...	36	0.83
	emb AL035581 SPBC1677 <i>S.pombe</i> chromosome II cosmid c1677.	36	0.83
45	emb AV425767 AV425767 AV425767 <i>Lotus japonicus</i> young plants (two...	36	0.83
	emb AI727538 AI727538 BNLGH18343 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	gb BE053957 BE053957 GA_Ea0033K12f <i>Gossypium arboreum</i> 7-10 dpa ...	35	1.1
	emb AI731384 AI731384 BNLGH18894 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	emb AW596016 AW596016 si96g09.y1 <i>Gm-c1032</i> Glycine max cDNA clone...	35	1.1
50	emb AI730998 AI730998 BNLGH18370 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	emb AJ276509 TAE276509 <i>Triticum aestivum</i> grp1 gene for glycine-r...	28	1.3
	gb B13527 B13527 jd421 Trypanosome Shotgun M13 genomic Trypanoso...	29	1.4
	gb U56698 CPU56698 <i>Ceratodon purpureus</i> phytochrome photoreceptor...	35	2.2
	emb AF079252 AF079252 <i>Dichanthium aristatum</i> granule-bound starch...	35	2.2
55	emb AJ133604 TAE133604 <i>Triticum aestivum</i> mRNA for alpha-gliadin ...	34	4.1

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<http://www.ncgr.org/cgi-bin/ff?wt1012a>
(257 letters)

Database: plantfungal
5 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
10	Sequences producing significant alignments:		(bits) Value
	emb AL115243 CNS01C9F Botrytis cinerea strain T4 cDNA library un...	29	5.7
	gb S69616 S69616 Ant18=dihydroflavonol-4-reductase [Hordeum vulg...	29	7.8

15 Query= WT1096_at 14691_at /id_source genbank /description no hits
found. /blast_score /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt1096|/ncgi)
20 <http://www.ncgr.org/cgi-bin/ff?wt1096>
(371 letters)

Database: plantfungal
25 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
30	Sequences producing significant alignments:		(bits) Value
	emb AW203566 AW203566 sf35f11.y1 Gm-c1028 Glycine max cDNA clone...	36	0.099
	emb AW776554 AW776554 EST335619 DSIL Medicago truncatula cDNA cl...	36	0.099
	emb AW171733 AW171733 N100627e rootphos(-) Medicago truncatula c...	36	0.099
	emb AW185514 AW185514 se80g03.y1 Gm-c1023 Glycine max cDNA clone...	36	0.099
35	emb AI777176 AI777176 EST258141 tomato resistant, Cornell Lycopen...	35	0.26
	gb C22084 C22084 C22084 Miyagawa-wase satsuma mandarin orange (M...	35	0.26
	emb AW755041 AW755041 PC10A02 Pine TriplEx pollen cone library P...	35	0.26
	emb AW218263 AW218263 EST303444 tomato radicle, 5 d post-imbibit...	35	0.26
	emb AI488300 AI488300 EST246622 tomato ovary, TAMU Lycopersicon ...	35	0.26
40	emb AA557085 AA557085 927 Loblolly pine N Pinus taeda cDNA clone...	35	0.26
	emb AW981718 AW981718 PC15H05 Pine TriplEx pollen cone library P...	35	0.26
	emb AW982079 AW982079 PC23E11 Pine TriplEx pollen cone library P...	35	0.35
	emb AF101786 AF101786 Pinus taeda clone PtaADH1 adhesive/proline...	35	0.35
	emb AA785548 AA785548 g8e04a1.f1 Aspergillus nidulans 24hr asexu...	35	0.35
45	emb AI812646 AI812646 17D5 Pine Lambda Zap Xylem library Pinus t...	35	0.35
	emb AI776730 AI776730 EST257830 tomato resistant, Cornell Lycopen...	34	0.49
	emb AW040418 AW040418 EST283282 tomato mixed elicitor, BTI Lycop...	34	0.49
	emb AI490164 AI490164 EST246756 tomato resistant, Cornell Lycopen...	34	0.49
	emb AA739624 AA739624 389 PtIFG2 Pinus taeda cDNA clone 8646M 3'...	34	0.49
50	emb AI490158 AI490158 EST246750 tomato resistant, Cornell Lycopen...	34	0.49
	emb AW625280 AW625280 EST319283 tomato radicle, 5 d post-imbibit...	34	0.49
	emb AA740016 AA740016 781 PtIFG2 Pinus taeda cDNA clone 9242M 3'...	34	0.49
	emb AW329045 AW329045 N200244e rootphos(-) Medicago truncatula c...	34	0.67
	emb AA556671 AA556671 526 Loblolly pine CA Pinus taeda cDNA clon...	34	0.67
55	emb AI416531 AI416531 sal0c07.y1 Gm-c1003 Glycine max cDNA clone...	33	0.92
	emb AI416664 AI416664 sal0c07.x1 Gm-c1003 Glycine max cDNA clone...	33	0.92
	gb BE023931 BE023931 sm94c10.y1 Gm-c1015 Glycine max cDNA clone ...	33	0.92
	emb AW064558 AW064558 ST33A05 Pine TriplEx shoot tip library Pin...	33	1.3
	gb BE033882 BE033882 MG01E10 MG Mesembryanthemum crystallinum cD...	33	1.3
60	emb AW011244 AW011244 ST18E01 Pine TriplEx shoot tip library Pin...	33	1.3
	gb BE034004 BE034004 MG03C08 MG Mesembryanthemum crystallinum cD...	33	1.3

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 emb|AA749493|AA749493 L30-34T3 Ice plant Lambda Uni-Zap XR expre... 33 1.3
 emb|AW042623|AW042623 ST24A10 Pine TriplEx shoot tip library Pin... 33 1.3
 emb|AW216739|AW216739 EST295453 tomato callus, TAMU Lycopersicon... 33 1.3
 5 emb|AA660660|AA660660 00548 MtRHE Medicago truncatula cDNA 5', m... 33 1.3
 emb|AW011516|AW011516 ST21G04 Pine TriplEx shoot tip library Pin... 33 1.3
 emb|AW310413|AW310413 sB5f11.x1 Gm-c1028 Glycine max cDNA clone... 32 1.7
 emb|AW043248|AW043248 ST31B02 Pine TriplEx shoot tip library Pin... 32 1.7
 emb|AW255053|AW255053 ML1348 peppermint glandular trichome Menth... 32 2.4
 10 emb|AW255347|AW255347 ML358 peppermint glandular trichome Menth... 32 2.4
 emb|AW349069|AW349069 GM210003B22D9R Gm-r1021 Glycine max cDNA 3... 31 3.3
 emb|AW597162|AW597162 sj74c10.y1 Gm-c1034 Glycine max cDNA clone... 31 3.3
 emb|AI482974|AI482974 EST242297 tomato shoot, Cornell Lycopersic... 31 3.3
 emb|AI482971|AI482971 EST242294 tomato shoot, Cornell Lycopersic... 31 3.3
 15 emb|AW568662|AW568662 si60e08.y1 Gm-r1030 Glycine max cDNA clone... 31 3.3
 emb|AI442234|AI442234 sa49d06.y1 Gm-c1004 Glycine max cDNA clone... 31 3.3
 emb|AI484234|AI484234 EST248461 tomato susceptible, Cornell Lyco... 31 3.3
 emb|AW568685|AW568685 si60g08.y1 Gm-r1030 Glycine max cDNA clone... 31 3.3
 emb|AW218238|AW218238 EST303419 tomato radicle, 5 d post-imbibit... 31 3.3
 20 emb|AW102024|AW102024 sd82b01.y1 Gm-c1009 Glycine max cDNA clone... 31 3.3
 emb|AI484230|AI484230 EST248457 tomato susceptible, Cornell Lyco... 31 3.3
 gb|BE020040|BE020040 sm38c04.y1 Gm-c1028 Glycine max cDNA clone ... 31 3.3
 emb|AW064689|AW064689 ST34E09 Pine TriplEx shoot tip library Pin... 31 4.5
 emb|AI212169|AI212169 w9d03a1.fl Aspergillus nidulans 24hr asexu... 31 4.5
 25 emb|AI938315|AI938315 sc42h10.y1 Gm-c1014 Glycine max cDNA clone... 31 4.5
 emb|AW010715|AW010715 ST11D03 Pine TriplEx shoot tip library Pin... 31 4.5
 emb|AW064688|AW064688 ST34E08 Pine TriplEx shoot tip library Pin... 31 4.5
 emb|AW705091|AW705091 sk57e09.y1 Gm-c1019 Glycine max cDNA clone... 30 6.2
 emb|AW218605|AW218605 EST303788 tomato radicle, 5 d post-imbibit... 30 6.2
 30 emb|AF039708|AF039708 Maackia amurensis early nodulin (ENOD2) mR... 30 8.5
 emb|AW747425|AW747425 WS1_68_B12.b1_A002 Water-stressed 1 (WS1) ... 30 8.5
 emb|AW687627|AW687627 NF011F08RT1F1074 Developing root Medicago ... 30 8.5
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 emb|AW745895|AW745895 WS1_38_C08.b1_A002 Water-stressed 1 (WS1) ... 30 8.5
 35 emb|AW683985|AW683985 NF004G11NR1F1000 Nodulated root Medicago t... 30 8.5
 emb|AQ639472|AQ639472 927P1-2C7.TV 927P1 Trypanosoma brucei geno... 30 8.5
 emb|AW747471|AW747471 WS1_68_B12.g1_A002 Water-stressed 1 (WS1) ... 30 8.5
 emb|AW208288|AW208288 M110945e GVSNN Medicago truncatula cDNA clo... 30 8.5

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45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

50 Score E
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emb|AI771551|AI771551 EST252651 tomato ovary, TAMU Lycopersicon ... 105 1e-22
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 55 emb|AI778651|AI778651 EST259530 tomato susceptible, Cornell Lyco... 105 1e-22
 emb|AI898070|AI898070 EST267513 tomato ovary, TAMU Lycopersicon ... 105 1e-22
 emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 105 1e-22
 emb|AW930095|AW930095 EST340552 tomato fruit mature green, TAMU ... 105 1e-22
 emb|AI894447|AI894447 EST263902 tomato callus, TAMU Lycopersicon... 105 1e-22
 60 emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 105 1e-22
 emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 104 2e-22

	emb AW399412 AW399412 EST309912 <i>L. pennellii</i> trichome, Cornell U...	104	2e-22
	emb AI773854 AI773854 EST254954 tomato resistant, Cornell Lycopersicon...	104	3e-22
	gb BE125244 BE125244 DG1_18_B07.b1_A002 Dark Grown 1 (DG1) Sorgh...	99	9e-21
	emb AI736542 AI736542 sb30b04.y1 Gm-c1009 Glycine max cDNA clone...	64	5e-17
5	emb AI938176 AI938176 sc40e07.y1 Gm-c1014 Glycine max cDNA clone...	84	2e-16
	emb AI938151 AI938151 sc40a07.y1 Gm-c1014 Glycine max cDNA clone...	84	3e-16
	emb AW133238 AW133238 se16b04.y1 Gm-c1013 Glycine max cDNA clone...	84	3e-16
	emb AW568464 AW568464 si59b03.y1 Gm-r1030 Glycine max cDNA clone...	84	3e-16
	emb AW832123 AW832123 sm30h02.y1 Gm-c1028 Glycine max cDNA clone...	84	5e-16
10	emb AI899328 AI899328 EST268771 tomato ovary, TAMU Lycopersicon ...	82	2e-15
	emb AW348772 AW348772 GM210003A22G1R Gm-r1021 Glycine max cDNA 3...	80	6e-15
	emb AI443600 AI443600 sa42b08.y1 Gm-c1004 Glycine max cDNA clone...	72	1e-12
	gb BE057559 BE057559 sn04a01.y1 Gm-c1015 Glycine max cDNA clone ...	70	5e-12
	emb AI896759 AI896759 EST266202 tomato callus, TAMU Lycopersicon...	61	3e-09
15	gb BE123900 BE123900 EST394025 <i>DSIL Medicago truncatula</i> cDNA clo...	58	2e-08
	emb AW030966 AW030966 EST274273 tomato callus, TAMU Lycopersicon...	34	8e-05
	emb AW185963 AW185963 se61h02.y1 Gm-c1019 Glycine max cDNA clone...	40	0.004
	gb T14912 T14912 crs394 lambdaZAPST <i>Ricinus communis</i> cDNA clone ...	40	0.004
	emb AW184959 AW184959 se84d10.y1 Gm-c1023 Glycine max cDNA clone...	40	0.004
20	emb AW217201 AW217201 EST295915 tomato callus, TAMU Lycopersicon...	29	0.010
	emb AI487153 AI487153 EST245475 tomato ovary, TAMU Lycopersicon ...	35	0.14
	emb AA556663 AA556663 518 Loblolly pine CA <i>Pinus taeda</i> cDNA clon...	35	0.26
	emb AW472418 AW472418 si24h07.y1 Gm-c1029 Glycine max cDNA clone...	29	0.37
	emb AW831124 AW831124 sm09c06.y1 Gm-c1027 Glycine max cDNA clone...	28	0.56
25	gb BE059192 BE059192 sn27d12.y1 Gm-c1016 Glycine max cDNA clone ...	32	1.3
	emb AW101722 AW101722 sd69d02.y1 Gm-c1008 Glycine max cDNA clone...	32	1.3
	emb AW395281 AW395281 sh46b07.y1 Gm-c1017 Glycine max cDNA clone...	32	1.8
	emb AW932541 AW932541 EST358384 tomato fruit mature green, TAMU ...	31	2.4
	emb AV428275 AV428275 AV428275 <i>Lotus japonicus</i> young plants (two...	31	2.4
30	emb AV415030 AV415030 AV415030 <i>Lotus japonicus</i> young plants (two...	31	2.4
	emb AW702436 AW702436 TgESTzz76b07.y1 TgRH*-Tachyzoite cDNA Toxo...	31	2.4
	emb AW621293 AW621293 EST312091 tomato root during/after fruit s...	31	2.4
	gb BE036447 BE036447 MO24G12 <i>MO Mesembryanthemum crystallinum</i> cD...	31	2.4
	emb AW509230 AW509230 sh92h07.y1 Gm-c1016 Glycine max cDNA clone...	31	2.4
35	emb AW034791 AW034791 EST278827 tomato callus, TAMU Lycopersicon...	31	2.4
	emb AI780125 AI780125 EST261004 tomato susceptible, Cornell Lyco...	31	2.4
	gb BE021558 BE021558 sm49e02.y1 Gm-c1028 Glycine max cDNA clone ...	31	2.4
	emb AW220250 AW220250 EST302733 tomato root during/after fruit s...	31	2.4
	emb AW442607 AW442607 EST307537 tomato mixed elicitor, BTI Lycop...	31	2.4
40	emb AW623982 AW623982 EST321927 tomato flower buds 3-8 mm, Corne...	29	2.5
	emb AW719534 AW719534 LjNEST5c5rW <i>Lotus japonicus</i> nodule library...	31	3.3
	emb AW926699 AW926699 HVSMEg0007O14 <i>Hordeum vulgare</i> pre-anthesis...	31	3.3
	emb AL035264 LMFL8032 <i>Leishmania major</i> Friedlin chromosome 4 cos...	30	4.5
	emb AF015462 AF015462 <i>Plasmodium falciparum</i> microsatellite 14D s...	30	4.5
45	emb AQ989347 AQ989347 Gm_ISb001_080_I14R ISU Soybean BAC Library...	30	4.5
	emb AL354553 LMFL232 <i>Leishmania major</i> Friedlin chromosome 14 cos...	30	6.2
	emb AL049498 SPCC645 <i>S.pombe</i> chromosome III cosmid c645.	30	6.2
	emb AI352775 AI352775 MB58-8A PZ204.BNlib <i>Brassica napus</i> cDNA cl...	30	6.2
	emb AZ216688 AZ216688 Sheared DNA-84G11.TF Sheared DNA Trypanoso...	30	6.2
50	emb AQ160113 AQ160113 mgxb0003K19r CUGI Rice Blast BAC Library P...	30	6.2
	emb AF105143 AF105143 <i>Brassica napus</i> chromosome N3 disease resis...	29	8.6
	emb AV394954 AV394954 AV394954 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
	emb AF162071 AF162071 <i>Mortierella verticillata</i> beta-tubulin 1 (b...	29	8.6
	emb AV395268 AV395268 AV395268 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
55	emb AI960376 AI960376 sc82g12.y1 Gm-c1018 Glycine max cDNA clone...	29	8.6
	emb AV393824 AV393824 AV393824 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
	emb AW711896 AW711896 f6e11ne.r1 <i>Neurospora crassa</i> evening cDNA ...	29	8.6
	emb AV396392 AV396392 AV396392 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
	emb AQ659750 AQ659750 Sheared DNA-16J7.TF Sheared DNA Trypanosom...	29	8.6
60	emb AL163505 LMFL3640 <i>Leishmania major</i> Friedlin chromosome 21 co...	29	8.6

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nova /gb_link

5 http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt788| /ncgi
http://www.ncgr.org/cgi-bin/ff?wt788
(528 letters)

10 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

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	emb AW156276 AW156276 se21h09.y1 Gm-c1015 Glycine max cDNA clone...	39	0.025	
	emb AW688406 AW688406 NF007A07ST1F1000 Developing stem Medicago ...	35	0.59	
20	emb AW729009 AW729009 GA__Ea0019F23 Gossypium arboreum 7-10 dpa ...	35	0.59	
	emb AI210929 AI210929 m0d12a1.r1 Aspergillus nidulans 24hr asexu...	34	0.81	
	emb AI212271 AI212271 x1d11a1.r1 Aspergillus nidulans 24hr asexu...	34	0.81	
	emb AI210928 AI210928 m0d12a1.f1 Aspergillus nidulans 24hr asexu...	34	0.81	
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	emb AW756661 AW756661 sl25e12.y1 Gm-c1027 Glycine max cDNA clone...	33	1.5	
	emb AW278522 AW278522 sf45e07.y1 Gm-c1009 Glycine max cDNA clone...	33	1.5	
	emb AW424313 AW424313 sh63h04.y1 Gm-c1015 Glycine max cDNA clone...	33	1.5	
30	emb AW696170 AW696170 NF103B07ST1F1060 Developing stem Medicago ...	33	1.5	
	emb AW569414 AW569414 si86g10.y1 Gm-c1031 Glycine max cDNA clone...	33	1.5	
	emb AW830833 AW830833 sm36c08.y1 Gm-c1028 Glycine max cDNA clone...	33	1.5	
	emb AW831982 AW831982 sm18e08.y1 Gm-c1027 Glycine max cDNA clone...	33	1.5	
	emb AW734341 AW734341 sk81h11.y1 Gm-c1016 Glycine max cDNA clone...	33	1.5	
35	emb Y07940 SSY07940 S.selaginoides chloroplast rbcL gene.	33	2.1	
	emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi...	32	4.0	
	emb AQ946352 AQ946352 Sheared DNA-45B22.TF Sheared DNA Trypanoso...	31	5.5	
	emb AW180477 AW180477 MgA0600f MgA Library Mycosphaerella gramin...	31	5.5	
	emb AQ651798 AQ651798 Sheared DNA-20J13.TR Sheared DNA Trypanoso...	31	5.5	

40 Query= afl21356_f at 15116_f at /id_source genbank /description
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(647 letters)

45 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

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55	emb AW667697 AW667697 GA__Ea0010E14 Gossypium arboreum 7-10 dpa ...	287	6e-77	
	emb AI778230 AI778230 EST259109 tomato susceptible, Cornell Lyco...	287	6e-77	
	emb AW218621 AW218621 EST303804 tomato radicle, 5 d post-imbibit...	287	6e-77	
	emb AW668548 AW668548 GA__Ea0014I16 Gossypium arboreum 7-10 dpa ...	287	6e-77	
	emb AW668413 AW668413 GA__Ea0013N18 Gossypium arboreum 7-10 dpa ...	287	6e-77	
60	emb AI782495 AI782495 EST263374 tomato susceptible, Cornell Lyco...	285	3e-76	
	emb AI779421 AI779421 EST260300 tomato susceptible, Cornell Lyco...	285	3e-76	

- emb|AI775630|AI775630 EST256730 tomato resistant, Cornell Lycopersicon... 285 3e-76
 gb|BE055389|BE055389 GA_Ea0026N20f Gossypium arboreum 7-10 dpa ... 284 5e-76
 emb|AI779420|AI779420 EST260299 tomato susceptible, Cornell Lycopersicon... 282 2e-75
 emb|AW349482|AW349482 GM210007A20G5R Gm-r1021 Glycine max cDNA 3... 282 2e-75
- 5
 emb|AW041006|AW041006 EST283870 tomato mixed elicitor, BTI Lycopersicon... 279 2e-74
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 emb|AW569109|AW569109 si63e02.y1 Gm-r1030 Glycine max cDNA clone... 275 2e-73
 emb|AW472050|AW472050 si19d05.y1 Gm-cl029 Glycine max cDNA clone... 273 8e-73
 emb|AW568096|AW568096 si68d05.y1 Gm-r1030 Glycine max cDNA clone... 273 1e-72
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 emb|AW508057|AW508057 si49e04.y1 Gm-r1030 Glycine max cDNA clone... 271 4e-72
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 emb|AI930828|AI930828 sc47g06.y1 Gm-cl015 Glycine max cDNA clone... 269 1e-71
 emb|AW035526|AW035526 EST281264 tomato callus, TAMU Lycopersicon... 266 1e-70
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 emb|AW729878|AW729878 GA_Ea0026I18 Gossypium arboreum 7-10 dpa ... 261 4e-69
 emb|AW101773|AW101773 sd70b02.y1 Gm-cl008 Glycine max cDNA clone... 261 4e-69
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 emb|AW559683|AW559683 EST314795 DSIR Medicago truncatula cDNA clone... 260 6e-69
 emb|AW317108|AW317108 sg44d09.y1 Gm-cl025 Glycine max cDNA clone... 260 8e-69
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 emb|AW094638|AW094638 EST287806 tomato mixed elicitor, BTI Lycopersicon... 255 3e-67
 emb|AW585325|AW585325 EST306020 KV2 Medicago truncatula cDNA clone... 251 3e-66
 emb|AW351217|AW351217 GM210010B20H5R Gm-r1021 Glycine max cDNA 3... 250 8e-66
 emb|AW666097|AW666097 sk32b07.y1 Gm-cl028 Glycine max cDNA clone... 248 4e-65
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 emb|AW756544|AW756544 sl23d11.y1 Gm-cl036 Glycine max cDNA clone... 247 6e-65
 emb|AA556985|AA556985 827 Loblolly pine N Pinus taeda cDNA clone... 237 6e-62
 emb|AW279163|AW279163 sf67b11.y1 Gm-cl013 Glycine max cDNA clone... 237 8e-62
 emb|AW201089|AW201089 se97f12.y1 Gm-cl027 Glycine max cDNA clone... 236 1e-61
 emb|AI162549|AI162549 A019P27U Hybrid aspen plasmid library Populus... 236 2e-61
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 emb|AW720300|AW720300 LjNEST20d9r Lotus japonicus nodule library... 236 2e-61
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 emb|AI440757|AI440757 sa53g03.y1 Gm-cl004 Glycine max cDNA clone... 234 6e-61
 emb|AW043308|AW043308 ST31G09 Pine TriplEx shoot tip library Pinus... 230 1e-59
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 emb|AI774108|AI774108 EST255208 tomato resistant, Cornell Lycopersicon... 227 7e-59
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 emb|AW065077|AW065077 ST39D01 Pine TriplEx shoot tip library Pinus... 225 2e-58
 emb|AW704118|AW704118 sk16b03.y1 Gm-cl028 Glycine max cDNA clone... 221 4e-57
 emb|AI507795|AI507795 sb12g09.y1 Gm-cl004 Glycine max cDNA clone... 216 1e-55
- 50
 emb|AW289649|AW289649 NXNV003G05F Nsf Xylem Normal wood Vertical... 215 2e-55
 emb|AV422946|AV422946 AV422946 Lotus japonicus young plants (two... 122 3e-55
 gb|T14824|T14824 crs266 lambdaZAPST Ricinus communis cDNA clone ... 212 2e-54
 emb|AW443507|AW443507 EST308437 tomato mixed elicitor, BTI Lycopersicon... 207 6e-53
 emb|AW226029|AW226029 ST76E07 Pine TriplEx shoot tip library Pinus... 207 8e-53
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 emb|AW747461|AW747461 WS1_68_B01.g1_A002 Water-stressed 1 (WS1) ... 181 1e-51
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 gb|BE054071|BE054071 GA_Ea0035D19f Gossypium arboreum 7-10 dpa ... 93 4e-50
 gb|C96251|C96251 C96251 Marchantia polymorpha immature sex organ... 98 5e-50
 emb|AI442544|AI442544 sa32h03.y1 Gm-cl004 Glycine max cDNA clone... 196 2e-49
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 emb|AI164569|AI164569 A065P13U Hybrid aspen plasmid library Populus... 180 2e-48
 emb|AW888188|AW888188 NXNV_105_F04_F Nsf Xylem Normal wood Vertical... 183 1e-45

emb|AI855650|AI855650 sc32c06.y1 Gm-c1014 Glycine max cDNA clone... 127 3e-45
 emb|AI777234|AI777234 EST258199 tomato resistant, Cornell Lycopen... 148 1e-44
 emb|AI165310|AI165310 A081P03U Hybrid aspen plasmid library Popu... 152 7e-44
 emb|AW870064|AW870064 NXNV_123_F09_F Nsf Xylem Normal wood Verti... 176 1e-43
 5 emb|AI484178|AI484178 EST249331 tomato resistant, Cornell Lycopen... 144 2e-43
 emb|AI162101|AI162101 A012P21U Hybrid aspen plasmid library Popu... 164 3e-42
 emb|AW255890|AW255890 ML976 peppermint glandular trichome Menta... 143 7e-42
 emb|AW733771|AW733771 sk84b01.y1 Gm-c1035 Glycine max cDNA clone... 149 7e-42
 emb|AW010084|AW010084 PC01E03 Pine TriplEx pollen cone library P... 160 7e-39
 10 emb|AI161700|AI161700 A005P46U Hybrid aspen plasmid library Popu... 150 3e-38
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 emb|AI774615|AI774615 EST255715 tomato resistant, Cornell Lycopen... 157 6e-38
 emb|AW651357|AW651357 EST329811 tomato germinating seedlings, TA... 157 6e-38
 emb|AW623884|AW623884 EST321829 tomato flower buds 3-8 mm, Corne... 157 6e-38
 15 emb|AI484189|AI484189 EST249342 tomato resistant, Cornell Lycopen... 157 9e-38
 gb|L37653|L37653 BNAESTGU Mustard flower buds Brassica rapa cDNA... 156 1e-37
 emb|AW944894|AW944894 EST336944 tomato flower buds 3-8 mm, Corne... 154 8e-37
 emb|AW726742|AW726742 GA_Ea0022J15 Gossypium arboreum 7-10 dpa ... 152 2e-36
 emb|AW694116|AW694116 NF072H11ST1F1095 Developing stem Medicago ... 150 2e-36
 20 emb|AW649234|AW649234 EST327688 tomato germinating seedlings, TA... 151 5e-36
 emb|AW725828|AW725828 GA_Ea0019N04 Gossypium arboreum 7-10 dpa ... 95 8e-36
 emb|AI777997|AI777997 EST258876 tomato susceptible, Cornell Lyco... 149 3e-35
 emb|AW317704|AW317704 sg56c06.y1 Gm-c1007 Glycine max cDNA clone... 148 4e-35
 emb|AW432260|AW432260 sh71d04.y1 Gm-c1015 Glycine max cDNA clone... 143 2e-33
 25 emb|AI165031|AI165031 A073p61u Hybrid aspen plasmid library Popu... 131 6e-32
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 30 emb|AI899479|AI899479 EST268922 tomato susceptible, Cornell Lyco... 124 7e-28
 emb|AI460396|AI460396 sa81a06.y1 Gm-c1004 Glycine max cDNA clone... 119 2e-26
 emb|AT002745|AT002745 AT002745 POSLM01 Pleurotus ostreatus cDNA ... 116 9e-26
 emb|AW508566|AW508566 si33e04.y1 Gm-r1030 Glycine max cDNA clone... 115 4e-25
 emb|AI166161|AI166161 B00964U Hybrid aspen plasmid library Popul... 113 1e-24

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 dehydrogenase [arabidopsis thaliana] /blast_score 0
 (3267 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

emb|AI486200|AI486200 EST244521 tomato ovary, TAMU Lycopersicon ... 377 e-103
 50 emb|AI894899|AI894899 EST264342 tomato callus, TAMU Lycopersicon... 357 4e-97
 emb|AI488742|AI488742 EST247081 tomato ovary, TAMU Lycopersicon ... 347 2e-94
 emb|AF042184|AF042184 Brassica napus lysine-ketoglutarate reduct... 334 1e-93
 emb|AI054604|AI054604 coau0001I01 Cotton Boll Abscission Zone cD... 319 3e-92
 emb|AW034280|AW034280 EST277851 tomato callus, TAMU Lycopersicon... 316 7e-85
 55 emb|AI894874|AI894874 EST264317 tomato callus, TAMU Lycopersicon... 307 4e-82
 emb|AW932187|AW932187 EST358030 tomato fruit mature green, TAMU ... 294 2e-78
 emb|AW933092|AW933092 EST358935 tomato fruit mature green, TAMU ... 287 4e-76
 emb|AW442160|AW442160 EST311556 tomato fruit red ripe, TAMU Lyco... 220 8e-74
 emb|AW681014|AW681014 WS1_8_B05.b1_A002 Water-stressed 1 (WS1) S... 275 1e-72
 60 emb|AW933411|AW933411 EST359350 tomato fruit mature green, TAMU ... 272 1e-71
 emb|AW931846|AW931846 EST357689 tomato fruit mature green, TAMU ... 264 3e-69

	emb AI485129 AI485129 EST243433 tomato ovary, TAMU Lycopersicon ...	253	8e-66
	emb AW035300 AW035300 EST280663 tomato callus, TAMU Lycopersicon...	241	3e-62
	emb AW934545 AW934545 EST353353 tomato flower buds 0-3 mm, Corne...	230	4e-59
	emb AI771941 AI771941 EST253041 tomato ovary, TAMU Lycopersicon ...	228	2e-58
5	emb AL022244 SPBC3B8 S.pombe chromosome II cosmid c3B8.	181	2e-56
	emb AW037965 AW037965 EST279609 tomato mixed elicitor, BTI Lycop...	211	2e-53
	emb AW931630 AW931630 EST357473 tomato fruit mature green, TAMU ...	208	3e-52
	emb AW035261 AW035261 EST280523 tomato callus, TAMU Lycopersicon...	142	4e-52
	emb AI896768 AI896768 EST266211 tomato callus, TAMU Lycopersicon...	192	2e-47
10	emb Z71665 SCYNR050C S.cerevisiae chromosome XIV reading frame O...	155	5e-47
	emb X77363 SCLYS9 S.cerevisiae LYS9 gene.	155	5e-47
	emb AW224200 AW224200 EST301107 tomato fruit red ripe, TAMU Lyco...	188	2e-46
	emb AW930672 AW930672 EST356515 tomato fruit mature green, TAMU ...	110	4e-45
	emb AI771935 AI771935 EST253035 tomato ovary, TAMU Lycopersicon ...	173	6e-42
15	emb AI899372 AI899372 EST268815 tomato ovary, TAMU Lycopersicon ...	172	1e-41
	emb AI486726 AI486726 EST245048 tomato ovary, TAMU Lycopersicon ...	110	2e-40
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	emb AW441656 AW441656 EST311052 tomato fruit red ripe, TAMU Lyco...	110	2e-38
	emb AI486762 AI486762 EST245084 tomato ovary, TAMU Lycopersicon ...	161	3e-38
20	emb AI488387 AI488387 EST246709 tomato ovary, TAMU Lycopersicon ...	160	6e-38
	emb AW093830 AW093830 EST287010 tomato mixed elicitor, BTI Lycop...	98	4e-33
	emb AV427683 AV427683 AV427683 Lotus japonicus young plants (two...	142	2e-32
	emb AI782310 AI782310 EST263189 tomato susceptible, Cornell Lyco...	139	1e-31
	emb AW432287 AW432287 sh71g03.y1 Gm-c1015 Glycine max cDNA clone...	82	6e-31
25	emb AL111972 CNS019QK Botrytis cinerea strain T4 cDNA library un...	136	1e-30
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30	emb AW038858 AW038858 EST280814 tomato mixed elicitor, BTI Lycop...	114	5e-24
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	emb AI487518 AI487518 EST245840 tomato ovary, TAMU Lycopersicon ...	110	6e-23
	emb AI486763 AI486763 EST245085 tomato ovary, TAMU Lycopersicon ...	110	6e-23
	emb AI399018 AI399018 NCW10A5T3 Westergaards Neurospora crassa c...	63	1e-21
35	emb AW031018 AW031018 EST274325 tomato callus, TAMU Lycopersicon...	101	4e-20
	emb AW932183 AW932183 EST358026 tomato fruit mature green, TAMU ...	72	9e-13
	emb AW096237 AW096237 EST289417 tomato mixed elicitor, BTI Lycop...	67	8e-10
	emb AA577639 AA577639 EST213 Sugarcane leaf roll Saccharum sp. c...	65	3e-09
	emb AW224318 AW224318 EST301045 tomato fruit red ripe, TAMU Lyco...	51	5e-05
40	emb AI900022 AI900022 sb97g03.y1 Gm-c1012 Glycine max cDNA clone...	50	1e-04
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	emb X77362 SCLYS1 S.cerevisiae LYS1 gene.	45	0.004
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45	gb U13233 CAU13233 Candida albicans saccharopine dehydrogenase (...)	40	0.078
	emb AL110979 CNS018Z0 Botrytis cinerea strain T4 cDNA library un...	35	0.079
	emb AL133156 SPAC227 S.pombe chromosome I cosmid c227.	40	0.15
	emb AF178855 AF178855 Candida albicans Crm1p (CRM1) gene, comple...	37	0.99
	emb AI667978 AI667978 TENG0800 T. Cruzi epimastigote normalised ...	36	1.4
50	emb AW310192 AW310192 sf32e10.x1 Gm-c1028 Glycine max cDNA clone...	36	1.4
	emb AW705872 AW705872 sk52a01.y1 Gm-c1019 Glycine max cDNA clone...	35	2.6
	emb AL355930 NCB208 Neurospora crassa DNA linkage group II BAC c...	35	3.5
	gb N82089 N82089 TgESTzy41f01.r1 TgRH Tachyzoite cDNA Toxoplasma...	35	3.5
	emb AW713255 AW713255 g6f04ne.fl Neurospora crassa evening cDNA ...	33	4.1
55	emb AW710105 AW710105 elc07ne.fl Neurospora crassa evening cDNA ...	33	4.1
	emb AW712320 AW712320 g1a02ne.fl Neurospora crassa evening cDNA ...	33	4.2
	emb AA451583 AA451583 AJK252 Onion seedling leaf cDNA library Al...	35	4.8
	emb AQ660868 AQ660868 Sheared DNA-27G4.TF Sheared DNA Trypanosom...	35	4.8
	emb AI773473 AI773473 EST254573 tomato resistant, Cornell Lycop...	30	5.4
60	emb X99000 CS39KBCIV S.cerevisiae 39kb DNA segment of chromosome...	34	6.7
	gb BE021261 BE021261 sm56g06.y1 Gm-c1028 Glycine max cDNA clone ...	34	6.7

	emb AA556567 AA556567 422 Loblolly pine C Pinus taeda cDNA clone...	34	6.7
	emb Z74265 SCYDL217C S.cerevisiae chromosome IV reading frame OR...	34	6.7
	emb Z73529 SCYPL173W S.cerevisiae chromosome XVI reading frame O...	34	6.7
	emb AI486066 AI486066 EST244387 tomato ovary, TAMU Lycopersicon ...	34	6.7
5	emb AV420631 AV420631 AV420631 Lotus japonicus young plants (two...	34	6.7
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	emb AL049181 PFMAL13P4 Plasmodium falciparum chromosome 13 strai...	34	9.2
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	emb AL033391 CAC20C1 C.albicans cosmid Ca20C1.	34	9.2
10	emb AF202183 AF202183 Glycine max isoflavone reductase homolog 1...	34	9.2
	emb AW648458 AW648458 EST326912 tomato germinating seedlings, TA...	34	9.2
	emb AA051847 AA051847 Cn0025-5 Cryptococcus neoformans, Stratage...	34	9.2
	emb AI960767 AI960767 sc90b07.y1 Gm-cl019 Glycine max cDNA clone...	34	9.2
	emb Z49384 SCYJL109C S.cerevisiae chromosome X reading frame ORF...	34	9.2
15	emb AF106954 AF106954 Brassica napus galactinol synthase (GS) mR...	34	9.2
	emb AW164589 AW164589 se73h03.y1 Gm-cl023 Glycine max cDNA clone...	34	9.2
	emb AW731148 AW731148 GA_Ea0010C07 Gossypium arboreum 7-10 dpa ...	34	9.2
	emb AW308914 AW308914 sf91g02.y1 Gm-cl019 Glycine max cDNA clone...	34	9.2
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20	emb AV423166 AV423166 AV423166 Lotus japonicus young plants (two...	34	9.2
	emb Z99164 SPAC29B12 S.pombe chromosome I cosmid c29B12.	29	9.4
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	emb AW565461 AW565461 LG1_344_F11.g1_A002 Light Grown 1 (LG1) So...	269	7e-71
	emb AW455238 AW455238 EST311898 tomato root during/after fruit s...	229	1e-63
	emb AW568861 AW568861 si73b10.y1 Gm-cl031 Glycine max cDNA clone...	139	3e-61
40	emb AI487264 AI487264 EST245586 tomato ovary, TAMU Lycopersicon ...	205	1e-55
	emb AI485585 AI485585 EST243906 tomato ovary, TAMU Lycopersicon ...	205	1e-54
	emb AW667985 AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ...	128	4e-54
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	emb AI897690 AI897690 EST267133 tomato ovary, TAMU Lycopersicon ...	205	7e-54
45	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	162	1e-53
	emb AI486547 AI486547 EST244868 tomato ovary, TAMU Lycopersicon ...	150	1e-53
	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	165	1e-53
	emb AI489882 AI489882 EST248221 tomato ovary, TAMU Lycopersicon ...	205	3e-53
	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	168	5e-53
50	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	163	9e-53
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	170	8e-52
	emb AI485022 AI485022 EST243302 tomato ovary, TAMU Lycopersicon ...	205	1e-51
	emb AI484547 AI484547 EST242777 tomato ovary, TAMU Lycopersicon ...	205	1e-51
	emb AI484020 AI484020 EST249891 tomato ovary, TAMU Lycopersicon ...	205	1e-51
55	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	160	2e-51
	emb AF142596 AF142596 Nicotiana tabacum LRR receptor-like protei...	144	2e-51
	emb AW616916 AW616916 EST323327 L. hirsutum trichome, Cornell Un...	145	3e-51
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	165	1e-50
	emb AI487456 AI487456 EST245778 tomato ovary, TAMU Lycopersicon ...	139	3e-50
60	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	154	7e-50
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	164	7e-50

- emb|AF220602|AF220602 *Lycopersicon pimpinellifolium* Rio Grande 7... 96 2e-49
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5 emb|AW266297|AW266297 L30-3030T3 Ice plant Lambda Uni-Zap XR exp... 169 3e-48
emb|AB008191|AB008191 *Brassica rapa* mRNA for SRK29, complete cds. 154 4e-48
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10 emb|X98520|BOSFR2 *B.oleracea* mRNA for receptor-like kinase, SFR2. 153 7e-47
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emb|AB032474|AB032474 *Brassica oleracea* SRK60 mRNA for S60 S-loc... 127 1e-46
emb|Y18260|BOY18260 *Brassica oleracea* mRNA for SRK15 protein, pa... 150 1e-46
15 gb|U20948|ITU20948 *Ipomoea trifida* receptor protein kinase (IRK1... 126 2e-46
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emb|AF088885|AF088885 *Nicotiana tabacum* receptor-like kinase CHR... 156 6e-46
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20 emb|Y14286|BOY14286 *Brassica oleracea* SFR3 gene, partial. 91 1e-45
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dbj|D38563|BOLRPKA *Brassica campestris* mRNA for receptor protein... 127 2e-45
dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 134 2e-45
25 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 145 2e-45
emb|AI898918|AI898918 EST268361 tomato ovary, TAMU *Lycopersicon* ... 183 5e-45
emb|AF131222|AF131222 *Lophopyrum elongatum* protein serine/threon... 138 2e-44
emb|AW756743|AW756743 sl26f10.y1 Gm-cl027 Glycine max cDNA clone... 181 2e-44
emb|AF220603|AF220603 *Lycopersicon esculentum* VFNT Cherry Pto lo... 96 2e-44
30 emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber *Gossypium* ... 132 3e-44
emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 151 4e-44
emb|AI489009|AI489009 EST247348 tomato ovary, TAMU *Lycopersicon* ... 117 7e-44
emb|AI483732|AI483732 EST249603 tomato ovary, TAMU *Lycopersicon* ... 177 4e-43
emb|AA738545|AA738545 SbRLK3 *Sorghum bicolor* cv. TX430 leaf Sorg... 153 6e-43
35 gb|U59315|LPU59315 *Lycopersicon pimpinellifolium* serine/threonin... 88 1e-42
gb|U02271|LEU02271 *Lycopersicon pimpinellifolium* Rio Grande-PtoR... 88 1e-42
emb|AJ245479|BNA245479 *Brassica napus* SII3, slk, srk, CePP, Fmt,... 80 2e-42
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emb|AW220490|AW220490 EST297043 tomato fruit mature green, TAMU ... 116 2e-42
40 gb|U28007|LEU28007 *Lycopersicon esculentum* Pto kinase interactor... 83 3e-42
emb|AW621706|AW621706 EST312504 tomato root during/after fruit s... 143 4e-42
emb|AW031255|AW031255 EST274630 tomato callus, TAMU *Lycopersicon*... 149 6e-42
emb|AW684940|AW684940 NF023C12NR1F1000 Nodulated root *Medicago* t... 113 6e-42
emb|AB000971|AB000971 *Brassica campestris* pseudogene for recepto... 78 8e-42
45 gb|U59316|LEU59316 *Lycopersicon esculentum* serine/threonine prot... 87 1e-41
emb|AW687233|AW687233 NF007D09RT1F1077 Developing root *Medicago* ... 93 1e-41
emb|AW220491|AW220491 EST297044 tomato fruit mature green, TAMU ... 116 2e-41
dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 81 2e-41
dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 81 2e-41
50 emb|AB041503|AB041503 *Populus nigra* PnPK1 mRNA for protein kinas... 77 3e-41
emb|AW220489|AW220489 EST297042 tomato fruit mature green, TAMU ... 112 3e-41
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emb|AI484701|AI484701 EST242962 tomato ovary, TAMU *Lycopersicon* ... 127 1e-40
55 emb|AA738544|AA738544 SbRLK2 *Sorghum bicolor* cv. TX430 leaf Sorg... 122 1e-40
emb|AW672145|AW672145 LG1_357_A10.b1_A002 Light Grown 1 (LG1) So... 167 2e-40
gb|U59317|LPU59317 *Lycopersicon pimpinellifolium* serine/threonin... 93 3e-40
gb|U13923|LEU13923 *Lycopersicon pimpinellifolium* serine/threonin... 93 3e-40
emb|Z73295|CRPK1 *C.roseus* mRNA for receptor-like protein kinase. 74 5e-40
60 gb|U59318|LEU59318 *Lycopersicon esculentum* serine/threonine prot... 92 6e-40
emb|AW729859|AW729859 GA__Ea0026H04 *Gossypium arboreum* 7-10 dpa ... 81 1e-39

emb|AW982539|AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi... 129 1e-39.
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 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 125 1e-39
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 5 emb|AW284352|AW284352 LG1_275_D12.g1_A002 Light Grown 1 (LG1) So... 165 2e-39
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 gb|BE053916|BE053916 GA__Ea0031D03f Gossypium arboreum 7-10 dpa ... 77 1e-38
 emb|AW760240|AW760240 sl59g07.y1 Gm-c1027 Glycine max cDNA clone... 130 2e-38
 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 73 3e-38
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 dbj|baa24440.1| (ab010407) phosphoglycerate dehydrogenase [arabidopsis
 thaliana] /blast_score 0
 20 (2127 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

25 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

30 emb|AW930291|AW930291 EST340748 tomato fruit mature green, TAMU ... 403 e-111
 emb|AW625643|AW625643 EST319550 tomato radicle, 5 d post-imbibit... 377 e-103
 emb|AW688234|AW688234 NF005A05ST1F1000 Developing stem Medicago ... 367 e-100
 emb|AW666282|AW666282 sk34f11.y1 Gm-c1028 Glycine max cDNA clone... 360 2e-98
 emb|AW691093|AW691093 NF041B09ST1F1000 Developing stem Medicago ... 332 5e-96
 35 gb|BE055044|BE055044 GA__Ea0031H08f Gossypium arboreum 7-10 dpa ... 332 9e-95
 emb|AW696933|AW696933 NF112E03ST1F1021 Developing stem Medicago ... 347 3e-94
 emb|AW926942|AW926942 HVSMEg0009B01 Hordeum vulgare pre-anthesis... 295 6e-89
 emb|AW737130|AW737130 EST338557 tomato flower buds, anthesis, Co... 325 1e-87
 emb|AW689358|AW689358 NF018C09ST1F1000 Developing stem Medicago ... 281 3e-85
 40 emb|AW650696|AW650696 EST329150 tomato germinating seedlings, TA... 179 2e-84
 emb|AW625020|AW625020 EST313849 tomato radicle, 5 d post-imbibit... 301 1e-80
 emb|AI813214|AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta... 297 2e-80
 emb|AW692700|AW692700 NF054C07ST1F1000 Developing stem Medicago ... 279 6e-80
 gb|BE036418|BE036418 MO24D12 MO Mesembryanthemum crystallinum cD... 258 2e-79
 45 gb|BE020170|BE020170 sm39e05.y1 Gm-c1028 Glycine max cDNA clone ... 293 3e-78
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 emb|AW731385|AW731385 GA__Ea0030K22 Gossypium arboreum 7-10 dpa ... 289 6e-77
 gb|BE052354|BE052354 GA__Ea0034P16f Gossypium arboreum 7-10 dpa ... 282 5e-75
 emb|AW687344|AW687344 NF008F03RT1F1029 Developing root Medicago ... 269 5e-71
 50 emb|AW926887|AW926887 HVSMEg0008N09 Hordeum vulgare pre-anthesis... 264 1e-69
 emb|AW944677|AW944677 00152 leafy spurge Lambda HybriZAP 2.1 two... 248 1e-64
 emb|AW727978|AW727978 GA__Ea0029C18 Gossypium arboreum 7-10 dpa ... 231 2e-61
 emb|AW755716|AW755716 sl08b12.y1 Gm-c1036 Glycine max cDNA clone... 234 2e-60
 emb|AW923236|AW923236 DGI_50_A11.g1_A002 Dark Grown 1 (DG1) Sorg... 233 3e-60
 55 gb|BE060782|BE060782 HVSMEg0013F14f Hordeum vulgare pre-anthesis... 226 7e-58
 emb|AW203801|AW203801 sf38d05.y1 Gm-c1028 Glycine max cDNA clone... 215 1e-54
 emb|AW317181|AW317181 sf38d05.x1 Gm-c1028 Glycine max cDNA clone... 200 4e-50
 emb|AW398821|AW398821 EST309321 L. pennellii trichome, Cornell U... 177 2e-43
 emb|AW650818|AW650818 EST329272 tomato germinating seedlings, TA... 148 2e-42
 60 emb|AW697347|AW697347 NF115F08ST1F1074 Developing stem Medicago ... 168 2e-40
 emb|AW428657|AW428657 Ljirnp22-731-a5 Ljirnp Lambda HybriZap ... 168 2e-40

- emb|AW695961|AW695961 NF101A09ST1F1068 Developing stem Medicago ... 168 2e-40
 emb|AV395160|AV395160 AV395160 Chlamydomonas reinhardtii C9 Chla... 164 2e-39
 emb|AW907004|AW907004 EST343231 potato stolon, Cornell Universit... 163 5e-39
 5 emb|AW736943|AW736943 NXNV_081_H10_F Nsf Xylem Normal wood Verti... 161 1e-38
 gb|BE123645|BE123645 NXNV_150_D07_F Nsf Xylem Normal wood Vertic... 158 1e-37
 gb|L47851|L47851 BNAF1389 Mustard flower buds Brassica rapa cDNA... 155 1e-36
 gb|BE058285|BE058285 sn14b01.y1 Gm-cl016 Glycine max cDNA clone ... 152 8e-36
 gb|BE055879|BE055879 GA_Ea0026P04f Gossypium arboreum 7-10 dpa ... 149 5e-35
 10 emb|AA660997|AA660997 00894 MtRHE Medicago truncatula cDNA 5' si... 72 2e-34
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 emb|AI165568|AI165568 A086P59U Hybrid aspen plasmid library Popu... 137 1e-31
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 emb|Z97052|SPCC4G3 S.pombe chromosome III cosmid c4G3. 82 7e-30
 15 gb|BE060772|BE060772 HVSMEg0013F04f Hordeum vulgare pre-anthesis... 99 2e-29
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 emb|AJ273311|AJ273311 AJ273311 Metarhizium anisopliae ARSEF 2575... 77 4e-28
 emb|AA840711|AA840711 CAN22 Anther cDNA library of Hot pepper Ca... 93 5e-28
 emb|AW688606|AW688606 NF009E07ST1F1000 Developing stem Medicago ... 124 2e-27
 20 emb|AC005761|AC005761 Leishmania major chromosome 3 clone L952 s... 78 5e-27
 emb|AL157811|SPAC186 S.pombe chromosome I cosmid c186. 90 2e-26
 gb|U18839|SCE9747 Saccharomyces cerevisiae chromosome V cosmids ... 80 2e-23
 emb|AL033389|SPBC1773 S.pombe chromosome II cosmid c1773. 106 1e-22
 emb|Z37997|SC9877 S.cerevisiae chromosome IX cosmid 9877. 80 2e-22
 25 emb|AW689996|AW689996 NF026G01ST1F1000 Developing stem Medicago ... 91 7e-20
 emb|AL031180|SPUNK4 S.pombe chromosome I cosmid c2E11. 99 2e-19
 dbj|D89185|D89185 Schizosaccharomyces pombe mRNA, partial cds, c... 99 2e-19
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 emb|AW736063|AW736063 EST332049 KV3 Medicago truncatula cDNA clo... 93 9e-18
 30 gb|BE054038|BE054038 GA_Ea0008F24f Gossypium arboreum 7-10 dpa ... 88 2e-16
 emb|AW599036|AW599036 gb01c10.y1 Moss EST library PPN Physcomitr... 87 6e-16
 gb|U43503|SCU43503 Saccharomyces cerevisiae chromosome XVI cosmi... 84 3e-15
 emb|AW283359|AW283359 LG1_223_C04.g1_A002 Light Grown 1 (LG1) So... 84 5e-15
 emb|AW625680|AW625680 EST319587 tomato radicle, 5 d post-imbibit... 83 1e-14
 35 emb|AI486949|AI486949 EST245271 tomato ovary, TAMU Lycopersicon ... 83 1e-14
 emb|Z71550|SCYNL274C S.cerevisiae chromosome XIV reading frame O... 83 1e-14
 emb|AW442114|AW442114 EST311510 tomato fruit red ripe, TAMU Lyco... 83 1e-14
 emb|AW030822|AW030822 EST274077 tomato callus, TAMU Lycopersicon... 83 1e-14
 emb|AI484846|AI484846 EST243107 tomato ovary, TAMU Lycopersicon ... 83 1e-14
 40 emb|AW442123|AW442123 EST311519 tomato fruit red ripe, TAMU Lyco... 83 1e-14
 emb|AW651324|AW651324 EST329778 tomato germinating seedlings, TA... 83 1e-14
 emb|AW647711|AW647711 EST307192 tomato germinating seedlings, TA... 83 1e-14
 emb|Z21493|MISTFDHD S.tuberosum mRNA for formate dehydrogenase. 83 1e-14
 emb|AI822999|AI822999 L30-850T3 Ice plant Lambda Uni-Zap XR expr... 82 1e-14
 45 emb|AW693443|AW693443 NF065D03ST1F1000 Developing stem Medicago ... 71 2e-14
 emb|AI488120|AI488120 EST246442 tomato ovary, TAMU Lycopersicon ... 80 5e-14
 emb|AT000538|AT000538 AT000538 Brassica rapa guard cell Brassica... 80 7e-14
 emb|AI490350|AI490350 EST248676 tomato ovary, TAMU Lycopersicon ... 79 9e-14
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 50 emb|AI490396|AI490396 EST248734 tomato ovary, TAMU Lycopersicon ... 78 2e-13
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 emb|AW037837|AW037837 EST279466 tomato mixed elicitor, BTI Lycop... 75 2e-12
 emb|AW266848|AW266848 L48-192T3 Ice plant Lambda Uni-Zap XR expr... 74 3e-12
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 55 emb|AI898003|AI898003 EST267446 tomato ovary, TAMU Lycopersicon ... 74 4e-12
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 60 emb|AW930862|AW930862 EST356705 tomato fruit mature green, TAMU ... 73 1e-11
 emb|AI899038|AI899038 EST268481 tomato ovary, TAMU Lycopersicon ... 73 1e-11

gb|BE055276|BE055276 GA_Ea0034L16f Gossypium arboreum 7-10 dpa ... 57 2e-11
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 emb|AW153099|AW153099 se34h11.y1 Gm-c1015 Glycine max cDNA clone... 71 4e-11
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 emb|AW164250|AW164250 se23h05.y1 Gm-c1015 Glycine max cDNA clone... 70 5e-11
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 (2458 letters)

15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

20 Score E
 Sequences producing significant alignments: (bits) Value

25 emb|AI898446|AI898446 EST267889 tomato ovary, TAMU Lycopersicon ... 209 e-108
 emb|AW217248|AW217248 EST295962 tomato callus, TAMU Lycopersicon... 245 3e-89
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 emb|AI485695|AI485695 EST244016 tomato ovary, TAMU Lycopersicon ... 261 5e-86
 emb|AI899197|AI899197 EST268640 tomato ovary, TAMU Lycopersicon ... 161 2e-78
 emb|AI485239|AI485239 EST243543 tomato ovary, TAMU Lycopersicon ... 291 1e-77
 emb|AW034573|AW034573 EST278257 tomato callus, TAMU Lycopersicon... 272 9e-72
 30 emb|AI488812|AI488812 EST247151 tomato ovary, TAMU Lycopersicon ... 251 1e-65
 emb|AW687082|AW687082 NF005G09RT1F1071 Developing root Medicago ... 182 7e-65
 emb|AI898248|AI898248 EST267691 tomato ovary, TAMU Lycopersicon ... 206 2e-64
 emb|AI483614|AI483614 EST249464 tomato ovary, TAMU Lycopersicon ... 238 1e-61
 emb|AI897089|AI897089 EST266532 tomato ovary, TAMU Lycopersicon ... 226 8e-58
 35 emb|AW774994|AW774994 EST334145 KV3 Medicago truncatula cDNA clo... 182 3e-56
 emb|AW559604|AW559604 EST314652 DSIR Medicago truncatula cDNA cl... 177 4e-53
 emb|AI485284|AI485284 EST243588 tomato ovary, TAMU Lycopersicon ... 206 5e-52
 emb|AI485664|AI485664 EST243985 tomato ovary, TAMU Lycopersicon ... 198 2e-49
 emb|AW774741|AW774741 EST333892 KV3 Medicago truncatula cDNA clo... 90 2e-48
 40 emb|AI487608|AI487608 EST245930 tomato ovary, TAMU Lycopersicon ... 187 3e-46
 emb|AI483438|AI483438 EST249259 tomato ovary, TAMU Lycopersicon ... 169 7e-41
 emb|AI485008|AI485008 EST243271 tomato ovary, TAMU Lycopersicon ... 157 3e-37
 emb|AI938737|AI938737 sb58c06.y1 Gm-c1018 Glycine max cDNA clone... 151 2e-35
 emb|AI967736|AI967736 Ljimpest11-837-a7 Ljimp Lambda HybriZap ... 147 4e-34
 45 emb|AW775688|AW775688 EST334753 DSIL Medicago truncatula cDNA cl... 108 8e-34
 emb|Z50161|SCC14ORFS S.cerevisiae orfs and LEU4, MET4, POL1, RAS... 60 1e-33
 emb|Z71382|SCYNL106C S.cerevisiae chromosome XIV reading frame O... 60 1e-33
 emb|AI973618|AI973618 sd07d04.y1 Gm-c1020 Glycine max cDNA clone... 141 3e-32
 emb|AI485392|AI485392 EST243713 tomato ovary, TAMU Lycopersicon ... 138 2e-31
 50 emb|X94335|SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 51 1e-29
 emb|Z75017|SCYOR109W S.cerevisiae chromosome XV reading frame OR... 51 1e-29
 emb|AL022103|SPBC2G2 S.pombe chromosome II cosmid c2G2. 78 3e-27
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 emb|Z38062|SC9687 S.cerevisiae chromosome IX cosmid 9687. 72 3e-27
 55 emb|AI488810|AI488810 EST247149 tomato ovary, TAMU Lycopersicon ... 121 3e-26
 gb|BE020060|BE020060 sm38e06.y1 Gm-c1028 Glycine max cDNA clone ... 118 2e-25
 emb|AW685248|AW685248 NF028A10NR1F1000 Nodulated root Medicago t... 116 2e-24
 emb|AW257207|AW257207 EST305344 KV2 Medicago truncatula cDNA clo... 75 2e-24
 emb|AV406995|AV406995 AV406995 Lotus japonicus young plants (two... 67 2e-23
 60 emb|AW034093|AW034093 EST277588 tomato callus, TAMU Lycopersicon... 111 3e-23
 emb|Z98763|SPAC9G1 S.pombe chromosome I cosmid c9G1. 59 9e-23

	emb AQ502761 AQ502761 V84A11 mTn-3xHA/lacZ Insertion Library Sac...	52	2e-22
	emb AI897134 AI897134 EST266577 tomato ovary, TAMU Lycopersicon ...	107	4e-22
	emb AI771644 AI771644 EST252744 tomato ovary, TAMU Lycopersicon ...	104	4e-21
	emb AW731056 AW731056 GA_Ea0008D13 Gossypium arboreum 7-10 dpa ...	100	5e-20
5	emb AV413397 AV413397 AV413397 Lotus japonicus young plants (two...	100	9e-20
	emb AW616540 AW616540 EST322951 L. hirsutum trichome, Cornell Un...	98	2e-19
	emb AL110506 SPBC577 S.pombe chromosome II cosmid c577.	74	2e-18
	emb AW126841 AW126841 ga16f04.y1 Moss EST library PPU Physcomitr...	94	4e-18
	emb AI780067 AI780067 EST260946 tomato susceptible, Cornell Lyco...	94	6e-18
10	emb AW687035 AW687035 NF005C05RT1F1037 Developing root Medicago ...	73	2e-17
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	emb AV415287 AV415287 AV415287 Lotus japonicus young plants (two...	90	5e-17
	gb BE124605 BE124605 EST393640 GVN Medicago truncatula cDNA clon...	65	6e-15
	emb AW220291 AW220291 EST302774 tomato root during/after fruit s...	68	1e-14
15	emb AQ644913 AQ644913 RPCI93-EcoRI-2C7.TV RPCI93-EcoRI Trypanoso...	53	2e-13
	emb AA495505 AA495505 c430 Zhou and Ragan 1993 Gracilaria gracil...	49	5e-13
	emb AW830613 AW830613 sm04c07.y1 Gm-c1027 Glycine max cDNA clone...	77	5e-13
	emb AW666237 AW666237 sk34b04.y1 Gm-c1028 Glycine max cDNA clone...	77	5e-13
	emb AW285758 AW285758 LG1_223_C03.b1_A002 Light Grown 1 (LG1) So...	74	5e-12
20	emb AQ658256 AQ658256 Sheared DNA-13C5.TR Sheared DNA Trypanosom...	73	1e-11
	emb AW704333 AW704333 sk18a03.y1 Gm-c1028 Glycine max cDNA clone...	71	5e-11
	emb AV390446 AV390446 AV390446 Chlamydomonas reinhardtii C9 Chla...	70	6e-11
	emb AL160371 LMFLCHR15 Leishmania major Friedlin assembled chrom...	64	8e-11
	emb AW695904 AW695904 NF099H04ST1F1043 Developing stem Medicago ...	49	2e-10
25	emb AZ048449 AZ048449 PSB67 Barley PstI genomic clones Hordeum v...	67	8e-10
	emb AW760518 AW760518 sl51d02.y1 Gm-c1027 Glycine max cDNA clone...	66	1e-09
	emb AW332143 AW332143 S4G7 AGS-1 Pneumocystis carinii f. sp. car...	36	1e-09
	emb AW687790 AW687790 NF013E04RT1F1034 Developing root Medicago ...	65	3e-09
	emb AI486692 AI486692 EST245014 tomato ovary, TAMU Lycopersicon ...	54	3e-09
30	emb AW333870 AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c...	36	5e-09
	emb AQ850639 AQ850639 LMAJFV1_lm41a04.x1 Leishmania major FV1 ra...	44	6e-09
	emb AW127178 AW127178 M110117 GVN Medicago truncatula cDNA clone...	63	1e-08
	emb AW616547 AW616547 EST322958 L. hirsutum trichome, Cornell Un...	62	2e-08
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35	emb AW693686 AW693686 NF068A05ST1F1036 Developing stem Medicago ...	62	3e-08
	emb AW208046 AW208046 M111077e DSIR Medicago truncatula cDNA clo...	61	5e-08
	emb AQ642482 AQ642482 RPCI93-EcoRI-1A17.TV RPCI93-EcoRI Trypanos...	53	7e-08
	emb AW686583 AW686583 NF039G02NR1F1000 Nodulated root Medicago t...	45	5e-07
	emb AQ849089 AQ849089 LMAJFV1_lm41a04.y1 Leishmania major FV1 ra...	44	6e-06
40	emb AI781410 AI781410 EST262277 tomato susceptible, Cornell Lyco...	52	2e-05
	emb AW617564 AW617564 EST323975 L. hirsutum trichome, Cornell Un...	49	2e-04
	emb AQ946427 AQ946427 Sheared DNA-49M8.TF Sheared DNA Trypanosom...	47	5e-04
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45	emb AQ655271 AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso...	38	0.004
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	emb AW437996 AW437996 ST83C09 Pine TriplEx shoot tip library Pin...	42	0.016
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50	emb AF263282 AF263282 Filobasidiella neoformans var. neoformans ...	34	0.64
	emb AW702543 AW702543 TgESTzz85a12.y1 TgRH*-Tachyzoite cDNA Toxo...	32	0.69
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60	emb AI482770 AI482770 EST242093 tomato shoot, Cornell Lycopersic...	35	2.6
	emb AQ653909 AQ653909 Sheared DNA-1G20.TR Sheared DNA Trypanosom...	35	2.6

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 (938 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10

Searching.....done

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	gb U68763 GMU68763	Glycine max putative transcription factor SCO...	71	1e-35
	emb Y18788 MSY18788	Medicago sativa mRNA for putative TFIIIA (or...	71	3e-35
	emb AF053077 AF053077	Nicotiana tabacum osmotic stress-induced z...	70	3e-33
	emb AW729218 AW729218	GA_Ea0024G18 Gossypium arboreum 7-10 dpa ...	71	5e-33
20	emb AW781249 AW781249	sk67b08.y1 Gm-c1016 Glycine max cDNA clone...	70	7e-31
	dbj D26086 PETZFP4	Petunia zinc-finger protein gene.	68	3e-30
	emb AW560934 AW560934	EST315982 DSIR Medicago truncatula cDNA cl...	68	8e-30
	emb AW775559 AW775559	EST334624 DSIL Medicago truncatula cDNA cl...	70	1e-29
	gb BE123920 BE123920	EST394045 DSIL Medicago truncatula cDNA clp...	70	1e-29
25	emb AI988657 AI988657	sd06b03.y1 Gm-c1020 Glycine max cDNA clone...	70	9e-29
	emb AW102472 AW102472	sd88f02.y1 Gm-c1009 Glycine max cDNA clone...	64	1e-28
	dbj D26084 PETZFDB2	Petunia mRNA for zinc-finger DNA binding pro...	69	1e-28
	dbj D26083 PETZFDB1	Petunia hybrida gene for zinc-finger DNA bin...	68	4e-28
	emb AI988290 AI988290	sc98f10.y1 Gm-c1020 Glycine max cDNA clone...	64	3e-27
30	emb AW706944 AW706944	sk08e10.y1 Gm-c1023 Glycine max cDNA clone...	69	2e-26
	emb AW153229 AW153229	se37f05.y1 Gm-c1015 Glycine max cDNA clone...	69	3e-26
	emb AW616587 AW616587	EST322998 L. hirsutum trichome, Cornell Un...	68	5e-26
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35	emb AI487287 AI487287	EST245609 tomato ovary, TAMU Lycopersicon ...	68	9e-26
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40	emb AF119050 AF119050	Datisca glomerata zinc-finger protein 1 (z...	71	2e-25
	gb BE059872 BE059872	sn38c04.y1 Gm-c1016 Glycine max cDNA clone ...	71	4e-25
	gb U76554 BRU76554	Brassica rapa zinc-finger protein-1 (BR42) mR...	63	9e-25
	gb U76555 BRU76555	Brassica rapa zinc-finger protein BcZFP1 (BcA...	62	3e-24
	emb AI966679 AI966679	sc55a11.y1 Gm-c1015 Glycine max cDNA clone...	64	4e-24
45	emb AW034622 AW034622	EST278306 tomato callus, TAMU Lycopersicon...	62	6e-24
	emb AI488218 AI488218	EST246540 tomato ovary, TAMU Lycopersicon ...	62	9e-24
	emb AW037956 AW037956	EST279600 tomato mixed elicitor, BTI Lycop...	59	4e-23
	emb Y16131 Y16131	Y16131 young root nodules Medicago sativa subs...	67	8e-23
	emb AW030858 AW030858	EST274148 tomato callus, TAMU Lycopersicon...	66	9e-23
50	emb AW032112 AW032112	EST275566 tomato callus, TAMU Lycopersicon...	68	5e-22
	emb AW625323 AW625323	EST319146 tomato radicle, 5 d post-imbibit...	59	8e-21
	emb AW033257 AW033257	EST276828 tomato callus, TAMU Lycopersicon...	66	2e-20
	emb AI485651 AI485651	EST243972 tomato ovary, TAMU Lycopersicon ...	62	2e-20
	emb AW033574 AW033574	EST277145 tomato callus, TAMU Lycopersicon...	66	2e-20
55	emb AI896031 AI896031	EST265474 tomato callus, TAMU Lycopersicon...	66	3e-20
	emb AI771191 AI771191	EST252387 tomato ovary, TAMU Lycopersicon ...	66	3e-20
	emb AW032357 AW032357	EST275811 tomato callus, TAMU Lycopersicon...	66	3e-20
	emb AW219736 AW219736	EST302218 tomato root during/after fruit s...	59	1e-19
	emb AW219517 AW219517	EST301915 tomato root during/after fruit s...	59	2e-19
60	emb AW706014 AW706014	sk64g01.y1 Gm-c1016 Glycine max cDNA clone...	69	1e-18
	emb AV426673 AV426673	AV426673 Lotus japonicus young plants (two...	60	5e-18

	emb AV423639 AV423639 AV423639 Lotus japonicus young plants (two...	66 7e-18
	gb BE021759 BE021759 sm62a09.y1 Gm-cl028 Glycine max cDNA clone ...	71 3e-17
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon...	55 4e-17
	emb AW720367 AW720367 LjNEST21g11r Lotus japonicus nodule librar...	64 6e-17
5	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA...	59 9e-17
	emb AB000455 AB000455 Petunia hybrida mRNA for PETHy;ZPT4-1, com...	60 1e-16
	gb BE058334 BE058334 sn14g01.y1 Gm-cl016 Glycine max cDNA clone ...	62 1e-16
	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon...	55 2e-16
	emb AV422432 AV422432 AV422432 Lotus japonicus young plants (two...	66 3e-16
10	emb AW277333 AW277333 sf80a11.y1 Gm-cl019 Glycine max cDNA clone...	64 4e-16
	emb AI900061 AI900061 sb98d02.y1 Gm-cl012 Glycine max cDNA clone...	64 5e-16
	emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t...	63 6e-16
	emb AI960244 AI960244 sc80g07.y1 Gm-cl018 Glycine max cDNA clone...	64 7e-16
	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD...	62 1e-15
15	emb AI736394 AI736394 sb28a06.y1 Gm-cl009 Glycine max cDNA clone...	67 5e-15
	emb AI894999 AI894999 EST264442 tomato callus, TAMU Lycopersicon...	68 9e-15
	emb AW622660 AW622660 EST313460 tomato root during/after fruit s...	68 9e-15
	emb AW755973 AW755973 sl11h06.y1 Gm-cl036 Glycine max cDNA clone...	64 4e-14
	emb AI938565 AI938565 sb55e03.y1 Gm-cl018 Glycine max cDNA clone...	64 4e-14
20	emb AB035133 AB035133 Petunia x hybrida gene for C2H2 zinc-finge...	52 1e-13
	emb AB006605 AB006605 Petunia x hybrida mRNA for ZPT3-3, complet...	52 1e-13
	emb AB035132 AB035132 Petunia x hybrida gene for C2H2 zinc-finge...	50 4e-13
	emb AB006597 AB006597 Petunia x hybrida mRNA for ZPT2-10, comple...	50 4e-13
	emb AB006606 AB006606 Petunia x hybrida mRNA for ZPT4-4, complet...	51 8e-13
25	emb AW684455 AW684455 NF017B06NR1F1000 Nodulated root Medicago t...	54 8e-13
	emb AW776204 AW776204 EST335269 DSIL Medicago truncatula cDNA cl...	65 1e-12
	emb AB000451 AB000451 Petunia hybrida mRNA for PETHy;ZPT2-5, com...	50 2e-12
	emb AI485306 AI485306 EST243610 tomato ovary, TAMU Lycopersicon ...	66 2e-12
	emb AW216968 AW216968 EST295682 tomato callus, TAMU Lycopersicon...	55 2e-12
30	emb AV422972 AV422972 AV422972 Lotus japonicus young plants (two...	60 3e-12
	emb AV423707 AV423707 AV423707 Lotus japonicus young plants (two...	60 3e-12
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35	emb AV418453 AV418453 AV418453 Lotus japonicus young plants (two...	60 3e-12
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	emb AV411580 AV411580 AV411580 Lotus japonicus young plants (two...	60 3e-12
	emb AV412455 AV412455 AV412455 Lotus japonicus young plants (two...	60 3e-12
	emb AB006600 AB006600 Petunia x hybrida mRNA for ZPT2-13, comple...	48 4e-12
40	emb AW687462 AW687462 NF009H03RT1F1031 Developing root Medicago ...	50 4e-12
	emb AB006603 AB006603 Petunia x hybrida mRNA for ZPT2-8, complet...	49 5e-12
	emb AB006601 AB006601 Petunia x hybrida mRNA for ZPT2-14, comple...	50 7e-12
	emb AI442517 AI442517 sa32e09.y1 Gm-cl004 Glycine max cDNA clone...	58 7e-12
	gb BE023156 BE023156 sm79a08.y1 Gm-cl015 Glycine max cDNA clone ...	69 1e-11
45	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds.	56 1e-11
	dbj D16416 WHTWZF1B Wheat mRNA for WZF1, complete cds.	56 1e-11
	emb AB006599 AB006599 Petunia x hybrida mRNA for ZPT2-12, comple...	48 1e-11
	emb AW685937 AW685937 NF031H10NR1F1000 Nodulated root Medicago t...	48 1e-11
	emb AV424248 AV424248 AV424248 Lotus japonicus young plants (two...	58 1e-11
50	emb AI775063 AI775063 EST256163 tomato resistant, Cornell Lycop...	59 2e-11
	emb AI484099 AI484099 EST249970 tomato ovary, TAMU Lycopersicon ...	59 2e-11
	emb AW738399 AW738399 EST339826 tomato flower buds, anthesis, Co...	59 2e-11
	emb AB006602 AB006602 Petunia x hybrida mRNA for ZPT2-7, complet...	49 2e-11
55	emb AI959966 AI959966 se35g05.x1 Gm-cl014 Glycine max cDNA clone...	50 2e-11

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60 (1352 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments:

(bits) Value

10	emb AJ000728 LEAJ728 Lycopersicon esculentum mRNA for MAP kinase...	555	e-157
	emb AF165186 AF165186 Nicotiana tabacum MAP kinase kinase mRNA, ...	540	e-153
	emb AW945105 AW945105 EST337156 tomato flower buds 3-8 mm, Corne...	318	6e-86
	emb AW756736 AW756736 sl26f02.y1 Gm-c1027 Glycine max cDNA clone...	174	9e-75
	dbj D31964 TOBNPK2 Tobacco mRNA for protein kinase (NPK2), compl...	183	8e-65
15	gb BE054500 BE054500 GA__Ea0031F11f Gossypium arboreum 7-10 dpa ...	165	1e-59
	emb AW220008 AW220008 EST302491 tomato root during/after fruit s...	228	6e-59
	emb AW624623 AW624623 EST322568 tomato flower buds 3-8 mm, Corne...	215	9e-55
	emb AI438023 AI438023 sa34h10.y1 Gm-c1004 Glycine max cDNA clone...	208	7e-53
	emb AW617901 AW617901 EST296829 L. hirsutum trichome, Cornell Un...	203	2e-51
20	emb AJ007393 YLI7393 Yarrowia lipolytica ste7 gene.	92	4e-49
	emb AW931392 AW931392 EST357235 tomato fruit mature green, TAMU ...	189	3e-47
	emb AW039087 AW039087 EST281060 tomato mixed elicitor, BTI Lycop...	183	2e-45
	emb Z99259 SPAC2C4 S.pombe chromosome I cosmid c2C4.	85	6e-43
	emb AW032808 AW032808 EST276367 tomato callus, TAMU Lycopersicon...	175	9e-43
	gb U07801 UMU07801 Ustilago maydis serine/threonine/tyrosine kin...	121	2e-42
25	emb AJ009609 BNA9609 Brassica napus mRNA for MAP4K alpha2 protein.	87	1e-41
	dbj D13001 YSCSSP32 Yeast Mkk1/SSP32 gene for Mkk1 protein kinas...	72	3e-41
	emb Z75139 SCYOR231W S.cerevisiae chromosome XV reading frame OR...	72	3e-41
	emb AF169644 AF169644 Glomerella cingulata MAP kinase kinase (EM...	82	7e-41
	emb AJ009608 BNA9608 Brassica napus mRNA for MAP4K alpha 1 protein.	82	8e-41
30	emb AW127406 AW127406 M110589 DSIL Medicago truncatula cDNA clon...	94	2e-39
	emb AJ225532 AJ225532 AJ225532 Absciscic acid-treated protonemata...	162	5e-39
	emb AZ215495 AZ215495 Sheared DNA-56D6.TR Sheared DNA Trypanosom...	113	3e-38
	dbj D13785 YSCMKK2 S.cerevisiae gene for Mkk2 protein kinase, co...	68	1e-37
	gb U72980 CAU72980 Candida albicans Map kinase kinase (STE7) gen...	128	2e-37
35	gb L19195 YSASTKIN Candida albicans (clone pKB66) serine/threoni...	128	2e-37
	emb AL109822 SPBC409 S.pombe chromosome II cosmid c409.	68	2e-37
	gb U43703 SCU43703 Saccharomyces cerevisiae chromosome XVI cosmi...	68	2e-37
	emb X62631 SPWIS1 S.pombe wis1 gene for protein kinase.	68	3e-37
	emb AW625928 AW625928 EST319823 tomato radicle, 5 d post-imbibit...	90	8e-37
40	emb AW348493 AW348493 GM210002B12A8R Gm-r1021 Glycine max cDNA 3...	154	1e-36
	emb AZ213240 AZ213240 Sheared DNA-102E10.TF Sheared DNA Trypanos...	140	3e-36
	emb AW497308 AW497308 ga57h06.y1 Moss EST library PPU Physcomitr...	150	2e-35
	emb Z49403 SCYJL128C S.cerevisiae chromosome X reading frame ORF...	78	5e-35
45	gb U12237 SCU12237 Saccharomyces cerevisiae suppressor of fluori...	78	5e-35
	gb J02946 YSCPBS2 Saccharomyces cerevisiae putative protein kina...	78	5e-35
	emb AJ243184 LIN243184 Leishmania infantum mkk gene for putative...	78	2e-34
	emb AW032663 AW032663 EST276222 tomato callus, TAMU Lycopersicon...	82	2e-34
	emb AJ243118 LME243118 Leishmania mexicana mkk gene for putative...	78	3e-34
50	emb AJ243187 LTR243187 Leishmania tropica mkk gene for putative ...	78	3e-34
	emb AJ243188 LMA243188 Leishmania major mkk gene for putative mi...	78	3e-34
	emb AJ243183 LAM243183 Leishmania amazonensis mkk gene for putat...	78	3e-34
	emb AJ243186 LAE243186 Leishmania aethiopica mkk gene for putati...	78	3e-34
	emb AW185502 AW185502 se80e12.y1 Gm-c1023 Glycine max cDNA clone...	85	6e-34
55	gb U16029 U16029 Leishmania donovani protein kinase (lpk) mRNA, ...	78	1e-33
	emb AJ243185 LDO243185 Leishmania donovani mkk gene for putative...	78	1e-33
	emb AI781759 AI781759 EST262638 tomato susceptible, Cornell Lyco...	97	3e-33
	gb BE059041 BE059041 sn24d08.y1 Gm-c1016 Glycine max cDNA clone ...	143	3e-33
	emb AW929787 AW929787 EST354057 tomato flower buds 8 mm to pre-a...	102	9e-32
60	emb AW981083 AW981083 EST392236 GVN Medicago truncatula cDNA clo...	88	3e-31
	gb BE036317 BE036317 MO23C02 MO Mesembryanthemum crystallinum cD...	82	1e-30

emb|AF069777|AF069777 Cryphonectria parasitica mitogen-activated... 66 2e-30
 emb|AW099876|AW099876 sd17g06.y2 Gm-cl012 Glycine max cDNA clone... 80 3e-30
 emb|AF249887|AF249887 Pneumocystis carinii map kinase kinase (mk... 72 6e-30
 emb|AW622016|AW622016 EST312814 tomato root during/after fruit s... 97 7e-29
 5 emb|Z69239|SPAC1D4 S.pombe chromosome I cosmid c1D4. 116 2e-28
 emb|X07445|SPBYR1 Fission yeast byr1 gene. 116 2e-28
 emb|Z67750|SC41KCIV S.cerevisiae DNA (cosmid 31A2; chromosome IV... 77 7e-28
 emb|X97751|SCIV23 S.cerevisiae chrIV genes STE7, CLB3, MSH5, RPC... 77 7e-28
 emb|Z74207|SCYDL159W S.cerevisiae chromosome IV reading frame OR... 77 8e-28
 10 gb|M14097|YSCSTE7 Yeast (S.cerevisiae) regulatory gene STE7, com... 77 8e-28
 dbj|D26601|TOBPK Tobacco mRNA for protein kinase, complete cds. 54 1e-27
 dbj|E05289|E05289 DNA encoding a protein kinase that is homologo... 54 1e-27
 emb|AL358652|LMFP1408 Leishmania major Friedlin chromosome 14 PA... 100 3e-27
 emb|AW349565|AW349565 GM210005A21F10R Gm-r1021 Glycine max cDNA ... 85 4e-27
 15 emb|AF169643|AF169643 Glomerella cingulata MAP kinase kinase (EM... 74 5e-27
 emb|AQ849880|AQ849880 LMAJFV1_lm51a11.x1 Leishmania major FV1 ra... 104 1e-26
 emb|AW564378|AW564378 LG1_292_H08.b1_A002 Light Grown 1 (LG1) So... 121 1e-26
 emb|AC005140|AC005140 Plasmodium falciparum chromosome 12 clone ... 88 2e-26
 emb|AW030150|AW030150 EST273405 tomato callus, TAMU Lycopersicon... 120 3e-26
 20 emb|Z28126|SCYKL126W S.cerevisiae chromosome XI reading frame OR... 84 5e-26
 gb|M21307|YSCPKN Yeast (S.cerevisiae) protein kinase (YPK1) gene... 84 7e-26
 emb|AW676925|AW676925 DG1_2_B05.b1_A002 Dark Grown 1 (DG1) Sorgh... 89 9e-26
 emb|Z49702|SC9718 S.cerevisiae chromosome XIII cosmid 9718. 85 9e-26
 gb|M24929|YSCYKR2A Saccharomyces cerevisiae protein kinase (YKR2... 85 9e-26
 25 emb|AI779511|AI779511 EST260390 tomato susceptible, Cornell Lyco... 118 1e-25
 emb|AZ048376|AZ048376 LMAJFV1_lm77f10.x1 Leishmania major FV1 ra... 100 1e-25
 gb|U11581|YSCHL5018 Saccharomyces cerevisiae chromosome VIII cos... 86 2e-25
 gb|M94719|YSCSTE20P Saccharomyces cerevisiae protein kinase (Ste... 86 2e-25
 gb|L04655|YSCSERKIN Saccharomyces cerevisiae serine/threonine ki... 86 2e-25
 30 emb|AW922296|AW922296 DG1_17_G11.g1_A002 Dark Grown 1 (DG1) Sorg... 116 4e-25
 emb|Z98763|SPAC9G1 S.pombe chromosome I cosmid c9G1. 92 4e-25
 emb|AE001376|AE001376 Plasmodium falciparum chromosome 2, sectio... 49 6e-25
 emb|Z97211|SPBC2F12 S.pombe chromosome II cosmid c2F12. 56 2e-24
 emb|Z98270|SPBC1D7 S.pombe chromosome II cosmid c1D7. 56 2e-24
 35 emb|AW351150|AW351150 GM210011A20C11R Gm-r1021 Glycine max cDNA ... 78 2e-24
 gb|M74293|YSPBYR2 Schizosaccharomyces pombe byr2 gene, complete ... 56 2e-24
 emb|X68851|SPSTE8A S.pombe ste8 gene encoding protein kinase. 56 2e-24
 emb|AJ238845|BNA238845 Brassica napus mRNA for MAP3K epsilon 1 p... 78 3e-24
 gb|L47210|YSASTPK Candida albicans serine/threonine protein kina... 86 8e-24
 40 gb|U73457|CAU73457 Candida albicans Cst20p (CST20) gene, complet... 86 8e-24
 emb|AJ005079|AJKL5079 Kluyveromyces lactis BCK1 gene, complete CDS. 51 8e-24
 emb|AF157632|AF157632 Schizosaccharomyces pombe MAPK kinase Skh1... 73 2e-23
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 emb|AF034090|AF034090 Neurospora crassa MAPKK kinase (nrc-1) gen... 58 2e-23
 45 emb|AQ501953|AQ501953 V11H7 mTn-3xHA/lacZ Insertion Library Sacc... 72 2e-23
 emb|AL034433|SPBC1604 S.pombe chromosome II cosmid c1604. 87 4e-23
 gb|U22371|SPU22371 Schizosaccharomyces pombe Pak1p (PAK1) mRNA, ... 87 5e-23
 gb|L41552|YSPSHK1A Schizosaccharomyces pombe Ste20 homologous pr... 87 5e-23

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Score E

Sequences producing significant alignments:

(bits) Value

	gb BE052137 BE052137 GA__Ea0031L11f <i>Gossypium arboreum</i> 7-10 dpa ...	257	8e-77
	emb AW727234 AW727234 GA__Ea0011E21 <i>Gossypium arboreum</i> 7-10 dpa ...	257	1e-76
5	emb AW728196 AW728196 GA__Ea0014P01 <i>Gossypium arboreum</i> 7-10 dpa ...	257	1e-76
	emb AW737982 AW737982 EST339409 tomato flower buds, anthesis, Co...	287	2e-76
	emb AW626347 AW626347 EST320254 tomato radicle, 5 d post-imbibit...	287	2e-76
	emb AW622517 AW622517 EST313317 tomato root during/after fruit s...	287	2e-76
	emb AW623663 AW623663 EST321608 tomato flower buds 3-8 mm, Corne...	287	2e-76
10	emb AW622008 AW622008 EST312806 tomato root during/after fruit s...	287	2e-76
	emb AI777165 AI777165 EST258130 tomato resistant, Cornell Lycope...	287	2e-76
	emb AW730733 AW730733 GA__Ea0027I13 <i>Gossypium arboreum</i> 7-10 dpa ...	254	7e-76
	emb AW705652 AW705652 sk50g08.y1 Gm-c1019 <i>Glycine max</i> cDNA clone...	248	1e-74
	emb AW755296 AW755296 sl01c07.y1 Gm-c1036 <i>Glycine max</i> cDNA clone...	245	6e-74
15	emb AW775898 AW775898 EST334963 DSIL <i>Medicago truncatula</i> cDNA cl...	243	2e-71
	emb AW774377 AW774377 EST333528 KV3 <i>Medicago truncatula</i> cDNA clo...	242	4e-71
	emb AW620616 AW620616 sj07e05.y1 Gm-c1032 <i>Glycine max</i> cDNA clone...	230	3e-69
	emb AW398755 AW398755 EST309255 <i>L. pennellii</i> trichome, Cornell U...	251	3e-68
	emb AW559353 AW559353 EST314401 DSIR <i>Medicago truncatula</i> cDNA cl...	231	6e-68
20	emb AI727590 AI727590 BNLGHi8481 Six-day Cotton fiber <i>Gossypium</i> ...	226	2e-67
	emb AW696709 AW696709 NF109H10ST1F1091 Developing stem <i>Medicago</i> ...	211	7e-67
	gb T24185 T24185 crs173 lambdaZAPST <i>Ricinus communis</i> cDNA clone ...	254	2e-66
	emb AW255061 AW255061 ML1356 peppermint glandular trichome <i>Menth...</i>	219	4e-64
	emb AW678629 AW678629 WS1_1_D02.b1_A002 Water-stressed 1 (WS1) S...	245	1e-63
25	emb AW672535 AW672535 LG1_360_B02.b1_A002 Light Grown 1 (LG1) So...	245	1e-63
	emb AW678699 AW678699 WS1_1_D02.b2_A002 Water-stressed 1 (WS1) S...	245	1e-63
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	emb AI899451 AI899451 EST268894 tomato susceptible, Cornell Lyco...	242	9e-63
	gb BE125791 BE125791 DG1_57_D06.b1_A002 Dark Grown 1 (DG1) Sorgh...	241	2e-62
30	emb AI482787 AI482787 EST242110 tomato shoot, Cornell Lycopersic...	241	2e-62
	gb BE123902 BE123902 EST394027 DSIL <i>Medicago truncatula</i> cDNA clo...	231	2e-62
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	emb AW185657 AW185657 se81h10.y1 Gm-c1023 <i>Glycine max</i> cDNA clone...	238	1e-61
	emb AW254869 AW254869 ML1292 peppermint glandular trichome <i>Menth...</i>	211	1e-61
35	emb AW255550 AW255550 ML584 peppermint glandular trichome <i>Mentha...</i>	237	4e-61
	emb AW704813 AW704813 sk55h01.y1 Gm-c1019 <i>Glycine max</i> cDNA clone...	236	5e-61
	emb AI895103 AI895103 EST264546 tomato callus, TAMU Lycopersicon...	232	7e-60
	gb BE059713 BE059713 sn35h07.y1 Gm-c1016 <i>Glycine max</i> cDNA clone ...	232	7e-60
	emb AW705371 AW705371 sk48b10.y1 Gm-c1019 <i>Glycine max</i> cDNA clone...	228	2e-58
40	emb AW755523 AW755523 sl05a05.y1 Gm-c1036 <i>Glycine max</i> cDNA clone...	223	4e-57
	emb AW727353 AW727353 GA__Ea0011L19 <i>Gossypium arboreum</i> 7-10 dpa ...	220	3e-56
	emb AW201709 AW201709 sf06d02.y1 Gm-c1027 <i>Glycine max</i> cDNA clone...	216	6e-55
	emb AW203472 AW203472 sf30f04.y1 Gm-c1028 <i>Glycine max</i> cDNA clone...	216	6e-55
	emb AI161953 AI161953 A010P20U Hybrid aspen plasmid library Popu...	149	2e-54
45	emb AI162696 AI162696 A022P09U Hybrid aspen plasmid library Popu...	152	2e-54
	emb AV410373 AV410373 AV410373 <i>Lotus japonicus</i> young plants (two...	186	4e-54
	emb AW217074 AW217074 EST295788 tomato callus, TAMU Lycopersicon...	213	5e-54
	emb AI441526 AI441526 sa67a03.y1 Gm-c1004 <i>Glycine max</i> cDNA clone...	177	2e-53
	emb AW678831 AW678831 WS1_1_D02.g1_A002 Water-stressed 1 (WS1) S...	208	2e-52
50	emb AW100277 AW100277 sd22a12.y2 Gm-c1012 <i>Glycine max</i> cDNA clone...	192	2e-52
	emb AW745340 AW745340 WS1_33_H02.b1_A002 Water-stressed 1 (WS1) ...	154	4e-48
	emb AW185605 AW185605 se79h09.y1 Gm-c1023 <i>Glycine max</i> cDNA clone...	193	6e-48
	emb AW278821 AW278821 sf99a06.y1 Gm-c1019 <i>Glycine max</i> cDNA clone...	192	8e-48
	gb BE035142 BE035142 MM03H05 MM <i>Mesembryanthemum crystallinum</i> cD...	178	1e-47
55	emb AW255911 AW255911 ML998 peppermint glandular trichome <i>Mentha...</i>	124	2e-47
	emb AW683421 AW683421 NF011G07LF1F1055 Developing leaf <i>Medicago</i> ...	190	4e-47
	emb AI778919 AI778919 EST259798 tomato susceptible, Cornell Lyco...	188	1e-46
	emb AI938231 AI938231 sc41d07.y1 Gm-c1014 <i>Glycine max</i> cDNA clone...	184	2e-45
	emb AW677289 AW677289 DG1_7_D03.b1_A002 Dark Grown 1 (DG1) Sorgh...	182	1e-44
60	emb AW287668 AW287668 LG1_244_H12.b1_A002 Light Grown 1 (LG1) So...	180	4e-44
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5 emb|AW255564|AW255564 ML599 peppermint glandular trichome Mentha... 137 7e-39
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15 emb|AI482794|AI482794 EST242117 tomato shoot, Cornell Lycopersic... 146 5e-34
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[arabidopsis thaliana] /blast_score 0
(2390 letters)

50 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	gb M96549 TOMHSC80P Tomato heat shock cognate protein 80 gene, 3...	577	0.0
	gb U55859 TAU55859 Triticum aestivum heat shock protein 80 mRNA,...	575	0.0
60	emb X98582 TAX98582 T.aestivum mRNA for HSP80-2 protein.	572	0.0
	emb X63195 NTHSP82 N.tabacum mRNA for heat shock protein 82.	601	0.0

	emb AF123259 AF123259	Lycopersicon esculentum heat shock protein...	483	0.0
	emb AF165818 AF165818	Guillardia theta nucleomorph 5S ribosomal ...	505	0.0
	emb AF042329 AF042329	Eimeria tenella heat shock protein 90 (hsp...	514	0.0
	gb M57386 THEHSP90	T.parva heat shock protein 90 (hsp90) mRNA, c...	500	0.0
5	emb Z29667 PFHESHP	P.falciparum (7) mRNA for heat-shock protein.	507	0.0
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	emb X87770 LIHSP83GN	L.infantum hsp83 gene.	454	0.0
	gb M92926 LEIHSP01	Leishmania amazonensis heat shock protein 83 ...	449	0.0
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15	emb AF212996 AF212996	Neurospora crassa heat shock protein 80 ge...	473	e-165
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45	emb AW186517 AW186517	se68g12.y1 Gm-c1019 Glycine max cDNA clone...	432	e-120
	gb BE055051 BE055051	GA_Ea0031H10f Gossypium arboreum 7-10 dpa ...	381	e-118
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50	emb AW011081 AW011081	ST16E03 Pine TriplEx shoot tip library Pin...	421	e-116
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 10 emb|AW220869|AW220869 EST297338 tomato fruit mature green, TAMU ... 398 e-109
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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5 emb|AW109013|AW109013 gate0002O16f Gossypium arboreum 7-10 dpa f... 179 4e-44
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60 emb|AW697097|AW697097 NF112C08ST1F1065 Developing stem Medicago ... 103 4e-21
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5 emb|AW924303|AW924303 WS1_52_H11.b1_A002 Water-stressed 1 (WS1) ... 99 7e-20
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35 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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emb|AF109654|AF109654 AF109654 Capsicum annuum root susceptible ... 169 3e-41
emb|AI352937|AI352937 MB74-5H PZ204.BNlib Brassica napus cDNA cl... 115 5e-40
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Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

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25 Database: plantfungal
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 dbj|E02108|E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100
 gb|M37753|SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple... 226 e-100
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 40 emb|X77990|BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99
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 45 gb|U22147|HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1) ... 265 1e-95
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 60 emb|A26451|A26451 Soya beta-1,3-glucanase plasmid pBR59 NdeI-Hin... 244 3e-92
 emb|X53129|PV13BDGL P. vulgaris mRNA for 1,3-beta-D-glucanase. 240 6e-91

- emb|X74905|LEQA *L.esculentum* TomQ'a mRNA for beta(1,3)glucanase. 105 2e-90
emb|X89717|PVB13GLUC *P.vulgaris* beta-1,3-glucanase gene. 243 3e-89
gb|U01902|U01902 *Solanum tuberosum* Datura endo-1,3-beta-D-glucan... 210 2e-88
emb|AJ131047|CAR131047 *Cicer arietinum* mRNA for glucan-endo-1,3-... 188 5e-88
5 emb|X74906|LEQB *L.esculentum* TomQ'b mRNA for beta(1,3)glucanase. 110 1e-86
emb|AF227953|AF227953 *Capsicum annuum* basic beta-1,3-glucanase (... 252 3e-86
emb|AF001523|AF001523 *Musa acuminata* beta-1, 3-glucanase mRNA, ... 148 5e-86
emb|AF004838|AF004838 *Musa acuminata* beta-1,3-glucanase mRNA, pa... 148 7e-86
gb|L02212|PEABETAGLU Pea beta-1,3-glucanase gene, complete cds. 180 1e-85
10 gb|S51479|S51479 beta-1,3-glucanase [*Pisum sativum*=peas, cultiva... 180 2e-85
emb|AF186083|AF186083 *AF186083 Populus alba* x *Populus tremula* ba... 218 5e-85
gb|M20620|TOBGLUBC *N.tabacum* beta-1,3-glucanase mRNA, clone pGL43. 207 4e-84
gb|U27179|MSU27179 *Medicago sativa* acidic glucanase mRNA, comple... 138 7e-79
gb|M60463|TOBGL153A Tobacco GL153 protein mRNA, complete cds. 99 3e-77
15 emb|AF141654|AF141654 *Nicotiana tabacum* beta-1,3-glucanase (GGL4... 99 5e-77
gb|M60460|TOBPR2A Tobacco PR2 protein mRNA, complete cds. 100 3e-76
gb|M59443|TOBGLUCB *N.tabacum* acidic beta-1,3-glucanase gene, com... 100 1e-75
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gb|M63634|TOBGCBREG *Nicotiana plumbaginifolia* beta(1,3)-glucanas... 268 2e-75
20 emb|X54431|NTSP41B Tobacco sp41b mRNA for (1-3)-beta-glucanase. 100 1e-74
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emb|X54430|NTSP41A Tobacco sp41a mRNA for (1-3)-beta-glucanase. 100 2e-74
gb|M96941|BLYGCNHVI *Hordeum vulgare* glucan endo-1,3-beta-glucosi... 93 8e-74
emb|AJ012751|CAR012751 *Cicer arietinum* mRNA for glucan endo-beta... 140 4e-73
25 gb|M20618|TOBGLUBA *N.tabacum* beta-1,3-glucanase mRNA, clones pGL... 207 9e-73
emb|Z15131|ASBGLUCAN *A.sativa* mRNA for beta glucanase. 158 1e-70
gb|M62740|BLYGLB2 *Hordeum vulgare* 1,3-1,4-beta-D glucan 4-glucan... 158 2e-70
emb|Z22874|TABETGLUB *T.aestivum* (1,3;1,4) beta glucanase mRNA, c... 158 2e-70
emb|Z22873|TABETGLUA *T.aestivum* beta glucanase mRNA, complete CDS. 158 3e-70
30 emb|X52572|HVBDG Barley DNA for (1-3,1-4)-beta-D-glucanase (EC 3... 158 1e-69
emb|X56775|HVGLB1 *H.vulgare* Glb 1 gene for 1-3,1-4-beta-D-glucan... 158 1e-69
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35 emb|AF034107|AF034107 *Glycine max* beta-1,3-glucanase 2 (SGlu2) g... 122 2e-67
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40 emb|AW216754|AW216754 EST295468 tomato callus, TAMU *Lycopersicon*... 202 7e-64
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45 gb|M96939|BLYGLCNHV *Hordeum vulgare* glucan endo-1,3-beta-glucosi... 121 3e-61
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gb|M23548|BLYGEH Barley (1->3)-beta-glucan endohydrolase mRNA, c... 92 7e-61
emb|Y18212|TAY18212 *Triticum aestivum* mRNA for beta-1,3-endogluc... 93 9e-61
emb|AF030771|AF030771 *Hordeum vulgare* beta-1,3-glucanase 2 (BGL3... 92 2e-60
50 gb|M62907|BLYCBGL32 *H.vulgare* L. (1-3)-beta-glucanase mRNA, comp... 92 2e-60
emb|A37992|A37992 Sequence 11 from Patent EP0616035: 92 2e-60
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emb|AF034109|AF034109 *Glycine max* beta-1,3-glucanase 4 (SGlu4) g... 139 2e-59
55 emb|AW033770|AW033770 EST277341 tomato callus, TAMU *Lycopersicon*... 122 3e-59
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60 emb|AI894452|AI894452 EST263907 tomato callus, TAMU *Lycopersicon*... 210 4e-57
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2 [arabidopsis thaliana] /blast_score 1.00e-112
15 (921 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

25 dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 144 7e-44
emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 132 9e-43
dbj|D38123|TOBBY4A Nicotiana tabacum mRNA for ERF1, complete cds. 134 6e-41
emb|AF245119|AF245119 Mesembryanthemum crystallinum AP2-related ... 161 5e-39
emb|AW267820|AW267820 EST305948 DSIR Medicago truncatula cDNA cl... 160 1e-38
30 emb|AB035270|AB035270 Matricaria chamomilla McEREBP1 mRNA for et... 155 5e-37
gb|U89255|LEU89255 Lycopersicon esculentum DNA-binding protein P... 138 3e-32
emb|AI771213|AI771213 EST252409 tomato ovary, TAMU Lycopersicon ... 135 1e-31
emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 134 1e-30
emb|AW729466|AW729466 GA_Ea0025B11 Gossypium arboreum 7-10 dpa ... 132 4e-30
35 emb|AF057373|AF057373 Nicotiana tabacum ethylene response elemen... 125 4e-28
emb|AW981151|AW981151 EST392345 DSIL Medicago truncatula cDNA cl... 124 8e-28
emb|AW396250|AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone... 116 2e-25
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40 emb|AI897834|AI897834 EST267277 tomato ovary, TAMU Lycopersicon ... 113 2e-24
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 (965 letters)

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 20 Sequences producing significant alignments: (bits) Value

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 25 emb|AF022775|AF022775 Nicotiana tabacum caffeoyl-CoA 3-O-methyl... 138 2e-67
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 30 gb|U13151|ZEU13151 Zinnia elegans S-adenosyl-L-methionine:trans-... 136 4e-66
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- emb|AI939180|AI939180 sc67h02.y1 Gm-c1016 Glycine max cDNA clone... 125 3e-54
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emb|AW424002|AW424002 sh59c10.y1 Gm-c1015 Glycine max cDNA clone... 115 2e-51
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emb|AW980337|AW980337 EST391490 GVN Medicago truncatula cDNA clo... 127 3e-50
20 emb|AW648499|AW648499 EST326953 tomato germinating seedlings, TA... 99 7e-50
emb|AW690185|AW690185 NF029D09ST1F1000 Developing stem Medicago ... 142 1e-49
emb|AI895091|AI895091 EST264534 tomato callus, TAMU Lycopersicon... 99 3e-49
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25 emb|AW684885|AW684885 NF022F07NR1F1000 Nodulated root Medicago t... 142 2e-47
emb|AA660318|AA660318 00189 MtrHE Medicago truncatula cDNA 5' si... 144 2e-47
emb|AW703717|AW703717 sk23e07.y1 Gm-c1028 Glycine max cDNA clone... 132 4e-47
emb|AW776435|AW776435 EST335500 DSIL Medicago truncatula cDNA cl... 142 5e-47
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30 emb|AW620537|AW620537 sj06d09.y1 Gm-c1032 Glycine max cDNA clone... 133 1e-46
emb|AI775483|AI775483 EST256583 tomato resistant, Cornell Lycops... 139 2e-46
gb|BE124333|BE124333 EST393368 GVN Medicago truncatula cDNA clon... 125 3e-46
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45 gb|BE059325|BE059325 sn31c09.y1 Gm-c1016 Glycine max cDNA clone ... 140 3e-43
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50 emb|AW774697|AW774697 EST333848 KV3 Medicago truncatula cDNA clo... 84 8e-42
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emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40
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emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40
emb|AI960196|AI960196 sc80a08.y1 Gm-c1018 Glycine max cDNA clone... 132 5e-40
60 emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39
emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39

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(925 letters)

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 10 661,018 sequences; 426,114,510 total letters

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	emb AJ012689 CAR012689 Cicer arietinum mRNA for ribonuclease T2.	384	e-106	
	gb U13256 NAU13256 Nicotiana alata RNase NE mRNA, complete cds.	361	4e-99	
	gb U19924 ZEU19924 Zinnia elegans wounding-induced ribonuclease ...	358	4e-98	
20	emb AB034638 AB034638 Nicotiana tabacum mRNA for RNase, complete...	353	1e-96	
	emb X79337 LERNAL L.esculentum mRNA for ribonuclease le.	212	2e-93	
	dbj D49529 D49529 Pyrus pyrifolia mRNA for ribonuclease, complet...	335	4e-91	
	emb AI486253 AI486253 EST244574 tomato ovary, TAMU Lycopersicon ...	212	2e-89	
	emb AI485206 AI485206 EST243510 tomato ovary, TAMU Lycopersicon ...	212	1e-81	
25	gb U19923 ZEU19923 Zinnia elegans ribonuclease mRNA, complete cds.	232	3e-80	
	emb X79338 LERNALX L.esculentum mRNA for ribonuclease lx.	177	1e-73	
	emb AB032257 AB032257 Nicotiana glutinosa NGR3 mRNA for RNase NG...	176	7e-70	
	emb AI484830 AI484830 EST243091 tomato ovary, TAMU Lycopersicon ...	212	7e-70	
	emb AW684365 AW684365 NF016B03NR1F1000 Nodulated root Medicago t...	251	7e-66	
30	emb AI489460 AI489460 EST247799 tomato ovary, TAMU Lycopersicon ...	212	3e-63	
	emb Y17444 LES17444 Lycopersicon esculentum RNALX gene, exons 1 ...	152	2e-57	
	emb AI772676 AI772676 EST253776 tomato resistant, Cornell Lycopersicon...	152	2e-57	
	emb AI775352 AI775352 EST256452 tomato resistant, Cornell Lycopersicon...	212	3e-56	
	gb BE037115 BE037115 MP15C03 MP Mesembryanthemum crystallinum cD...	153	4e-55	
35	emb AF000939 AF000939 Hordeum vulgare aleurone ribonuclease mRNA...	89	7e-55	
	gb M83668 NELSTORAGE Nelumbo nucifera storage protein mRNA, comp...	127	2e-54	
	emb AI812905 AI812905 22D1 Pine Lambda Zap Xylem library Pinus t...	165	3e-54	
	emb AI488432 AI488432 EST246771 tomato ovary, TAMU Lycopersicon ...	211	5e-54	
	emb AW775298 AW775298 EST334363 DSIL Medicago truncatula cDNA cl...	200	7e-54	
40	emb AW279538 AW279538 s90h05.y1 Gm-c1019 Glycine max cDNA clone...	188	6e-47	
	emb AF000940 AF000940 Hordeum vulgare ribonuclease gene, complet...	116	2e-44	
	gb BE060583 BE060583 HVSMEg0012L03f Hordeum vulgare pre-anthesis...	74	5e-42	
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	emb AI777654 AI777654 EST258449 tomato susceptible, Cornell Lycopersicon...	152	2e-41	
45	emb AW596890 AW596890 sj84b03.y1 Gm-c1034 Glycine max cDNA clone...	162	3e-39	
	gb BE060118 BE060118 HVSMEg0011I10f Hordeum vulgare pre-anthesis...	89	6e-37	
	gb BE060590 BE060590 HVSMEg0012L10f Hordeum vulgare pre-anthesis...	89	2e-36	
	emb AW704136 AW704136 sk16e03.y1 Gm-c1028 Glycine max cDNA clone...	145	4e-34	
	emb AW289659 AW289659 NXNV003D07F Nsf Xylem Normal wood Vertical...	109	8e-32	
50	gb U19794 MDU19794 Malus domestica S-like RNase gene, partial cds.	76	2e-25	
	emb AI967855 AI967855 Ljimpest14-054-a9 Ljimp Lambda HybriZap ...	109	4e-23	
	emb Y17446 LES17446 Lycopersicon esculentum RNALX gene, exons 1 ...	104	1e-21	
	dbj D64012 LUFRNLC2 Luffa cylindrica mRNA for ribonuclease (RNase...	95	1e-20	
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	emb AW216541 AW216541 EST295255 tomato callus, TAMU Lycopersicon...	43	6e-19	
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	gb BE124916 BE124916 EST393951 GVN Medicago truncatula cDNA clon...	44	4e-18	

	emb AB032256 AB032256 <i>Nicotiana glutinosa</i> NGR2 mRNA for RNase NG...	41	9e-18
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	emb AW775566 AW775566 EST334631 <i>DSIL Medicago truncatula</i> cDNA cl...	44	1e-17
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5	emb AB034248 AB034248 <i>Volvox carteri</i> vml mRNA for S-like RNase,...	58	8e-17
	emb AF176533 AF176533 <i>Solanum chacoense</i> self-incompatibility rib...	82	2e-16
	emb AI416638 AI416638 sa17c06.y1 <i>Gm-c1004 Glycine max</i> cDNA clone...	45	6e-16
	emb X96465 AHS2RNASE <i>A.hispanicum</i> mRNA for S2-Rnase.	60	2e-15
	emb AB028153 AB028153 <i>Prunus avium</i> mRNA for S1-RNase, complete cds.	56	3e-15
10	emb AW223027 AW223027 EST299838 tomato fruit red ripe, TAMU Lyco...	43	4e-15
	emb AW224120 AW224120 EST300931 tomato fruit red ripe, TAMU Lyco...	43	5e-15
	emb AW223831 AW223831 EST300642 tomato fruit red ripe, TAMU Lyco...	43	5e-15
	emb AF191732 AF191732 <i>Solanum chacoense</i> self-incompatibility rib...	82	6e-15
	emb AB010306 AB010306 <i>Prunus avium</i> mRNA for S3-RNase, complete cds.	57	2e-14
15	emb X76065 LPSRNASE <i>L.peruvianum</i> mRNA for S-RNase S3.	60	2e-14
	emb AB010304 AB010304 <i>Prunus avium</i> mRNA for S2-RNase, partial cds.	60	4e-14
	emb AI729649 AI729649 BNLGHi13860 Six-day Cotton fiber <i>Gossypium</i> ...	45	9e-14
	emb AI729386 AI729386 BNLGHi13239 Six-day Cotton fiber <i>Gossypium</i> ...	45	1e-13
	emb AW671991 AW671991 LG1_353_B05.b1_A002 Light Grown 1 (LG1) So...	45	1e-13
20	gb S61768 S61768 S (S5)=self-incompatibility {3' region} [<i>Lycopersicon</i> ...	60	1e-13
	emb X56897 SCSIAP3 <i>S.chacoense</i> mRNA for self-incompatibility ass...	63	1e-13
	emb AW563386 AW563386 LG1_214_C01.b1_A002 Light Grown 1 (LG1) So...	45	1e-13
	emb AB011470 AB011470 <i>Prunus dulcis</i> mRNA for Sc-RNase, complete ...	60	3e-13
	emb AB011469 AB011469 <i>Prunus dulcis</i> mRNA for Sb-RNase, complete ...	57	4e-13
25	emb AW623083 AW623083 EST321028 tomato flower buds 3-8 mm, <i>Cornel</i> ...	43	8e-13
	emb AW034883 AW034883 EST279112 tomato callus, TAMU <i>Lycopersicon</i> ...	43	8e-13
	emb AF232304 AF232304 <i>Solanum chacoense</i> gametophytic self-incomp...	58	1e-12
	emb Z26583 LPSLGS6 <i>L.peruvianum</i> (Mill) self-incompatibility glyc...	56	1e-12
	emb AB011471 AB011471 <i>Prunus dulcis</i> mRNA for Sd-RNase, partial cds.	57	1e-12
30	emb AV427528 AV427528 AV427528 <i>Lotus japonicus</i> young plants (two...	74	2e-12
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	dbj E01266 E01266 cDNA encoding S2-protein linked to part of its...	56	1e-11
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40	emb AJ271062 PHY271062 <i>Petunia hybrida</i> mRNA for Sv-ribonuclease ...	62	2e-11
	emb AB016522 AB016522 <i>Petunia x hybrida</i> mRNA for SB1-ribonucleas...	62	2e-11
	emb AB026981 AB026981 <i>Prunus salicina</i> mRNA for Sa-RNase, partial...	56	3e-11
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	gb U19791 MDU19791 <i>Malus domestica</i> S5-RNase (S) mRNA, partial cds.	38	4e-11
45	emb X96466 AHS4RNASE <i>A.hispanicum</i> mRNA for S4-Rnase.	46	7e-11
	gb M81686 PETSXPROB <i>Petunia hybrida</i> Sx-protein (self-incompatibi...	58	1e-10
	emb Z26581 LPSLGS7 <i>L.peruvianum</i> (Mill) mRNA for self-incompatabi...	51	2e-10
	emb X56896 SCSIAP <i>S.chacoense</i> mRNA for self-incompatibility asso...	62	3e-10
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	dbj D63887 D63887 <i>Nicotiana alata</i> mRNA for ribonuclease, complet...	61	3e-10
	emb AF105363 AF105363 <i>Lycium andersonii</i> self-incompatibility rib...	66	4e-10
	gb U07362 PHU07362 <i>Petunia hybrida</i> S1 self-incompatibility ribon...	62	4e-10
55	gb L40542 POTDSCS <i>Solanum carolinense</i> self-incompatibility ribon...	65	7e-10

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Database: plantfungal

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5

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Sequences producing significant alignments:

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	emb AI782831 AI782831 EST263710 tomato susceptible, Cornell Lyco...	270	1e-71
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40	emb AW034079 AW034079 EST277574 tomato callus, TAMU Lycopersicon...	77	3e-13
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45	emb Z83835 LEZEAXAN L.esculentum mRNA for zeaxanthin epoxidase.	59	1e-07
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60	emb AL115728 CNS01CMW Botrytis cinerea strain T4 cDNA library un...	36	0.80
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 15 gb|BE122310|BE122310 894019A08.y1 C. reinhardtii CC-1690, normal... 35 2.1
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 35 emb|AF008953|AF008953 Octomeles sumatrana 18S ribosomal RNA gene... 34 3.9
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55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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60 Score E
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- emb|AI896318|AI896318 EST265761 tomato callus, TAMU Lycopersicon... 182 5e-65
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 5 emb|AW432288|AW432288 sh71g05.y1 Gm-c1015 Glycine max cDNA clone... 200 5e-50
 emb|AI730535|AI730535 BNLGHi7007 Six-day Cotton fiber Gossypium ... 152 1e-49
 emb|AF085168|AF085168 Triticum aestivum receptor-like protein ki... 77 2e-46
 emb|AF085166|AF085166 Hordeum vulgare receptor-like kinase gene,... 86 2e-45
 emb|AF085167|AF085167 Hordeum vulgare receptor-like kinase ARK1A... 85 3e-45
 10 gb|U51330|TAU51330 Triticum aestivum leaf rust resistance kinase... 82 8e-45
 emb|AF100771|AF100771 Hordeum vulgare receptor-like kinase (Hv3A... 100 2e-44
 gb|U78762|TAU78762 Triticum aestivum receptor-like kinase ARK1AS... 86 2e-44
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15 emb|AW934655|AW934655 EST353547 tomato flower buds 0-3 mm, Corne... 93 3e-34
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Database: plantfungal

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- emb|AI731648|AI731648 BNLGHi10360 Six-day Cotton fiber Gossypium... 182 2e-61
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15 emb|AL096874|SPBC1539 S.pombe chromosome II cosmid c1539. 57 5e-29
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45 gb|U33057|SCD9717 Saccharomyces cerevisiae chromosome IV cosmids... 34 2.6
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments: (bits) Value

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15 emb|AW933869|AW933869 EST359712 tomato fruit mature green, TAMU ... 287 1e-76
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25 emb|AW033083|AW033083 EST276642 tomato callus, TAMU Lycopersicon... 275 8e-73
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emb|AF162779|AF162779 Trypanosoma cruzi Tc45-calreticulin precur... 143 2e-60
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60 (757 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments:

(bits) Value

	gb U70666 BNU70666 Brassica napus pathogenesis-related protein P...	323	3e-89
10	gb U21849 BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds.	323	3e-89
	gb U64806 BNU64806 Brassica napus pathogenesis-related protein P...	209	4e-86
	emb AI352851 AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl...	311	5e-84
	emb AI352893 AI352893 MB72-6D PZ204.BNlib Brassica napus cDNA cl...	165	3e-62
	emb AW217013 AW217013 EST295727 tomato callus, TAMU Lycopersicon...	152	4e-60
15	emb AW219671 AW219671 EST302153 tomato root during/after fruit s...	151	1e-59
	emb AW092403 AW092403 EST285583 tomato mixed elicitor, BTI Lycop...	151	1e-59
	emb AI895090 AI895090 EST264533 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW625930 AW625930 EST319825 tomato radicle, 5 d post-imbibit...	151	1e-59
	emb AW032514 AW032514 EST276073 tomato callus, TAMU Lycopersicon...	151	1e-59
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	emb AW034206 AW034206 EST277777 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW219480 AW219480 EST301878 tomato root during/after fruit s...	151	1e-59
	emb AW092623 AW092623 EST285803 tomato mixed elicitor, BTI Lycop...	151	1e-59
25	emb AW040954 AW040954 EST283818 tomato mixed elicitor, BTI Lycop...	151	1e-59
	emb AW034454 AW034454 EST278025 tomato callus, TAMU Lycopersicon...	151	1e-59
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35	emb AW329241 AW329241 N200453e rootphos(-) Medicago truncatula c...	160	1e-58
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50	emb X14065 NTPRP1 Nicotiana tabacum gene for basic form of patho...	140	5e-55
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	emb X52555 NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat...	116	1e-52
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55	emb AW053720 AW053720 L30-1612T3 Ice plant Lambda Uni-Zap XR exp...	112	4e-52
	emb AW559969 AW559969 EST315017 DSIR Medicago truncatula cDNA cl...	81	4e-52
	emb AI352801 AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl...	194	1e-51
	emb X17681 NTPR1CA Tobacco gene for pathogenesis-related protein...	111	2e-51
	emb X05454 NTPR1CR Nicotiana tabacum mRNA for PR-1c protein.	111	2e-51
60	emb X12487 NTPR1C Tobacco mRNA fragment for pathogenesis-related...	111	2e-51
	emb AJ011520 LES011520 Lycopersicon esculentum pr1a (P4) gene.	98	1e-50

gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50
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 5 emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50
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 10 emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
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 emb|AW034882|AW034882 EST279111 tomato callus, TAMU Lycopersicon... 95 1e-49
 emb|AW031086|AW031086 EST274393 tomato callus, TAMU Lycopersicon... 116 1e-49
 emb|X74939|HVPR1AR H.vulgare HvPR-1a mRNA for a basic PR-1-type... 114 2e-49
 20 emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49
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 25 emb|Y08804|LEPR1B1 L.esculentum mRNA for PR protein. 92 7e-49
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55 Database: plantfungal
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60 Score E
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	emb AI782780 AI782780 EST263659 tomato susceptible, Cornell Lyco...	259	4e-77
	emb AI486671 AI486671 EST244993 tomato ovary, TAMU Lycopersicon ...	241	4e-70
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50	emb AW350847 AW350847 GM210009B20G5R Gm-r1021 Glycine max cDNA 3...	106	2e-24
	emb AI776960 AI776960 EST251986 tomato callus, TAMU Lycopersicon...	111	2e-23
	emb AW781088 AW781088 sl88h09.y1 Gm-cl037 Glycine max cDNA clone...	111	3e-23
	emb AW039011 AW039011 EST280984 tomato mixed elicitor, BTI Lycop...	111	3e-23
	emb AW617273 AW617273 EST323684 L. hirsutum trichome, Cornell Un...	106	7e-22
55	gb BE022211 BE022211 sm72b10.y1 Gm-cl028 Glycine max cDNA clone ...	106	7e-22
	emb AW668188 AW668188 GA_Ea0013B18 Gossypium arboreum 7-10 dpa ...	105	2e-21
	emb AA824914 AA824914 CT202.SK Tomato Leaf cDNA from cv. VFNT ch...	93	6e-21
	emb AT000374 AT000374 AT000374 Apple peel cDNA library Malus x d...	102	1e-20
	emb AW623583 AW623583 EST321528 tomato flower buds 3-8 mm, Corne...	69	7e-20
60	emb AI495394 AI495394 sa97d10.y1 Gm-cl1004 Glycine max cDNA clone...	98	2e-19
	emb AI725563 AI725563 BNLGHi12127 Six-day Cotton fiber Gossypium...	67	5e-18

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5 emb|AI894661|AI894661 EST264104 tomato callus, TAMU Lycopersicon... 68 3e-10
emb|AW217336|AW217336 EST296159 tomato flower buds 0-3 mm, Corne... 67 7e-10
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emb|AW164084|AW164084 Ljirnp19-528-f6 Ljirnp Lambda HybriZap ... 56 1e-06
emb|AJ249962|DCA249962 Daucus carota mRNA for potassium channel ... 55 3e-06
10 emb|AW184978|AW184978 se85a09.y1 Gm-c1023 Glycine max cDNA clone... 54 4e-06
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emb|AW041519|AW041519 EST284383 tomato mixed elicitor, BTI Lycop... 51 3e-05
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15 emb|AW928912|AW928912 EST337700 tomato flower buds 8 mm to pre-a... 48 2e-04
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emb|AC016528|AC016528 Leishmania major chromosome 35 clone L4123... 35 1.7
35 emb|AI781524|AI781524 EST262403 tomato susceptible, Cornell Lyco... 31 2.0
gb|U28374|YSCD9740 Saccharomyces cerevisiae chromosome IV cosmid... 35 2.3
emb|AW399566|AW399566 EST310066 L. pennellii trichome, Cornell U... 35 2.3
gb|BE034738|BE034738 ML03G05 ML Mesembryanthemum crystallinum cD... 35 2.3
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40 emb|AW648153|AW648153 EST326607 tomato germinating seedlings, TA... 35 2.3
gb|M74798|HEVHMGR3A Hevea brasiliensis 3-hydroxy-3-methylglutary... 34 4.4
emb|AW728887|AW728887 GA_Ea0018B11 Gossypium arboreum 7-10 dpa ... 34 4.4
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55 emb|AI489346|AI489346 EST247685 tomato ovary, TAMU Lycopersicon ... 79 2e-28
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emb|AW509006|AW509006 si38h07.y1 Gm-r1030 Glycine max cDNA clone... 79 2e-26
emb|AW685404|AW685404 NF028H10NR1F1000 Nodulated root Medicago t... 74 2e-24
60 emb|AW781320|AW781320 sk68d07.y1 Gm-c1016 Glycine max cDNA clone... 86 2e-24
emb|AI897832|AI897832 EST267275 tomato ovary, TAMU Lycopersicon ... 78 1e-23

- emb|AW102460|AW102460 sd88d10.y1 Gm-c1009 Glycine max cDNA clone... 70 2e-22
emb|AI490284|AI490284 EST248610 tomato ovary, TAMU Lycopersicon ... 103 2e-22
emb|AI487362|AI487362 EST245684 tomato ovary, TAMU Lycopersicon ... 72 3e-20
gb|BE125690|BE125690 DG1_54_A02.g1_A002 Dark Grown 1 (DG1) Sorgh... 96 3e-19
5 emb|X80231|LTCAMA L.tarentolae CAM A gene for calmodulin. 73 1e-18
emb|AL115248|CNS01C9K Botrytis cinerea strain T4 cDNA library un... 65 4e-18
dbj|D10521|TETCALW T.pyriformis mRNA for calmodulin. 73 7e-18
gb|M76407|SLECALMODU Stylonychia lemnae calmodulin gene, complet... 74 9e-18
emb|AF007889|AF007889 Symbiodinium microadriaticum calmodulin (S... 74 1e-17
10 emb|AF078679|AF078679 Olea europaea calcium-binding protein (PCA... 57 2e-17
emb|X56511|TBCALUBG T. brucei genes for calmodulin, EFH5 and ubi... 77 2e-17
emb|X52096|TCCALB2 Trypanosoma cruzi CalA2 calmodulin gene. 77 2e-17
emb|AF030033|AF030033 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 75 2e-17
emb|X90560|PPCAMPROT Physcomitrella patens mRNA for calmodulin. 71 2e-17
15 gb|U91642|POU91642 Pleurotus ostreatus calmodulin mRNA, complete... 75 2e-17
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emb|X85091|MPCAM M.pyrifera mRNA for calmodulin. 74 2e-17
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emb|Y08373|TGCM T.gondii mRNA for calmodulin. 74 2e-17
20 gb|C96396|C96396 C96396 Marchantia polymorpha immature sex organ... 73 3e-17
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emb|AB041711|AB041711 Chara corallina cccam1 mRNA for calmodulin... 75 4e-17
25 gb|J05116|ACKCAL A.klebsiana calmodulin gene, complete cds. 75 4e-17
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emb|AI328739|AI328739 a6d02ne.fl Neurospora crassa evening cDNA ... 74 6e-17
emb|AF034964|AF034964 Glomerella cingulata calmodulin (cam) mRNA... 74 6e-17
gb|U12505|HCCMD Histoplasma capsulatum 186AS calmodulin mRNA, co... 74 8e-17
30 gb|M34540|PARCAM P.tetraurelia calmodulin gene, complete cds. 74 8e-17
gb|S68025|S68025 CAM=calmodulin [Paramecium tetraurelia, Genomic... 74 8e-17
emb|AW164773|AW164773 se77e12.y1 Gm-c1023 Glycine max cDNA clone... 64 8e-17
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35 emb|AW126204|AW126204 N100049e rootphos(-) Medicago truncatula c... 57 8e-17
emb|X52242|TTCALM T.thermophila mRNA for calmodulin. 73 1e-16
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emb|AW625406|AW625406 EST319229 tomato radicle, 5 d post-imbibit... 62 1e-16
gb|K02944|TRBCMRSG Trypanosoma brucei gambiense calmodulin genes... 73 2e-16
40 gb|M88307|BNACALM Brassica juncea calmodulin mRNA, complete cds. 73 2e-16
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emb|X89890|BPCALMGEN B.pilosa mRNA for calmodulin. 73 2e-16
emb|AW099396|AW099396 sd39h01.y1 Gm-c1016 Glycine max cDNA clone... 76 2e-16
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45 emb|AL112713|CNS01AB5 Botrytis cinerea strain T4 cDNA library un... 73 2e-16
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emb|AW738989|AW738989 gb23c06.y1 Moss EST library PPN Physcomitr... 73 3e-16
gb|U48693|TAU48693 Triticum aestivum calmodulin TaCaM3-1 mRNA, c... 73 4e-16
gb|M27303|BLYCAMA Barley cam gene encoding calmodulin, complete ... 73 4e-16
60 gb|BE033450|BE033450 ME02B08 ME Mesembryanthemum crystallinum cD... 73 4e-16
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	emb AW730911 AW730911 GA_Ea0029I11 <i>Gossypium arboreum</i> 7-10 dpa ...	73	4e-16
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5	emb AF030032 AF030032 <i>Phaseolus vulgaris</i> calmodulin (CaM) mRNA, ...	73	4e-16
	gb L01431 SOYSCAM2X Soybean calmodulin (SCaM-2) mRNA, complete cds.	73	4e-16
	emb Y09853 CACAM <i>Cicer arietinum</i> mRNA for CaM protein.	73	4e-16
	gb L01432 SOYSCAM3X Soybean calmodulin (SCaM-3) mRNA, complete cds.	73	4e-16
	gb U49104 TAU49104 <i>Triticum aestivum</i> calmodulin TaCaM3-3 mRNA, c...	73	4e-16
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	emb Z12839 LLCALMOD <i>Lilium longiflorum</i> mRNA encoding calmodulin.	73	4e-16
	gb L18912 LILCALMODU <i>Lilium longiflorum</i> calmodulin mRNA, complet...	73	4e-16
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	emb AF097311 AF097311 <i>Stevia rebaudiana</i> kaurene synthase (KS22-1)...	88	5e-31
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55	emb AF067601 AF067601 <i>Clarkia breweri</i> linalool synthase 1 (LIS1)...	86	1e-17
	gb U43904 CMU43904 <i>Cucurbita maxima</i> ent-kaurene synthase B mRNA,...	63	5e-17
	emb AI485628 AI485628 EST243949 tomato ovary, TAMU <i>Lycopersicon</i> ...	60	3e-15
	emb AI485623 AI485623 EST243944 tomato ovary, TAMU <i>Lycopersicon</i> ...	55	9e-14
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	emb AW255432 AW255432 ML454 peppermint glandular trichome <i>Mentha</i> ...	56	1e-08

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40	emb AW255052 AW255052 ML1347 peppermint glandular trichome Menth...	55	2e-06
	emb AW254888 AW254888 ML1312 peppermint glandular trichome Menth...	55	2e-06
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	emb AB015675 AB015675 Lycopersicon esculentum CPS mRNA for copal...	54	5e-06
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45	emb AF175323 AF175323 Mentha longifolia limonene synthase mRNA, ...	54	6e-06
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	emb AF139205 AF139205 Abies grandis beta-phellandrene synthase (...)	52	2e-05
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55	emb AW254876 AW254876 ML1300 peppermint glandular trichome Menth...	49	2e-04
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	emb AF051899 AF051899 Salvia officinalis 1,8-cineole synthase mR...	48	4e-04
	emb AF006193 AF006193 Abies grandis (-)-4S-limonene synthase mRN...	47	5e-04
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 10 emb|AW255471|AW255471 ML495 peppermint glandular trichome *Mentha...* 40 0.087
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35 Database: plantfungal
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	emb AB022732 AB022732 <i>Glycyrrhiza echinata</i> CYP Ge-31 mRNA for cy...	376	e-149
	emb AJ238439 CAR238439 <i>Cicer arietinum</i> mRNA for a cytochrome P45...	377	e-147
45	emb AJ012581 CAR012581 <i>Cicer arietinum</i> mRNA for cytochrome P450.	376	e-147
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	emb AJ000478 HTCYP81L <i>Helianthus tuberosus</i> mRNA for cytochrome P...	225	4e-84
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55	emb AW307234 AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone...	275	6e-73
	emb AW234443 AW234443 sf25c03.y1 Gm-c1028 Glycine max cDNA clone...	273	3e-72
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60	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber <i>Gossypium</i> ...	188	2e-62
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- emb|AW329224|AW329224 N200436e rootphos(-) Medicago truncatula c... 228 1e-58
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 5 emb|AI774414|AI774414 EST255514 tomato resistant, Cornell Lycopen... 152 9e-56
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 10 dbj|E13663|E13663 cDNA encoding cytochrome P450 which is induced... 116 5e-50
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 emb|AW676742|AW676742 DG1_14_A08.g1_A002 Dark Grown 1 (DG1) Sorg... 116 1e-49
 emb|AI731081|AI731081 BNLGHi8648 Six-day Cotton fiber Gossypium ... 198 1e-49
 emb|AW257188|AW257188 EST305325 KV2 Medicago truncatula cDNA clo... 152 2e-49
 15 emb|AW309826|AW309826 sf25c03.x1 Gm-cl028 Glycine max cDNA clone... 196 5e-49
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 20 emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 160 4e-47
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 25 emb|Y10982|GMP450CP6 Glycine max mRNA for cytochrome P450-like p... 159 9e-47
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 emb|AF124372|AF124372 Nicotiana tabacum NT7 mRNA, partial cds. 145 1e-46
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 30 emb|AF156976|AF156976 Gerbera hybrida flavone synthase II (CYP93... 103 2e-46
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 dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 157 1e-45
 emb|AW616482|AW616482 EST322893 L. hirsutum trichome, Cornell Un... 124 2e-45
 emb|AW617814|AW617814 EST324213 L. hirsutum trichome, Cornell Un... 124 2e-45
 35 emb|AF155332|AF155332 Petunia x hybrida flavonoid 3'-hydroxylase... 183 2e-45
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 45 emb|AW309498|AW309498 sf20c05.x1 Gm-cl028 Glycine max cDNA clone... 178 1e-43
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 emb|AW616066|AW616066 EST296823 L. hirsutum trichome, Cornell Un... 122 1e-43
 50 emb|AW255096|AW255096 ML139 peppermint glandular trichome Mentha... 162 2e-43
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 55 emb|AB023636|AB023636 Glycyrrhiza echinata CYP Ge-8 mRNA for cyt... 107 4e-42
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 5 emb|AB022733|AB022733 Glycyrrhiza echinata CYP Ge-51 mRNA for cy... 104 4e-41
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Database: plantfungal
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35 gb|U64925|NTU64925 Nicotiana tabacum geranylgeranylated protein ... 260 1e-68
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 40 emb|AW685484|AW685484 NF030E02NR1F1000 Nodulated root Medicago t... 171 2e-41
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 45 emb|AI780050|AI780050 EST260929 tomato susceptible, Cornell Lyco... 138 9e-32
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 emb|AI780139|AI780139 EST261018 tomato susceptible, Cornell Lyco... 86 7e-16
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 50 emb|AW774764|AW774764 EST333915 KV3 Medicago truncatula cDNA clo... 62 7e-09
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 55 emb|AW926585|AW926585 HVSMEg0007J19 Hordeum vulgare pre-anthesis... 29 0.025
 emb|AW032321|AW032321 EST275775 tomato callus, TAMU Lycopersicon... 28 0.026
 emb|AW736598|AW736598 EST333090 KV3 Medicago truncatula cDNA clo... 37 0.39
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	emb AW933326 AW933326 EST359169 tomato fruit mature green, TAMU ...	26	1.5
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	emb AW256609 AW256609 EST304746 KV2 Medicago truncatula cDNA clo...	34	2.6
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	emb AI485664 AI485664 EST243985 tomato ovary, TAMU Lycopersicon ...	195	8e-49
	emb AW774741 AW774741 EST333892 KV3 Medicago truncatula cDNA clo...	90	2e-48
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	emb AI485008 AI485008 EST243271 tomato ovary, TAMU Lycopersicon ...	157	2e-37
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	emb AL022103 SPBC2G2 S.pombe chromosome II cosmid c2G2.	79	1e-27
	emb X79743 SCBPPS S.cerevisiae BET1, PAN1 PRI1 and STS1 genes.	72	2e-27
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20	emb AW333870 AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c...	36	4e-09
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	emb AW127178 AW127178 M110117 GVN Medicago truncatula cDNA clone...	63	8e-09
	emb AW399291 AW399291 EST309791 L. pennellii trichome, Cornell U...	62	2e-08
	emb AW616547 AW616547 EST322958 L. hirsutum trichome, Cornell Un...	62	2e-08
25	emb AW693686 AW693686 NF068A05ST1F1036 Developing stem Medicago ...	62	2e-08
	emb AW208046 AW208046 M111077e DSIR Medicago truncatula cDNA clo...	61	4e-08
	emb AQ642482 AQ642482 RPCI93-EcoRI-1A17.TV RPCI93-EcoRI Trypanos...	53	6e-08
	emb AW686583 AW686583 NF039G02NR1F1000 Nodulated root Medicago t...	45	5e-07
	emb AQ849089 AQ849089 LMAJFV1_lm41a04.y1 Leishmania major FV1 ra...	44	5e-06
30	emb AI781410 AI781410 EST262277 tomato susceptible, Cornell Lyco...	52	2e-05
	emb AW617564 AW617564 EST323975 L. hirsutum trichome, Cornell Un...	49	2e-04
	emb AQ946427 AQ946427 Sheared DNA-49M8.TF Sheared DNA Trypanosom...	47	4e-04
	emb AW099113 AW099113 sd34f04.y1 Gm-c1012 Glycine max cDNA clone...	46	0.001
	emb Z74807 SCYOL065C S.cerevisiae chromosome XV reading frame OR...	29	0.002
35	emb AQ655271 AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso...	38	0.004
	emb AW685854 AW685854 NF031A06NR1F1000 Nodulated root Medicago t...	43	0.007
	emb AW437996 AW437996 ST83C09 Pine TriplEx shoot tip library Pin...	42	0.014
	emb AI440709 AI440709 sa62e11.y1 Gm-c1004 Glycine max cDNA clone...	31	0.021
	emb AW979881 AW979881 EST341528 tomato root deficiency, Cornell ...	37	0.45
40	gb M28064 PFAHRKP Plasmodium brasilianum DNA homologous to the h...	37	0.45
	emb AF263282 AF263282 Filobasidiella neoformans var. neoformans ...	34	0.54
	emb AW702543 AW702543 TgESTzz85a12.y1 TgRH*-Tachyzoite cDNA Toxo...	32	0.58
	emb AQ651205 AQ651205 Sheared DNA-30N15.TF Sheared DNA Trypanoso...	37	0.62
	emb AQ945454 AQ945454 Sheared DNA-54H22.TF Sheared DNA Trypanoso...	37	0.62
45	emb AZ214873 AZ214873 Sheared DNA-109E2.TR Sheared DNA Trypanoso...	37	0.62
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	emb AL049180 PFMAL13P1 Plasmodium falciparum chromosome 13 strai...	36	1.2
	emb Z74892 BO15H11 B.oleracea mRNA for glycine-rich protein.	36	1.2
	emb AW774740 AW774740 EST333891 KV3 Medicago truncatula cDNA clo...	36	1.2
50	emb Z38060 SC5610 S.cerevisiae chromosome IX sequence derived fr...	36	1.2
	emb AL031745 PFMAL1P2 Plasmodium falciparum chromosome 1 strain ...	35	2.2

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(1690 letters)

60 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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5	emb X74421 STG6PDH	S.tuberosum mRNA for glucose-6-phosphate dehy...	911 0.0
	emb AF012862 AF012862	Petroselinum crispum cytosolic glucose-6-p...	841 0.0
	emb AJ001770 NTTCG9	Nicotiana tabacum mRNA for cytosolic glucose...	893 0.0
	gb U18238 MSU18238	Medicago sativa glucose-6-phosphate dehydroge...	900 0.0
10	emb AF012863 AF012863	Petroselinum crispum cytosolic glucose-6-p...	887 0.0
	emb AJ001769 NTTCG6	Nicotiana tabacum mRNA cytosolic glucose-6-p...	895 0.0
	emb AF097663 AF097663	Mesembryanthemum crystallinum cytoplasmic ...	754 0.0
	emb AB011441 AB011441	Triticum aestivum WESR5 mRNA for glucose-6...	500 e-141
	emb X70373 KLLTZWF	K.lactis LET1 gene and ZWF gene for glucose-...	231 e-138
15	emb Z69381 SCCXIV39K	S.cerevisiae 38,855 bp segment of chromosom...	244 e-136
	gb M34709 YSCG6PD	S.cerevisiae glucose-6-phosphate dehydrogenase...	244 e-136
	emb X57336 SCMET19	S. cerevisiae MET19 gene for glucose-6-phosph...	244 e-136
	emb Z71517 SCYNL241C	S.cerevisiae chromosome XIV reading frame O...	244 e-136
	emb AJ010712 STU010712	Solanum tuberosum mRNA for glucose-6-phos...	240 e-136
20	emb X99405 NTG6PD	N.tabacum mRNA for chloroplast glucose-6-phosp...	242 e-135
	emb AF012861 AF012861	Petroselinum crispum plastidic glucose-6-p...	248 e-135
	emb AI730607 AI730607	BNLGHi7371 Six-day Cotton fiber Gossypium ...	481 e-135
	emb X87942 ANG6PDHSE	A.niger mRNA for glucose-6-phosphate dehydr...	225 e-132
	emb AW686120 AW686120	NF038D09NR1F1000 Nodulated root Medicago t...	472 e-132
25	emb AJ132346 DBI132346	Dunaliella bioculata mRNA for plastidic g...	235 e-132
	emb AW925642 AW925642	HVSMEg0005C04 Hordeum vulgare pre-anthesis...	465 e-130
	emb AJ001772 NTTPG18	Nicotiana tabacum mRNA for plastidic glucos...	243 e-129
	emb AW930385 AW930385	EST340938 tomato fruit mature green, TAMU ...	444 e-124
	emb AW831416 AW831416	sm22g09.y1 Gm-c1028 Glycine max cDNA clone...	434 e-121
30	emb X83923 STG6PDHPI	S.tuberosum mRNA for glucose-6-phosphate de...	249 e-118
	emb AJ000182 SO000182	Spinacia oleracea mRNA for glucose-6-phosp...	242 e-117
	emb AJ001771 NTTPG16	Nicotiana tabacum mRNA for plastidic glucos...	247 e-116
	emb AI491202 AI491202	EST241911 tomato shoot, Cornell Lycopersic...	368 e-116
	emb AL121764 SPAC9	S.pombe chromosome I cosmid c9.	196 e-116
35	emb AW233801 AW233801	sf26h03.y1 Gm-c1028 Glycine max cDNA clone...	415 e-115
	emb Z95395 SPAC3A12	S.pombe chromosome I cosmid c3A12.	196 e-108
	emb AW288048 AW288048	N100892e rootphos(-) Medicago truncatula c...	387 e-106
	emb AW685333 AW685333	NF027C04NR1F1000 Nodulated root Medicago t...	356 e-105
	emb X77830 ANWGGSDA	A.nidulans (WG096) gsdA gene.	130 e-102
40	emb AJ006246 CCA6246	Cyanidium caldarium mRNA for glucose-6-phos...	239 e-102
	emb AJ000184 SO000184	Spinacia oleracea mRNA for glucose-6-phosp...	242 e-100
	emb AJ000183 SO000183	Spinacia oleracea mRNA for glucose-6-phosp...	190 3e-99
	emb X84001 ANDNAG6PD	A.nidulans g6pd gene.	130 2e-98
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45	emb AW761534 AW761534	sl68h05.y1 Gm-c1027 Glycine max cDNA clone...	356 4e-97
	emb X74988 PFGLPH	P.falciparum gene for glucose-6-phosphate dehy...	192 5e-89
	emb AW560329 AW560329	EST315377 DSIR Medicago truncatula cDNA cl...	323 2e-87
	gb M80655 PFAG6PD	Plasmodium falciparum glucose-6-phosphate dehy...	192 1e-86
	emb AW497059 AW497059	ga53c08.y1 Moss EST library PPU Physcomitr...	319 5e-86
50	emb AW216550 AW216550	EST295264 tomato callus, TAMU Lycopersicon...	188 6e-84
	emb AW219903 AW219903	EST302386 tomato root during/after fruit s...	305 7e-82
	emb AW180861 AW180861	MgA1030fMgA Library Mycosphaerella gramin...	226 5e-80
	emb AW616585 AW616585	EST322996 L. hirsutum trichome, Cornell Un...	175 7e-80
	emb AW309937 AW309937	sf26h03.x1 Gm-c1028 Glycine max cDNA clone...	294 1e-78
55	emb AW031447 AW031447	EST274901 tomato callus, TAMU Lycopersicon...	166 6e-78
	emb AI894720 AI894720	EST264163 tomato callus, TAMU Lycopersicon...	291 1e-77
	emb AW690515 AW690515	NF030E09ST1F1000 Developing stem Medicago ...	174 3e-77
	emb AW736245 AW736245	EST332231 KV3 Medicago truncatula cDNA clo...	278 7e-76
	emb AW455246 AW455246	EST311906 tomato root during/after fruit s...	155 6e-75
60	emb AW980010 AW980010	EST310488 tomato root deficiency, Cornell ...	153 3e-74
	emb AL023595 SPCC794	S.pombe chromosome III cosmid c794.	177 1e-73

- emb|AW255521|AW255521 ML551 peppermint glandular trichome Mentha... 270 3e-71
 emb|AW567621|AW567621 si65f02.y1 Gm-r1030 Glycine max cDNA clone... 264 1e-69
 emb|AW689492|AW689492 NF019H04ST1F1000 Developing stem Medicago ... 128 3e-69
 emb|AW737104|AW737104 EST338531 tomato flower buds, anthesis, Co... 141 1e-64
 5 emb|AW255222|AW255222 ML216 peppermint glandular trichome Mentha... 142 2e-64
 emb|AW737079|AW737079 EST338506 tomato flower buds, anthesis, Co... 141 3e-64
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 emb|AQ952407|AQ952407 Sheared DNA-32N19.TF Sheared DNA Trypanoso... 84 2e-60
 10 emb|AA787466|AA787466 n3fl1a1.r1 Aspergillus nidulans 24hr asexu... 229 4e-59
 emb|AW254983|AW254983 ML1164 peppermint glandular trichome Menth... 134 2e-58
 emb|AW617385|AW617385 EST323796 L. hirsutum trichome, Cornell Un... 141 2e-57
 emb|AI773327|AI773327 EST254427 tomato resistant, Cornell Lycopers... 222 5e-57
 emb|AW704079|AW704079 sk27e10.y1 Gm-cl028 Glycine max cDNA clone... 219 6e-56
 15 emb|X77829|ANNGSDA A.niger (N400) gsdA gene. 131 4e-55
 emb|AW286177|AW286177 LG1_328_D07.g1_A002 Light Grown 1 (LG1) So... 216 4e-55
 emb|AW617091|AW617091 EST323502 L. hirsutum trichome, Cornell Un... 138 5e-55
 emb|AI777244|AI777244 EST258209 tomato resistant, Cornell Lycopers... 150 1e-54
 emb|AV424412|AV424412 AV424412 Lotus japonicus young plants (two... 205 9e-52
 20 emb|AQ875204|AQ875204 V123H11 mTn-3xHA/lacZ Insertion Library, s... 192 1e-49
 emb|AV416113|AV416113 AV416113 Lotus japonicus young plants (two... 196 4e-49
 emb|Z99568|SPAC3C7 S.pombe chromosome I cosmid c3C7. 95 1e-48
 emb|AQ500574|AQ500574 V36G4 mTn-3xHA/lacZ Insertion Library Sacc... 127 6e-48
 emb|AI187687|AI187687 p280 Porphyra yezoensis in Lambda UniZAP P... 87 1e-47
 25 emb|AJ279688|BPE279688 Betula pendula partial mRNA for Glucose-6... 93 7e-47
 emb|AW700124|AW700124 gb34g09.y1 Moss EST library PPN Physcomitr... 187 3e-46
 emb|AW223852|AW223852 EST300663 tomato fruit red ripe, TAMU Lyco... 141 6e-46
 emb|AW774199|AW774199 EST333350 KV3 Medicago truncatula cDNA clo... 143 3e-45
 emb|AW621290|AW621290 EST312088 tomato root during/after fruit s... 138 3e-43
 30 emb|AW980083|AW980083 EST341594 tomato root deficiency, Cornell ... 133 2e-42
 emb|AZ217409|AZ217409 Sheared DNA-90C8.TR Sheared DNA Trypanosom... 90 3e-42
 emb|AI941197|AI941197 sb85g11.y1 Gm-cl010 Glycine max cDNA clone... 169 7e-41
 emb|AW224136|AW224136 EST300947 tomato fruit red ripe, TAMU Lyco... 141 3e-40
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 35 emb|AU036687|AU036687 Schizosaccharomyces pombe genomic clone ha... 98 3e-38
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 40 emb|AJ130773|LDI130773 Laminaria digitata mRNA for glucose-6-pho... 131 2e-29
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Score E
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60 emb|AW725454|AW725454 GA_Ea0018A14 Gossypium arboreum 7-10 dpa ... 238 8e-81
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- gb|U34860|SCU34860 *Saccharomyces cerevisiae* origin recognition c... 122 2e-33
 dbj|D38172|YSCTEM1P Yeast gene for GTP-binding protein Tem1p, co... 122 2e-33
 emb|AI988573|AI988573 sd04c11.y1 Gm-c1020 Glycine max cDNA clone... 142 3e-33
 emb|Y12314|SPSPG1GEN *S.pombe* spg1 gene. 67 9e-20
 5 emb|AJ001587|SPAJ1587 *Schizosaccharomyces pombe* sid3 gene. 67 9e-20
 emb|AW776339|AW776339 EST335404 *DSIL* *Medicago truncatula* cDNA cl... 67 5e-14
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 10 gb|L08690|YSCGSP1X Yeast GTP-binding protein (GSP1) gene, comple... 32 2e-06
 gb|L08691|YSCGSP2X Yeast GTP-binding protein (GSP2) gene, comple... 32 2e-06
 emb|X71946|SCCNR2A *S.cerevisiae* CNR2 gene. 32 2e-06
 emb|X71945|SCCNR1A *S.cerevisiae* CNR1 gene. 32 2e-06
 dbj|D17748|TETTRAN *Tetrahymena thermophila* mRNA for Ran/TC4, com... 33 3e-06
 15 dbj|D21825|TETPRAN *Tetrahymena pyriformis* mRNA for Ran/TC4, comp... 33 3e-06
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 gb|U17085|TBU17085 *Trypanosoma brucei brucei* RAN/TC4 GTPase homo... 29 0.43
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 40 emb|AW040005|AW040005 EST282496 tomato mixed elicitor, BTI Lycop... 35 0.56
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 45 emb|AV414769|AV414769 AV414769 *Lotus japonicus* young plants (two... 35 0.62
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 emb|Z73961|LJRAC1 *L.japonicus* mRNA for small GTP-binding protein... 35 0.62
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 55 emb|AW694335|AW694335 NF075C06ST1F1049 Developing stem *Medicago* ... 35 0.62
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 60 gb|BE054534|BE054534 GA_Ea0033M19f *Gossypium arboreum* 7-10 dpa ... 35 0.62
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	gb S79308 S79308 Rac13=21.8 kda GTP-binding protein [Gossypium h...	35	0.62
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5	gb BE055015 BE055015 GA__Ea0001G03f Gossypium arboreum 7-10 dpa ...	35	0.62
	emb AW690086 AW690086 NF028B10ST1F1000 Developing stem Medicago ...	35	0.62
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45	Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done		
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	emb A26875 A26875 R.sativus AFP1 gene.	166	7e-43
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	gb U18556 RSU18556 Raphanus sativus antifungal protein 2 preprot...	160	1e-38
	emb X97319 RSEFP3 R.sativus mRNA for antifungal protein 3.	133	8e-37
	gb U59459 BNU59459 Brassica napus antifungal protein mRNA, compl...	135	2e-36
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	emb A27062 A27062 C.benedictus AMP2 sequence.	73 1e-12
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5	emb A27064 A27064 C.ternatea AMP1 sequence.	58 8e-10
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Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters

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 40 (1194 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Score E
 Sequences producing significant alignments: (bits) Value

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments: (bits) Value

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45 emb|Y10098|HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... 300 2e-80
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Database: plantfungal
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20 Database: plantfungal
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25 Score E
Sequences producing significant alignments: (bits) Value

emb|X61488|BNCHITIN B.napus mRNA for chitinase. 453 e-166
30 gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 212 1e-95
gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 211 4e-95
emb|X57187|PVCHITIN P.vulgaris mRNA for chitinase. 135 8e-86
dbj|D45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 136 5e-82
emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 185 5e-81
emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 182 8e-80
35 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 156 4e-79
emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 156 4e-79
dbj|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 119 4e-78
dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 119 7e-78
dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 119 1e-77
40 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase class 4 (p... 103 6e-77
gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 105 1e-75
gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 84 7e-73
gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 140 1e-72
gb|BE034428|BE034428 MH04G02 MH Mesembryanthemum crystallinum cD... 139 3e-72
45 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 133 2e-70
gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 131 1e-69
emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 239 1e-66
gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 130 2e-66
emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 177 5e-66
50 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 167 9e-65
emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 172 2e-64
gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 165 4e-64
gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 111 7e-64
gb|U52847|DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... 162 2e-63
55 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 93 4e-63
gb|U52848|DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 161 1e-62
emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem Medicago ... 144 2e-62
gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 141 1e-59
emb|AW680953|AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S... 139 4e-58
60 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 147 3e-57
emb|AI897217|AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... 177 4e-57

- emb|AI776153|AI776153 EST257241 tomato resistant, Cornell Lycopersicon... 177 5e-56
 emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 141 2e-55
 gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 86 3e-55
 emb|AW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 140 6e-55
 5 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 138 3e-54
 emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 137 4e-54
 emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 98 1e-53
 emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 134 2e-53
 emb|AW924422|AW924422 WS1_69_C06.b1_A002 Water-stressed 1 (WS1) ... 139 4e-53
 10 emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 130 7e-53
 gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 86 8e-53
 emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 116 2e-52
 gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 116 1e-51
 gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 116 1e-51
 15 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 117 9e-51
 emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 124 2e-50
 gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 141 6e-50
 emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 149 1e-49
 emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 165 4e-49
 20 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 120 4e-49
 emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 115 9e-49
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 112 1e-48
 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 112 1e-48
 emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 115 1e-48
 25 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 140 2e-48
 gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 83 3e-48
 gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 112 5e-48
 emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 112 5e-48
 emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 139 9e-48
 30 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 139 9e-48
 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 118 3e-47
 emb|AF061806|AF061806 Elaeagnus umbellata basic chitinase mRNA, ... 118 4e-47
 gb|M94105|ALCCHITIN Allium sativum chitinase mRNA, 3' end. 116 7e-47
 emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 120 2e-46
 35 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 116 3e-46
 emb|AW922596|AW922596 DG1_46_C01.b1_A002 Dark Grown 1 (DG1) Sorg... 79 3e-46
 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 116 3e-46
 gb|BE034267|BE034267 MH02D06 MH Mesembryanthemum crystallinum cD... 74 3e-46
 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 122 4e-46
 40 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 116 4e-46
 emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 112 7e-46
 emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 121 9e-46
 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 109 1e-45
 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 112 2e-45
 45 emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 135 2e-45
 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 116 2e-45
 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 109 2e-45
 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 116 3e-45
 gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 109 6e-45
 50 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 108 8e-45
 emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 147 2e-44
 gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 141 4e-44
 emb|AA739579|AA739579 344 PtIFG2 Pinus taeda cDNA clone 8562M 3'... 107 1e-43
 emb|AW560048|AW560048 EST315096 DSIR Medicago truncatula cDNA cl... 116 1e-43
 55 emb|A23396|A23396 B.vulgaris gene for chitinase 76. 105 3e-43
 emb|AW267781|AW267781 EST305909 DSIR Medicago truncatula cDNA cl... 115 4e-43
 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 108 8e-43
 emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 125 1e-42
 emb|AI352718|AI352718 MB46-29 PZ204.BNlib Brassica napus cDNA cl... 144 4e-42
 60 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 80 5e-42
 emb|AI729668|AI729668 BNLGHi13889 Six-day Cotton fiber Gossypium... 111 2e-41

emb|AF061805|AF061805 Elaeagnus umbellata acidic chitinase mRNA,... 116 3e-41
 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 117 4e-41
 emb|Z15138|LECHI14 L.esculentum mRNA for chitinase (partial). 114 1e-40
 gb|U30465|LEU30465 Lycopersicon esculentum class II chitinase (C... 114 2e-40
 5 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 100 1e-39

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 (1116 letters)

15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

20 Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
25	emb AW671006 AW671006 LG1_278_H12.b1_A002 Light Grown 1 (LG1) So...	81	6e-28
	emb AA520813 AA520813 TgESTzz64d07.r1 TgME49 invivo Bradyzoite c...	38	0.16
	gb U43491 SCU43491 Saccharomyces cerevisiae cosmid clone pEOA156...	37	0.31
	emb Z74916 SCYOR008C S.cerevisiae chromosome XV reading frame OR...	37	0.31
	gb U39481 SCU39481 Saccharomyces cerevisiae Slglp (SLG1) gene, c...	37	0.31
30	emb AA680906 AA680906 LmFrAm0494 Leishmania major Amastigote ful...	33	1.0
	emb AF193903 AF193903 Cafeteria roenbergensis mitochondrial DNA,...	35	1.1
	emb AF229795 AF229795 Vigna radiata beta galactosidase mRNA, com...	35	1.5
	emb AW683786 AW683786 NF001A06NR1F1038 Nodulated root Medicago t...	35	1.5
	emb AC005802 AC005802 Leishmania major chromosome 3 clone L6202 ...	34	2.1
	emb AC005893 AC005893 Leishmania major chromosome 3 clone L822 s...	34	2.1
35	emb AA520166 AA520166 TgESTzz39b08.s1 TgME49 invivo Bradyzoite c...	34	2.9
	emb AW618793 AW618793 EST320779 L. pennellii trichome, Cornell U...	34	2.9
	emb AW306460 AW306460 se51a02.y1 Gm-c1017 Glycine max cDNA clone...	34	2.9
	emb AQ502036 AQ502036 V10E12 mTn-3xHA/lacZ Insertion Library Sac...	33	3.9
40	gb U87148 HVU87148 Hordeum vulgare nucellin mRNA, complete cds.	33	3.9
	emb AF017430 AF017430 Hordeum vulgare EEA1 mRNA, complete cds.	33	3.9
	emb AQ500344 AQ500344 V41B12 mTn-3xHA/lacZ Insertion Library Sac...	33	3.9
	emb Z71686 SCYNR071C S.cerevisiae chromosome XIV reading frame O...	33	3.9
	emb AQ501720 AQ501720 V15F6 mTn-3xHA/lacZ Insertion Library Sacc...	33	3.9
	emb AQ872965 AQ872965 V56D9 mTn-3xHA/lacZ Insertion Library, str...	33	3.9
45	emb AW126050 AW126050 N100246e rootphos(-) Medicago truncatula c...	33	5.4
	emb AW127669 AW127669 M110413 DSLC Medicago truncatula cDNA clon...	33	5.4
	emb AW126177 AW126177 N100022e rootphos(-) Medicago truncatula c...	33	5.4
	emb AW126137 AW126137 N100334e rootphos(-) Medicago truncatula c...	33	5.4
	emb AW509583 AW509583 ga61f07.y1 Moss EST library PPU Physcomitr...	33	5.4
50	emb AQ503147 AQ503147 V44D10 mTn-3xHA/lacZ Insertion Library Sac...	33	5.4
	emb AQ501343 AQ501343 V23B5 mTn-3xHA/lacZ Insertion Library Sacc...	33	5.4
	emb Z98559 SPAC23C11 S.pombe chromosome I cosmid c23C11.	33	5.4
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	emb AW925272 AW925272 HVSMEg0001G19 Hordeum vulgare pre-anthesis...	33	5.4
55	emb AA783066 AA783066 alh02c9.r1 Aspergillus nidulans 24hr asexu...	26	5.7
	emb AC013353 AC013353 Trypanosoma brucei chromosome VI clone RPC...	32	7.4
	emb AV409938 AV409938 AV409938 Lotus japonicus young plants (two...	32	7.4
	emb AW780906 AW780906 sl86c03.y1 Gm-c1037 Glycine max cDNA clone...	32	7.4
	emb AI443278 AI443278 sa46f11.y1 Gm-c1004 Glycine max cDNA clone...	32	7.4
60	emb AW156670 AW156670 se29c01.y1 Gm-c1015 Glycine max cDNA clone...	32	7.4
	emb AW277786 AW277786 sf86e12.y1 Gm-c1019 Glycine max cDNA clone...	32	7.4

emb|AE001432|AE001432 Plasmodium falciparum chromosome 2, sectio... 32 7.4
emb|AW734710|AW734710 sk98e12.y1 Gm-c1035 Glycine max cDNA clone... 32 7.4
emb|AW099005|AW099005 sd33a02.y1 Gm-c1012 Glycine max cDNA clone... 32 7.4
emb|AW704821|AW704821 sk40a01.y1 Gm-c1019 Glycine max cDNA clone... 32 7.4
5 emb|AW277436|AW277436 sf82a10.y1 Gm-c1019 Glycine max cDNA clone... 32 7.4
emb|AW459299|AW459299 sh23c01.y1 Gm-c1016 Glycine max cDNA clone... 32 7.4
emb|AV407743|AV407743 AV407743 Lotus japonicus young plants (two... 32 7.4
emb|AW757240|AW757240 sl30h11.y1 Gm-c1027 Glycine max cDNA clone... 32 7.4

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emb|caal7552.1| (al021961) phosphoglycerate dehydrogenase - like
protein [arabidopsis thaliana] /blast_score 0 /ec_number /family
dehydrogenase /chip nova /gb_link
15 http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi
http://www.ncgr.org/cgi-bin/ff?al021961
(1812 letters)

20 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

25 Score E
Sequences producing significant alignments: (bits) Value

emb|AW930291|AW930291 EST340748 tomato fruit mature green, TAMU ... 415 e-115
emb|AW625643|AW625643 EST319550 tomato radicle, 5 d post-imbibit... 398 e-110
30 emb|AW666282|AW666282 sk34f11.y1 Gm-c1028 Glycine max cDNA clone... 393 e-108
emb|AW650696|AW650696 EST329150 tomato germinating seedlings, TA... 226 e-103
emb|AW691093|AW691093 NF041B09ST1F1000 Developing stem Medicago ... 355 e-102
emb|AW926942|AW926942 HVSMEg0009B01 Hordeum vulgare pre-anthesis... 339 e-102
gb|BE055044|BE055044 GA_Ea0031H08f Gossypium arboreum 7-10 dpa ... 341 2e-99
35 emb|AW696933|AW696933 NF112E03ST1F1021 Developing stem Medicago ... 357 4e-98
emb|AW731385|AW731385 GA_Ea0030K22 Gossypium arboreum 7-10 dpa ... 344 2e-95
emb|AW688234|AW688234 NF005A05ST1F1000 Developing stem Medicago ... 348 6e-95
gb|BE036418|BE036418 MO24D12 MO Mesembryanthemum crystallinum cD... 279 1e-94
gb|BE052354|BE052354 GA_Ea0034P16f Gossypium arboreum 7-10 dpa ... 346 3e-94
40 emb|AW423801|AW423801 sh52b02.y1 Gm-c1017 Glycine max cDNA clone... 339 4e-92
emb|AI813214|AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta... 336 4e-92
emb|AW692700|AW692700 NF054C07ST1F1000 Developing stem Medicago ... 304 7e-87
emb|AW737130|AW737130 EST338557 tomato flower buds, anthesis, Co... 318 1e-85
emb|AW727978|AW727978 GA_Ea0029C18 Gossypium arboreum 7-10 dpa ... 285 3e-80
45 gb|BE020170|BE020170 sm39e05.y1 Gm-c1028 Glycine max cDNA clone ... 291 1e-77
emb|AW944677|AW944677 00152 leafy spurge Lambda HybriZAP 2.1 two... 291 1e-77
emb|AW926887|AW926887 HVSMEg0008N09 Hordeum vulgare pre-anthesis... 280 3e-74
emb|AW689358|AW689358 NF018C09ST1F1000 Developing stem Medicago ... 253 3e-73
emb|AW755716|AW755716 sl08b12.y1 Gm-c1036 Glycine max cDNA clone... 267 2e-70
50 emb|AW625020|AW625020 EST313849 tomato radicle, 5 d post-imbibit... 253 4e-66
gb|BE060782|BE060782 HVSMEg0013F14f Hordeum vulgare pre-anthesis... 234 1e-60
emb|AW687344|AW687344 NF008F03RT1F1029 Developing root Medicago ... 215 1e-54
emb|AV395160|AV395160 AV395160 Chlamydomonas reinhardtii C9 Chla... 208 1e-52
emb|AW907004|AW907004 EST343231 potato stolon, Cornell Universit... 205 7e-52
55 emb|AW398821|AW398821 EST309321 L. pennellii trichome, Cornell U... 201 2e-50
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emb|AW923236|AW923236 DG1_50_A11.g1_A002 Dark Grown 1 (DG1) Sorg... 191 1e-47
emb|AW428657|AW428657 Ljirnp22-731-a5 Ljirnp Lambda HybriZap ... 185 8e-46
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60 emb|AW736943|AW736943 NXNV_081_H10_F Nsf Xylem Normal wood Verti... 180 3e-44
emb|AW697347|AW697347 NF115F08ST1F1074 Developing stem Medicago ... 175 9e-43

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10	emb AL031180 SPUNK4 S.pombe chromosome I cosmid c2E11.	103	1e-36
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	emb AW317181 AW317181 sf38d05.x1 Gm-cl028 Glycine max cDNA clone...	148	1e-34
	dbj E12500 E12500 Nucleotide sequence of eta gene of cephalospor...	89	2e-34
	emb Z97052 SPCC4G3 S.pombe chromosome III cosmid c4G3.	83	2e-33
15	emb AA840711 AA840711 CAN22 Anther cDNA library of Hot pepper Ca...	101	5e-33
	emb AL157811 SPAC186 S.pombe chromosome I cosmid c186.	98	1e-32
	emb AJ273311 AJ273311 AJ273311 Metarhizium anisopliae ARSEF 2575...	91	1e-32
	gb BE058285 BE058285 sn14b01.y1 Gm-cl016 Glycine max cDNA clone ...	138	1e-31
	gb BE060772 BE060772 HVSMEg0013F04f Hordeum vulgare pre-anthesis...	95	2e-31
20	gb U18839 SCE9747 Saccharomyces cerevisiae chromosome V cosmids ...	84	6e-31
	emb AC005761 AC005761 Leishmania major chromosome 3 clone L952 s...	78	7e-31
	emb AW693956 AW693956 NF071B03ST1F1027 Developing stem Medicago ...	89	5e-30
	emb AI165568 AI165568 A086P59U Hybrid aspen plasmid library Popu...	132	5e-30
	emb Z37997 SC9877 S.cerevisiae chromosome IX cosmid 9877.	84	5e-30
25	emb AW599036 AW599036 gb01c10.y1 Moss EST library PPN Physcomitr...	116	5e-25
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	emb AL033389 SPBC1773 S.pombe chromosome II cosmid c1773.	105	3e-22
	emb Z71550 SCYNL274C S.cerevisiae chromosome XIV reading frame O...	89	8e-22
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35	emb AW689996 AW689996 NF026G01ST1F1000 Developing stem Medicago ...	86	7e-16
	emb AQ874261 AQ874261 V105E9 mTn-3xHA/lacZ Insertion Library, st...	84	2e-15
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50	dbj D88272 D88272 Hordeum vulgare mRNA for formate dehydrogenase...	75	2e-12
	emb AI488120 AI488120 EST246442 tomato ovary, TAMU Lycopersicon ...	74	3e-12
	emb AW780701 AW780701 sl75g02.y1 Gm-cl027 Glycine max cDNA clone...	55	3e-12
	emb AW266848 AW266848 L48-192T3 Ice plant Lambda Uni-Zap XR expr...	74	4e-12
55	emb AW693443 AW693443 NF065D03ST1F1000 Developing stem Medicago ...	66	4e-12
	dbj D49433 D49433 Pumpkin colne HPR2 hydroxypyruvate reductases ...	72	1e-11
	dbj D49432 D49432 Pumpkin clone HPR1 hydroxypyruvate reductases ...	72	1e-11
	emb AW278707 AW278707 sf96b06.y1 Gm-cl019 Glycine max cDNA clone...	72	1e-11
	gb U01067 PUMHPR Cucurbita pepo Halloween NADH-dependent hydroxy...	72	2e-11
	emb AI490396 AI490396 EST248734 tomato ovary, TAMU Lycopersicon ...	71	3e-11
60	emb X14609 CSNDHR Cucumis sativus mRNA for NAPH-dependent hydrox...	70	5e-11
	emb AJ001429 RGDMANDER Rhodotorula graminis mRNA for D-mandelate...	70	6e-11

emb|AW040337|AW040337 EST283201 tomato mixed elicitor, BTI Lycop... 70 6e-11
 emb|AW037837|AW037837 EST279466 tomato mixed elicitor, BTI Lycop... 70 6e-11
 emb|AL033497|CAC49C10 C.albicans cosmid Ca49C10. 70 6e-11
 emb|AI897727|AI897727 EST267170 tomato ovary, TAMU Lycopersicon ... 69 9e-11
 5 emb|AI898454|AI898454 EST267897 tomato ovary, TAMU Lycopersicon ... 69 9e-11

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 10 emb|caa23036.1| (al035394) putative na+/h+-exchanging protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
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 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035394| /ncgi
 http://www.ncgr.org/cgi-bin/ff?al035394
 (2463 letters)

15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

20 Searching.....done

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				(bits) Value
	Sequences producing significant alignments:			
25	emb AW736388 AW736388 EST332307 KV3 Medicago truncatula cDNA clo...	243	5e-63	
	emb AW622441 AW622441 EST313229 tomato root during/after fruit's...	204	2e-51	
	emb AL157994 SPAC105 S.pombe chromosome I cosmid c105.	192	1e-47	
	emb AQ841817 AQ841817 T134068 Soybean RFLP probe Glycine max gen...	186	8e-46	
	emb X77087 SJ100567 S.cerevisiae (S288C) J0909, J0911, J0914 and...	150	5e-35	
30	emb Z49369 SCYJL094C S.cerevisiae chromosome X reading frame ORF...	150	5e-35	
	emb AW774205 AW774205 EST333356 KV3 Medicago truncatula cDNA clo...	120	8e-28	
	emb AW559356 AW559356 EST314404 DSIR Medicago truncatula cDNA cl...	104	2e-23	
	emb AQ361449 AQ361449 mgxb0004G06r CUGI Rice Blast BAC Library P...	59	4e-16	
	emb AT000678 AT000678 AT000678 Brassica rapa guard cell Brassica...	79	2e-13	
35	emb AV409975 AV409975 AV409975 Lotus japonicus young plants (two...	59	5e-11	
	emb AT000552 AT000552 AT000552 Brassica rapa guard cell Brassica...	57	6e-07	
	emb AW980088 AW980088 EST341613 tomato root deficiency, Cornell ...	45	8e-07	
	emb AW307241 AW307241 s54e09.y1 Gm-c1009 Glycine max cDNA clone...	48	1e-06	
	emb AW334422 AW334422 S34F3 AGS-1 Pneumocystis carinii f. sp. ca...	52	2e-05	
40	emb AQ842018 AQ842018 T134304 Soybean RFLP probe Glycine max gen...	47	1e-04	
	emb AV410314 AV410314 AV410314 Lotus japonicus young plants (two...	40	0.010	
	emb AW163886 AW163886 Ljimpest17-312-a12 Ljirnp Lambda HybriZap...	34	0.019	
	emb AQ849208 AQ849208 LMAJFV1_lm43f12.y1 Leishmania major FV1 ra...	41	0.042	
	emb AW690188 AW690188 NF029E07ST1F1000 Developing stem Medicago ...	35	0.044	
45	emb Y15086 CFHEPABC Cylindrotheca fusiformis hepA, hepB, hepC ge...	39	0.21	
	emb AL112906 CNS01AGI Botrytis cinerea strain T4 cDNA library un...	38	0.28	
	emb AW725682 AW725682 GA__Ea0019E05 Gossypium arboreum 7-10 dpa ...	37	0.54	
	emb AW727060 AW727060 GA__Ea0011B07 Gossypium arboreum 7-10 dpa ...	36	1.0	
	emb AL034559 PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq...	36	1.4	
	emb AF127331 AF127331 Euplotes crassus histone H1-1 (H1-1) gene,...	36	1.4	
50	emb AW729298 AW729298 GA__Ea0024K04 Gossypium arboreum 7-10 dpa ...	28	1.6	
	emb AL139794 LMFP1105 Leishmania major Friedlin chromosome 4 PAC...	35	1.9	
	emb AB028188 AB028188 Penicillium digitatum DNA fragment contain...	35	2.6	
	emb Z48093 GVEITS133 G.verna DNA for internal transcribed spacer...	28	3.2	
	emb AL353012 SPBC1711 S.pombe chromosome II cosmid c1711.	35	3.6	
55	gb BE036059 BE036059 MO19C02 MO Mesembryanthemum crystallinum cD...	35	3.6	
	gb BE036176 BE036176 MO20A07 MO Mesembryanthemum crystallinum cD...	35	3.6	
	emb AW693672 AW693672 NF067B05ST1F1044 Developing stem Medicago ...	35	3.6	
	emb AJ274013 AJ274013 AJ274013 Metarhizium anisopliae ARSEF 2575...	35	3.6	
	gb U80041 AFU80041 Avena fatua Af10-protein mRNA, complete cds.	34	5.0	
60	emb AI612607 AI612607 TENG0370 T. Cruzi epimastigote normalised ...	34	5.0	
	emb X04693 SOPCG Spinach gene for plastocyanin.	34	5.0	

emb|AW010989|AW010989 ST15D02 Pine TriplEx shoot tip library Pin... 34 5.0
 emb|AB013876|AB013876 Chlorella vulgaris gene, a unique region o... 34 5.0
 emb|AZ215593|AZ215593 Sheared DNA-74E9.TR Sheared DNA Trypanosom... 34 6.8
 emb|AQ845769|AQ845769 LMAJFV1_lm25g04.x1 Leishmania major FV1 ra... 34 6.8
 5 gb|M33825|TRBMVAT5A T.brucei MVAT5-like variant surface glycopro... 34 6.8
 emb|AC005802|AC005802 Leishmania major chromosome 3 clone L6202 ... 34 6.8
 emb|AQ640120|AQ640120 927P1-18A3.TP 927P1 Trypanosoma brucei gen... 34 6.8
 emb|AW299087|AW299087 EST305761 KV2 Medicago truncatula cDNA clo... 34 6.8
 emb|AQ163144|AQ163144 mgxb0023A11r CUGI Rice Blast BAC Library P... 34 6.8
 10 emb|AF183445|CLITSYDK1 Codonopsis lanceolata internal transcribe... 34 6.8
 emb|AC005893|AC005893 Leishmania major chromosome 3 clone L822 s... 34 6.8
 gb|L06030|TRBVSGH Trypanosoma brucei MVAT5-RX2 variant surface g... 34 6.8
 gb|L04971|TRBVSGM Trypanosoma brucei variant surface glycoprotei... 34 6.8
 emb|AW564995|AW564995 LG1_313_B04.b1_A002 Light Grown 1 (LG1) So... 34 6.8
 15 emb|AI050199|AI050199 TENU1447 T. cruzi epimastigote normalized ... 34 6.8
 emb|AW597619|AW597619 sj96f04.y1 Gm-cl023 Glycine max cDNA clone... 34 6.8
 emb|AF224499|AF224499 Triticum aestivum KNOTTED-1-like homeobox ... 34 6.8
 gb|N60227|N60227 TgESTzy10g08.r1 TgRH Tachyzoite cDNA Toxoplasma... 33 9.4
 emb|X68032|MTENOD12 M.truncatula ENOD12 gene. 33 9.4
 20 emb|AW126974|AW126974 gal6h04.y1 Moss EST library PPU Physcomitr... 33 9.4
 emb|AA274329|AA274329 TgESTzz24g03.s1 TgME49 invivo Bradyzoite c... 33 9.4
 gb|BE054344|BE054344 GA_Ea0035E03f Gossypium arboreum 7-10 dpa ... 33 9.4
 emb|AA009393|AA009393 TgESTzz08e11.r1 TgME49 Tachyzoite cDNA Tox... 33 9.4
 emb|Y16262|DCY16262 Daucus carota mRNA for neutral invertase. 33 9.4
 25 gb|BE035627|BE035627 MO12F02 MO Mesembryanthemum crystallinum cD... 33 9.4
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30 Query= AC002387.185_at 13631_at /id_source genbank /description
 gb|aab82634.1| (ac002387) putative transketolase precursor
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&cuid=gb|ac002387| /ncgi
 http://www.ncgr.org/cgi-bin/ff?ac002387
 35 (2371 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

45 emb|Z50099|STTKETMR S.tuberosum mRNA for transketolase. 1372 0.0
 gb|L76554|SPITRAN Spinacia oleracea transketolase mRNA, chloropl... 1350 0.0
 emb|Y15781|CAY15781 Capsicum annuum mRNA for plastid transketola... 1344 0.0
 emb|A52295|A52295 Sequence 1 from Patent EP0723017. 1283 0.0
 emb|Z46648|CPTKT7 C.plantagineum tkt7 gene for transketolase. 1063 0.0
 50 emb|Z46647|CPTKT10 C.plantagineum tkt10 gene for transketolase. 1038 0.0
 emb|Z46646|CPTKT3 C.plantagineum tkt3 gene for transketolase. 1014 0.0
 emb|AJ249787|CPA249787 Cyanophora paradoxa mRNA for putative tra... 557 0.0
 emb|AL033501|CAC41C10 C.albicans cosmid Ca41C10. 253 e-175
 emb|AC007872|AC007872 The sequence of an Aspergillus parasiticus... 167 e-158
 55 gb|H55032|H55032 HHU58a Sorghum bicolor cv. TX430 Sorghum bicolo... 233 e-151
 emb|AC005299|AC005299 emericella nidulans chromosome viii cosmid... 166 e-147
 emb|AC004395|AC004395 Emericella nidulans Chromosome VIII Cosmid... 166 e-147
 emb|AW443928|AW443928 EST308858 tomato mixed elicitor, BTI Lycop... 468 e-131
 emb|AW667519|AW667519 GA_Ea0009J09 Gossypium arboreum 7-10 dpa ... 463 e-129
 60 emb|AI778813|AI778813 EST259692 tomato susceptible, Cornell Lycop... 453 e-126
 emb|AW776720|AW776720 EST335785 DSIL Medicago truncatula cDNA cl... 450 e-125

- emb|AW695194|AW695194 NF092E10ST1F1082 Developing stem Medicago ... 370 e-124
emb|AI774685|AI774685 EST255785 tomato resistant, Cornell Lycopersicon ... 444 e-123
emb|AW618386|AW618386 EST320372 *L. pennellii* trichome, Cornell U... 434 e-120
gb|BE052708|BE052708 GA_Ea0031N21f *Gossypium arboreum* 7-10 dpa ... 431 e-119
5 emb|AW737315|AW737315 EST338838 tomato flower buds, anthesis, Co... 409 e-113
emb|AW694020|AW694020 NF071G12ST1F1099 Developing stem Medicago ... 406 e-112
gb|BE060293|BE060293 HVSMEg0011O04f *Hordeum vulgare* pre-anthesis... 405 e-112
emb|AW649769|AW649769 EST328223 tomato germinating seedlings, TA... 377 e-111
emb|AW234850|AW234850 sf19h07.y1 Gm-c1028 Glycine max cDNA clone... 399 e-110
10 emb|AW760220|AW760220 sl59e08.y1 Gm-c1027 Glycine max cDNA clone... 388 e-106
emb|AW929526|AW929526 EST338314 tomato flower buds 8 mm to pre-a... 386 e-106
emb|AW596420|AW596420 sj12c01.y1 Gm-c1032 Glycine max cDNA clone... 380 e-104
emb|AI730390|AI730390 BNLGHi6849 Six-day Cotton fiber *Gossypium* ... 302 e-102
emb|AI778812|AI778812 EST259691 tomato susceptible, Cornell Lyco... 372 e-102
15 emb|AW720123|AW720123 LjNEST14e4r *Lotus japonicus* nodule library... 369 e-101
emb|AW697121|AW697121 NF115C09ST1F1069 Developing stem Medicago ... 334 e-101
emb|AW726320|AW726320 GA_Ea0021F03 *Gossypium arboreum* 7-10 dpa ... 354 1e-99
emb|AQ841855|AQ841855 T134114 Soybean RFLP probe Glycine max gen... 358 4e-98
emb|AW564025|AW564025 LG1_281_F10.b1_A002 Light Grown 1 (LG1) So... 359 4e-98
20 emb|AW979915|AW979915 EST341564 tomato root deficiency, Cornell ... 349 6e-95
emb|AI781665|AI781665 EST262544 tomato susceptible, Cornell Lyco... 348 1e-94
emb|Z26486|PSTKTG *P. stipitis* TKT gene for transketolase. 261 8e-93
emb|AW039152|AW039152 EST281387 tomato mixed elicitor, BTI Lycopersicon ... 339 7e-92
gb|BE053034|BE053034 GA_Ea0031O21f *Gossypium arboreum* 7-10 dpa ... 338 9e-92
25 emb|AW691000|AW691000 NF040C09ST1F1000 Developing stem Medicago ... 338 9e-92
emb|AW290149|AW290149 NXNV012F12F Nsf Xylem Normal wood Vertical... 337 2e-91
emb|AW203636|AW203636 sf36e03.y1 Gm-c1028 Glycine max cDNA clone... 332 6e-90
emb|AI966148|AI966148 sc34c04.y1 Gm-c1014 Glycine max cDNA clone... 330 4e-89
emb|Z71255|SCCHR XVI *S. cerevisiae* chromosome XVI 165536 bp sequen... 225 2e-88
30 gb|U51033|YSCP9513 *Saccharomyces cerevisiae* chromosome XVI cosmi... 225 2e-88
emb|Z49219|SC9499X *S. cerevisiae* chromosome XVI cosmid 9499. 225 2e-88
emb|X73224|SCTKL1 *S. cerevisiae* TKL1 gene for transketolase. 225 2e-88
emb|AL033385|SPBC2G5 *S. pombe* chromosome II cosmid c2G5. 198 2e-87
emb|AV388967|AV388967 AV388967 *Chlamydomonas reinhardtii* C9 Chla... 322 8e-87
35 emb|AV391940|AV391940 AV391940 *Chlamydomonas reinhardtii* C9 Chla... 321 1e-86
emb|AW587453|AW587453 IPPGHZ0039 Cotton fiber and embryo Lambda ... 276 3e-86
gb|U65983|KLU65983 *Kluyveromyces lactis* transketolase (TKL1) gen... 211 1e-85
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40 emb|AA660853|AA660853 00748 MtRHE *Medicago truncatula* cDNA 5' si... 282 1e-83
emb|AV393839|AV393839 AV393839 *Chlamydomonas reinhardtii* C9 Chla... 230 1e-83
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emb|AW776795|AW776795 EST335860 DSIL *Medicago truncatula* cDNA cl... 307 2e-82
45 emb|AW694632|AW694632 NF078D05ST1F1045 Developing stem Medicago ... 285 4e-82
emb|AV391577|AV391577 AV391577 *Chlamydomonas reinhardtii* C9 Chla... 304 1e-81
emb|AV388182|AV388182 AV388182 *Chlamydomonas reinhardtii* C9 Chla... 304 2e-81
emb|AW688641|AW688641 NF009H10ST1F1000 Developing stem Medicago ... 282 8e-80
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50 emb|AW695046|AW695046 NF082H06ST1F1059 Developing stem Medicago ... 297 3e-79
emb|X78993|SCRACII *S. cerevisiae* genomic DNA 70kb region of the r... 200 3e-79
emb|X73532|SCTKL2 *S. cerevisiae* gene for transketolase. 200 3e-79
emb|Z35985|SCYBR116C *S. cerevisiae* chromosome II reading frame OR... 200 3e-79
emb|AW564318|AW564318 LG1_290_F06.b1_A002 Light Grown 1 (LG1) So... 293 4e-78
55 emb|AW201472|AW201472 sf03e09.y1 Gm-c1027 Glycine max cDNA clone... 292 6e-78
emb|AB025004|AB025004 *Cicer arietinum* mRNA for transketolase, pa... 292 8e-78
emb|AW746874|AW746874 WS1_56_C06.b1_A002 Water-stressed 1 (WS1) ... 291 2e-77
emb|AW776336|AW776336 EST335401 DSIL *Medicago truncatula* cDNA cl... 290 4e-77
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60 emb|AV395290|AV395290 AV395290 *Chlamydomonas reinhardtii* C9 Chla... 288 1e-76
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 dbj|D89172|D89172 Schizosaccharomyces pombe mRNA, partial cds, c... 171 3e-73
 emb|AV394221|AV394221 AV394221 Chlamydomonas reinhardtii C9 Chla... 275 4e-73
 emb|AV387871|AV387871 AV387871 Chlamydomonas reinhardtii C9 Chla... 275 1e-72
 5 emb|AI162975|AI162975 A028P14U Hybrid aspen plasmid library Popu... 273 1e-72
 emb|AJ234429|HVU234429 Hordeum vulgare partial mRNA; clone cMWG0... 271 1e-71
 emb|AW398784|AW398784 EST309284 L. pennellii trichome, Cornell U... 271 2e-71
 gb|BE056580|BE056580 894010C09.y1 C. reinhardtii CC-1690, normal... 267 2e-70
 emb|AW694944|AW694944 NF081G03ST1F1023 Developing stem Medicago ... 258 4e-70
 10 emb|AW041543|AW041543 EST284407 tomato mixed elicitor, BTI Lycop... 265 8e-70
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 emb|AQ842006|AQ842006 T134292 Soybean RFLP probe Glycine max gen... 263 4e-69
 15 emb|AI726103|AI726103 BNLGHi5028 Six-day Cotton fiber Gossypium ... 260 3e-68
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 emb|AA819992|AA819992 L0-171M13R Ice plant Lambda Uni-Zap XR exp... 258 1e-67
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 emb|AI563214|AI563214 EST00338 watermelon lambda zap library Cit... 249 1e-65
 20 emb|AF086822|AF086822 Candida boidinii dihydroxyacetone synthase... 163 7e-65
 emb|AW696579|AW696579 NF106E10ST1F1082 Developing stem Medicago ... 249 7e-65
 gb|M63302|YSCTRANSK S.cerevisiae transketolase gene, complete cds. 168 5e-64

25 Query= AL022347.46_at 13659_at /id_source genbank /description
 emb|caa18462.1| (al022347) serine/threonine kinase-like protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022347| /ncgi
 30 http://www.ncgr.org/cgi-bin/ff?al022347
 (2037 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

35 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

40 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 385 e-125
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 343 e-111
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 348 e-109
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 346 e-109
 45 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 347 e-109
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 333 e-108
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 342 e-107
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 328 e-106
 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 334 e-105
 50 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 329 e-104
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 205 e-104
 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 326 e-103
 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 330 e-103
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 336 e-102
 55 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 325 e-101
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 emb|Y12530|BOARLKGEN B.oleraceae gene encoding serine/threonine ... 131 1e-95
 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 282 3e-94
 dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 281 3e-93
 60 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 276 4e-93
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- emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 275 9e-91
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5 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 127 2e-88
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emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 313 4e-84
10 emb|X79432|BOSRK3 B.oleracea SRK3 gene. 118 6e-84
emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 112 8e-84
emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 113 7e-83
emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 113 1e-82
emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 122 9e-82
15 gb|BE057261|BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ... 296 4e-79
emb|AW831390|AW831390 sm22a06.y1 Gm-c1028 Glycine max cDNA clone... 216 1e-75
emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 126 2e-75
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20 emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 221 3e-72
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dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 125 8e-71
emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 268 1e-70
emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 188 7e-68
25 emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 242 2e-66
emb|AI896155|AI896155 EST265598 tomato callus, TAMU Lycopersicon... 172 3e-65
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30 emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 166 1e-61
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45 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 109 1e-53
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50 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 136 1e-51
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55 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 135 2e-50
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60 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 192 1e-47
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 15 gb|U59318|LEU59318 Lycopersicon esculentum serine/threonine prot... 105 1e-45
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 25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005662|/ncgi)
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 30 Database: plantfungal
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 50 emb|AI898538|AI898538 EST267981 tomato ovary, TAMU Lycopersicon ... 303 1e-81
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 55 emb|AW029697|AW029697 EST272952 tomato callus, TAMU Lycopersicon... 299 2e-80
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25	emb AI485781 AI485781 EST244102 tomato ovary, TAMU Lycopersicon ...	240	1e-62
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	emb AI485480 AI485480 EST243801 tomato ovary, TAMU Lycopersicon ...	221	5e-57
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30	emb AI771831 AI771831 EST252931 tomato ovary, TAMU Lycopersicon ...	219	3e-56
	emb AI488694 AI488694 EST247033 tomato ovary, TAMU Lycopersicon ...	216	2e-55
	emb AI897044 AI897044 EST266487 tomato ovary, TAMU Lycopersicon ...	216	2e-55
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35	gb BE036025 BE036025 MO18F06 MO Mesembryanthemum crystallinum cD...	197	1e-49
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	emb AA660966 AA660966 00863 MtrHE Medicago truncatula cDNA 5' si...	193	2e-48
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	emb AW687876 AW687876 NF014D11RT1F1093 Developing root Medicago ...	179	2e-44
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	emb AI771730 AI771730 EST252830 tomato ovary, TAMU Lycopersicon ...	171	5e-42
45	emb AI895638 AI895638 EST265081 tomato callus, TAMU Lycopersicon...	164	9e-40
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	emb AW981333 AW981333 EST392486 DSIL Medicago truncatula cDNA cl...	156	3e-37
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50	emb AW563884 AW563884 LG1_272_D05.b1_A002 Light Grown 1 (LG1) So...	136	3e-31
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55	emb AI725304 AI725304 1170 PtiFG2 Pinus taeda cDNA clone 9256r, ...	78	2e-18
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 10 emb|AW443870|AW443870 EST308800 tomato mixed elicitor, BTI Lycop... 41 0.011
 emb|AW678240|AW678240 WS1_14_G12.b1_A002 Water-stressed 1 (WS1) ... 37 0.26
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 gb|U10549|ANU10549 Aspergillus niger protein kinase C (pkcA) gen... 35 0.94
 gb|U74447|ZAU74447 Zinnia angustifolia internal transcribed spac... 33 0.95
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 (159 letters)

25 Database: plantfungal
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	emb AW661015 AW661015 832009D11.y1 C. reinhardtii CC-125 nutrien...	23	2.7
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	emb AL354533 LMFL6294 Leishmania major Friedlin chromosome 21 co...	26	4.1
	gb N98018 N98018 2045C3 czapPFDd2.1, Debopam Chakrabarti Plasmod...	26	4.1
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50	emb AW650822 AW650822 EST329276 tomato germinating seedlings, TA...	26	4.1
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55	emb AL136536 SPBC1703 S.pombe chromosome II cosmid c1703.	26	4.1
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50	emb AJ002236 LPJ002236 Lycopersicon pimpinellifolium Cf-9 resist...	103	2e-57
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	emb A57130 A57130 Sequence 1 from Patent WO9531564.	122	4e-57
	gb U42445 U42445 Lycopersicon pimpinellifolium leucine rich repe...	122	4e-57
	emb A57133 A57133 Sequence 4 from Patent WO9531564.	122	4e-57
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	emb A67432 A67432 Sequence 5 from Patent WO9743429.	109	1e-52
	emb AF053996 AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr...	101	5e-49
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60	emb A67434 A67434 Sequence 7 from Patent WO9743429.	127	7e-49
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Database: plantfungal
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 35 gb|U22525|KLU22525 Kluyveromyces lactis high affinity glucose tr... 109 3e-36
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 45 emb|AI780094|AI780094 EST260973 tomato susceptible, Cornell Lycopersicon... 139 7e-35
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 15 emb|AI778757|AI778757 EST259636 tomato susceptible, Cornell Lyco... 89 1e-19
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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| emb X70981 SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase. | 127 | 6e-99 |
| emb Y09423 NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... | 136 | 8e-98 |
| emb X71654 SMCYP71B3 S.melongena CYP71A2 mRNA for hydroxylase. | 124 | 9e-95 |
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| 40 emb Y10489 GMC450CP1 G.max mRNA for putative cytochrome P450, cl... | 90 | 1e-84 |
| emb X70982 SMCYPEG3 S.melongena CYP71A3 mRNA for P450 hydroxylase. | 126 | 3e-74 |
| emb Y09424 NRCYP71A6 N.racemosa mRNA for cytochrome P450, CYP71A... | 154 | 3e-65 |
| dbj E13663 E13663 cDNA encoding cytochrome P450 which is induced... | 71 | 9e-63 |
| dbj D83968 SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... | 71 | 9e-63 |
| 45 emb AF022157 AF022157 Glycine max cytochrome P450 monooxygenase ... | 126 | 3e-61 |
| emb AW053855 AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... | 103 | 1e-53 |
| emb Y09920 HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... | 94 | 1e-50 |
| emb Y10098 HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... | 94 | 1e-50 |
| emb AF022459 AF022459 Glycine max cytochrome P450 monooxygenase ... | 105 | 4e-50 |
| 50 emb AJ238612 CRO238612 Catharanthus roseus mRNA for cytochrome P... | 89 | 2e-49 |
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http://www3.ncbi.nlm.nih.gov/htbin-
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20 (1368 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

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60 gb|BE055475|BE055475 GA_Ea0035I12f Gossypium arboreum 7-10 dpa ... 69 5e-19
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- emb|AW781424|AW781424 sl78a07.y1 Gm-c1037 Glycine max cDNA clone... 95 9e-19
 emb|Z25802|PHUDPRHAX P.hybrida mRNA for UDP rhamnose: anthocyani... 68 9e-19
 emb|AI967768|AI967768 Ljirnp11-882-f3 Ljirnp Lambda HybriZap ... 95 1e-18
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 5 emb|AB012115|AB012115 Vigna mungo UFGlyT mRNA for UDP-glycose:fl... 89 1e-18
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 emb|AW677595|AW677595 DG1_8_E07.g1_A002 Dark Grown 1 (DG1) Sorgh... 94 2e-18
- 10 Query= AL021961.3_at 15042_at /id_source genbank /description
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- Database: plantfungal
 20 661,018 sequences; 426,114,510 total letters
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 emb|Z19568|PDCIALDHA P.deltoides encoding cinnamyl alcohol dehyd... 310 e-146
 30 emb|A24083|A24083 pPOPCAD1 cinnamyl alcohol dehydrogenase cDNA. 311 e-146
 emb|AF217957|AF217957 Populus tremuloides cinnamyl alcohol dehyd... 309 e-145
 emb|X62344|NTCAD19MR N.tabacum CAD19 mRNA for cinnamyl alcohol d... 302 e-145
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 40 emb|X72675|PACINALDA P.abies mRNA for cinnamyl alcohol dehydroge... 240 e-124
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 50 emb|X92855|LEMTD L.esculentum exon 1 of MTD gene. 130 6e-77
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 60 emb|AW350274|AW350274 GM210007B20B7R Gm-r1021 Glycine max cDNA 3... 262 1e-69
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- emb|AW031628|AW031628 EST275082 tomato callus, TAMU Lycopersicon... 182 7e-69
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5 emb|AW684815|AW684815 NF021D07NR1F1000 Nodulated root Medicago t... 230 1e-62
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10 emb|AF146691|AF146691 Lycopersicon esculentum cultivar Rio Grand... 194 1e-58
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15 emb|AI488134|AI488134 EST246456 tomato ovary, TAMU Lycopersicon ... 210 2e-53
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20 gb|BE123743|BE123743 NXNV_153_E12_F Nsf Xylem Normal wood Vertic... 187 4e-49
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25 emb|AW775567|AW775567 EST334632 DSIL Medicago truncatula cDNA cl... 105 7e-45
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30 emb|AI729035|AI729035 BNLGHi12406 Six-day Cotton fiber Gossypium... 174 9e-43
emb|AW666266|AW666266 sk34e03.y1 Gm-c1028 Glycine max cDNA clone... 108 2e-42
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35 emb|AV412798|AV412798 AV412798 Lotus japonicus young plants (two... 137 6e-40
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40 emb|AW776649|AW776649 EST335714 DSIL Medicago truncatula cDNA cl... 94 1e-38
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55 emb|AF067082|AF067082 Apium graveolens mannitol dehydrogenase (M... 127 9e-32
emb|AW234172|AW234172 sf22a12.y1 Gm-c1028 Glycine max cDNA clone... 134 1e-30
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emb|AW218822|AW218822 EST301302 tomato root during/after fruit s... 84 2e-29
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Database: plantfungal
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 emb|AW096641|AW096641 EST289821 tomato mixed elicitor, BTI Lycop... 27 8.9
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 40 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi)
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45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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50 Score E.
 Sequences producing significant alignments: (bits) Value

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	gb BE036234 BE036234 MO21C12 MO Mesembryanthemum crystallinum cD...	78	1e-13
	emb AW286123 AW286123 LG1_261_F11.b1_A002 Light Grown 1 (LG1) So...	64	5e-13
	emb AW626069 AW626069 EST319976 tomato radicle, 5 d post-imbibit...	69	1e-12
35	gb BE095283 BE095283 00344 leafy spurge Lambda HybriZAP 2.1 two-...	62	1e-12
	emb AW677160 AW677160 DG1_5_D03.b1_A002 Dark Grown 1 (DG1) Sorgh...	62	2e-12
	emb AW677332 AW677332 DG1_5_F03.g1_A002 Dark Grown 1 (DG1) Sorgh...	70	2e-11
	gb BE022753 BE022753 sm88a02.y1 Gm-cl015 Glycine max cDNA clone ...	61	5e-11
	emb AW424028 AW424028 sh59f09.y1 Gm-cl015 Glycine max cDNA clone...	62	8e-11
40	emb X70064 PDBSPA P.deltoides gene for poplar bark storage protein.	63	3e-09
	emb AW119934 AW119934 sd54g12.y1 Gm-cl016 Glycine max cDNA clone...	54	4e-09
	emb AW677125 AW677125 DG1_5_F03.b1_A002 Dark Grown 1 (DG1) Sorgh...	43	5e-07
	gb BE058421 BE058421 sn15h03.y1 Gm-cl016 Glycine max cDNA clone ...	56	6e-07
	emb AW119941 AW119941 sd54h12.y1 Gm-cl016 Glycine max cDNA clone...	46	1e-06
45	gb BE037054 BE037054 MP13H01 MP Mesembryanthemum crystallinum cD...	55	1e-06
	gb BE036004 BE036004 MO17H11 MO Mesembryanthemum crystallinum cD...	51	1e-06
	gb BE035382 BE035382 MO03G01 MO Mesembryanthemum crystallinum cD...	54	2e-06
	emb AW127599 AW127599 M110330 DSLC Medicago truncatula cDNA clon...	44	3e-06
	gb BE095282 BE095282 00343 leafy spurge Lambda HybriZAP 2.1 two-...	52	5e-06
50	emb AW287592 AW287592 LG1_244_A09.b1_A002 Light Grown 1 (LG1) So...	40	6e-06
	emb AA557101 AA557101 943 Loblolly pine N Pinus taeda cDNA clone...	47	2e-04
	gb BE037091 BE037091 MP14F10 MP Mesembryanthemum crystallinum cD...	47	2e-04
	gb M25340 POPCHIC Populus sp. chitinase mRNA fragment, clone 4.	46	6e-04
	gb BE036753 BE036753 MP04H07 MP Mesembryanthemum crystallinum cD...	46	6e-04
55	gb BE037437 BE037437 MP21A08 MP Mesembryanthemum crystallinum cD...	34	8e-04
	gb BE037490 BE037490 MP21G12 MP Mesembryanthemum crystallinum cD...	45	9e-04
	emb AU036852 AU036852 AU036852 Cryptomeria japonica seedling lea...	41	0.015
	emb AA556425 AA556425 280 Loblolly pine C Pinus taeda cDNA clone...	41	0.015
	gb BE036626 BE036626 MP02H12 MP Mesembryanthemum crystallinum cD...	40	0.021
60	emb AW458345 AW458345 sh86h01.y1 Gm-cl016 Glycine max cDNA clone...	30	0.052
	gb BE034872 BE034872 ML05E09 ML Mesembryanthemum crystallinum cD...	38	0.10

emb|AW729858|AW729858 GA_Ea0026H02 Gossypium arboreum 7-10 dpa ... 36 0.37
 emb|AQ953583|AQ953583 Sheared DNA-53H18.TF Sheared DNA Trypanoso... 36 0.51
 gb|BE036480|BE036480 MP03G10 MP Mesembryanthemum crystallinum cD... 36 0.51
 emb|Z00044|CHNTXX Nicotiana tabacum chloroplast genome DNA. 35 0.70
 5 emb|AL160939|L1356CX Leishmania major Friedlin cosmid L1356.3 t3... 34 1.8
 gb|BE036897|BE036897 MP08B09 MP Mesembryanthemum crystallinum cD... 34 1.8
 emb|AI730722|AI730722 BNLGHi7729 Six-day Cotton fiber Gossypium ... 34 1.8
 emb|AB030726|AB030726 Nicotiana tabacum mRNA for DNA (cytosine-5... 34 2.5
 emb|AW397331|AW397331 sg77e08.y1 Gm-c1007 Glycine max cDNA clone... 34 2.5
 10 emb|AI210350|AI210350 i0c03a1.r1 Aspergillus nidulans 24hr asexu... 34 2.5
 emb|AA786346|AA786346 l3g09a1.fl Aspergillus nidulans 24hr asexu... 34 2.5
 emb|AW397063|AW397063 sg66e08.y1 Gm-c1007 Glycine max cDNA clone... 34 2.5
 emb|AI327733|AI327733 i0c03a1.fl Aspergillus nidulans 24hr asexu... 34 2.5
 emb|AW672119|AW672119 LG1_357_F07.b1_A002 Light Grown 1 (LG1) So... 33 3.4
 15 emb|AJ270207|ECA270207 Entodinium caudatum partial mRNA fro puta... 33 3.4
 emb|AW672133|AW672133 LG1_357_D07.b1_A002 Light Grown 1 (LG1) So... 33 3.4
 emb|AQ847463|AQ847463 LMAJFV1_lm34c05.y1 Leishmania major FV1 ra... 33 4.7
 emb|AZ212142|AZ212142 Sheared DNA-70G10.TF Sheared DNA Trypanoso... 32 6.4
 emb|AI163630|AI163630 A045p06u Hybrid aspen plasmid library Popu... 32 6.4
 20 emb|AL354532|LMFL1177 Leishmania major Friedlin chromosome 21 co... 30 6.9
 emb|AJ243516|NCR243516 Neurospora crassa partial nca-3 gene for ... 32 8.8
 emb|AL116648|CNS01DCG Botrytis cinerea strain T4 cDNA library un... 27 9.3
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 emb|caa50677.1|(x71794) peroxidase [arabidopsis thaliana]
 25 /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
 (1236 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

30

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

35

gb|M60729|HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge... 744 0.0
 emb|A00741|A00741 A.rusticana synthetic gene (reverse complement... 692 0.0
 emb|A00740|A00740 A.rusticana synthetic gene for peroxidase. 692 0.0
 dbj|E01651|E01651 cDNA encoding horseradish peroxidase. 692 0.0
 40 gb|M37157|HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge... 371 e-133
 emb|X97349|PTPXP2PER P.trichocarpa mRNA for anionic peroxidase P... 473 e-132
 emb|X97350|PTPXP3PER P.trichocarpa mRNA for anionic peroxidase P... 469 e-131
 dbj|D83224|POPP01 Populus nigra mRNA for peroxidase, complete cds. 468 e-131
 gb|M37156|HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge... 363 e-130
 45 emb|X97348|PTPXP1PER P.trichocarpa mRNA for anionic peroxidase P... 463 e-129
 dbj|D30652|POPPA Populus kitakamiensis mRNA for peroxidase, part... 441 e-123
 emb|X97351|PTPXP4PER P.trichocarpa mRNA for anionic peroxidase P... 383 e-120
 dbj|D30653|POPPB Populus kitakamiensis mRNA for peroxidase, part... 356 e-112
 emb|AF149277|AF149277 Phaseolus vulgaris peroxidase 1 precursor ... 227 e-107
 50 gb|L36157|ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple... 229 e-107
 emb|AF007211|AF007211 Glycine max peroxidase precursor (GMIPER1)... 229 e-106
 gb|L07554|LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA... 381 e-105
 emb|X90692|MSRNAPE1A M.sativa mRNA for peroxidase 1A. 211 e-105
 dbj|D90115|HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i... 296 e-103
 55 emb|AJ242742|IBA242742 Ipomoea batatas mRNA for peroxidase (pod ... 138 2e-97
 emb|AF149280|AF149280 Phaseolus vulgaris peroxidase 5 precursor ... 142 4e-97
 emb|X90693|MSRNAPE1B M.sativa mRNA for peroxidase 1B. 231 1e-95
 emb|X90694|MSRNAPE1C M.sativa mRNA for peroxidase 1C. 226 7e-94
 gb|L36111|SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 210 2e-89
 60 emb|AI959837|AI959837 sc94h07.y1 Gm-c1019 Glycine max cDNA clone... 228 6e-89
 emb|AF244924|AF244924 Spinacia oleracea peroxidase prx15 precurs... 208 9e-88

- emb|AW559660|AW559660 EST314772 DSIR Medicago truncatula cDNA cl... 236 1e-87
 emb|AW774581|AW774581 EST333732 KV3 Medicago truncatula cDNA clo... 236 7e-87
 emb|AF155124|AF155124 Gossypium hirsutum bacterial-induced perox... 215 2e-86
 emb|AW981426|AW981426 EST392579 DSIL Medicago truncatula cDNA cl... 236 2e-85
 5 emb|AB042103|AB042103 Asparagus officinalis AspPOX1 mRNA for per... 209 2e-85
 emb|AF244923|AF244923 Spinacia oleracea peroxidase prx14 precurs... 205 9e-85
 emb|AJ250121|PAB250121 Picea abies mRNA for SPI2 protein (spi2 g... 253 1e-83
 emb|AW775762|AW775762 EST334827 DSIL Medicago truncatula cDNA cl... 236 6e-83
 emb|Y10466|SOPR XR5 S.oleracea mRNA for peroxidase, clone PC18. 218 3e-82
 10 emb|AW775425|AW775425 EST334490 DSIL Medicago truncatula cDNA cl... 208 1e-81
 emb|AW685437|AW685437 NF029D09NR1F1000 Nodulated root Medicago t... 230 9e-80
 emb|AB024439|AB024439 Scutellaria baicalensis mRNA for peroxidas... 209 2e-79
 emb|AF244922|AF244922 Spinacia oleracea peroxidase prx13 precurs... 212 3e-79
 emb|X57564|ARNEUPERO A.rusticana mRNA for neutral peroxidase. 115 6e-78
 15 emb|AW776273|AW776273 EST335338 DSIL Medicago truncatula cDNA cl... 222 1e-77
 emb|AW267813|AW267813 EST305941 DSIR Medicago truncatula cDNA cl... 200 1e-76
 emb|X91232|MARNAPRX M.annua mRNA for peroxidase. 196 5e-76
 emb|AF049881|AF049881 Linum usitatissimum peroxidase FLXPER4 (PE... 207 7e-76
 emb|AW256487|AW256487 EST304624 KV2 Medicago truncatula cDNA clo... 200 9e-76
 20 emb|AW775890|AW775890 EST334955 DSIL Medicago truncatula cDNA cl... 200 3e-74
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 gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 86 2e-73
 gb|U41657|GMU41657 Glycine max seed coat peroxidase isozyme (SPO... 159 3e-73
 emb|AB027752|AB027752 Nicotiana tabacum mRNA for peroxidase, com... 197 5e-73
 25 gb|L36110|SSNPEROXIA Stylosanthes humilis peroxidase mRNA. 199 5e-73
 gb|M37636|ARCPNC1 Arachis hypogaea cationic peroxidase (PNC1) mR... 204 7e-73
 emb|AW685235|AW685235 NF027H10NR1F1000 Nodulated root Medicago t... 236 9e-73
 emb|AW278775|AW278775 sf97d02.y1 Gm-cl019 Glycine max cDNA clone... 155 1e-72
 emb|X71593|LECEV11A L.esculentum CEVI-1 mRNA. 99 2e-72
 30 gb|J02979|TOBPXDLF Nicotiana tabacum lignin-forming peroxidase m... 100 2e-72
 emb|AW559945|AW559945 EST314993 DSIR Medicago truncatula cDNA cl... 233 2e-72
 emb|AW980744|AW980744 EST391897 GVN Medicago truncatula cDNA clo... 235 5e-70
 emb|Y10467|SOPR XR6 S.oleracea mRNA for peroxidase, clone PC23. 105 1e-69
 dbj|D83225|POPP02 Populus nigra peroxidase gene, complete cds. 196 2e-69
 35 gb|M74103|TOBANPER Nicotiana sylvestris anionic peroxidase mRNA,... 205 6e-69
 emb|AF043234|AF043234 Striga asiatica ferriprotein porphyrin-con... 211 1e-68
 gb|BE034991|BE034991 MM01A12 MM Mesembryanthemum crystallinum cD... 202 6e-68
 emb|AW574244|AW574244 EST316835 GVN Medicago truncatula cDNA clo... 202 1e-67
 emb|Y10465|SOPR XR4 S.oleracea mRNA for peroxidase, clone PC44. 98 3e-67
 40 emb|AW686084|AW686084 NF038B07NR1F1000 Nodulated root Medicago t... 236 5e-67
 emb|AW561032|AW561032 EST316080 DSIR Medicago truncatula cDNA cl... 203 7e-67
 emb|X56011|TAPERO Wheat mRNA for peroxidase. 111 2e-66
 emb|AW185769|AW185769 se59d08.y1 Gm-cl019 Glycine max cDNA clone... 219 4e-65
 emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase. 96 2e-64
 45 gb|BE033422|BE033422 ME01E09 ME Mesembryanthemum crystallinum cD... 184 4e-64
 emb|AB024438|AB024438 Scutellaria baicalensis mRNA for peroxidas... 205 7e-64
 gb|M91374|CUSPREPERA Cucumis sativus peroxidase mRNA, complete cds. 76 2e-63
 gb|L24120|LINFLXP Linum usitatissimum peroxidase precursor (FLXP... 167 2e-63
 gb|M91372|CUSPREPERB Cucumis sativus peroxidase mRNA, complete cds. 134 2e-63
 50 emb|AF043235|AF043235 Striga asiatica ferriprotein porphyrin-con... 199 3e-63
 emb|AW288002|AW288002 N100846e rootphos(-) Medicago truncatula c... 182 7e-63
 emb|AW126121|AW126121 N100318e rootphos(-) Medicago truncatula c... 216 1e-62
 gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 133 5e-62
 emb|AW687443|AW687443 NF009F07RT1F1062 Developing root Medicago ... 235 1e-61
 55 emb|AW687957|AW687957 NF001D11ST1F1000 Developing stem Medicago ... 236 3e-61
 emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidas... 163 3e-61
 emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 133 5e-61
 emb|AI496388|AI496388 sb04a11.y1 Gm-cl004 Glycine max cDNA clone... 224 6e-61
 emb|AW686765|AW686765 NF042E07NR1F1000 Nodulated root Medicago t... 222 8e-61
 60 dbj|D38050|POPP1 Aspen prx3a gene for peroxidase, complete cds. 121 9e-61
 emb|AW704659|AW704659 sk54h10.y1 Gm-cl019 Glycine max cDNA clone... 149 9e-61

emb|Y10464|SOPR3 S.oleracea mRNA for peroxidase, clone PC42. 80 3e-60
emb|AW705730|AW705730 sk51b02.y1 Gm-c1019 Glycine max cDNA clone... 149 8e-60
gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 100 9e-60
gb|U12314|CCU12314 Cenchrus ciliaris clone PX7 peroxidase mRNA, ... 105 9e-60
5 emb|AI938533|AI938533 sb46h09.y1 Gm-c1015 Glycine max cDNA clone... 145 1e-59
emb|AW705617|AW705617 sk50d03.y1 Gm-c1019 Glycine max cDNA clone... 149 2e-59
emb|AI781859|AI781859 EST262738 tomato susceptible, Cornell Lyco... 102 2e-59
emb|AF149278|AF149278 Phaseolus vulgaris peroxidase 3 precursor ... 90 3e-59
gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 102 4e-59
10 emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59
emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 156 8e-59
gb|M32742|CUSCUPER C.sativus peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58
emb|AW705946|AW705946 sk52h07.y1 Gm-c1019 Glycine max cDNA clone... 224 6e-58

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/chip nova /gb_link

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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?x68592>
(1530 letters)

25 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

30
Score E
Sequences producing significant alignments: (bits) Value

emb|AF006489|AF006489 Gossypium hirsutum adenine nucleotide tran... 325 0.0
emb|X62123|STANTG S.tuberosum ant gene for ADP/ATP translocator. 328 0.0
35 gb|U89839|LEU89839 Lycopersicon esculentum ADP/ATP translocator ... 327 0.0
emb|X57557|STANT1 S.tuberosum PANT1 mRNA for adenine nucleotide ... 635 0.0
emb|AJ003197|LAAJ3197 Lupinus albus mRNA for adenine nucleotide ... 331 e-175
emb|X80023|TTADPATP T.turgidum mRNA for ADP/ATP carrier. 322 e-172
emb|X65194|CRANT C.reinhardtii mRNA CRANT for mitochondrial ADP/... 348 e-149
40 emb|AL023634|SPBC530 S.pombe chromosome II cosmid c530. 265 e-139
emb|Z49974|SPANC1GN S.pombe ANC1 gene for adenine nucleotide car... 265 e-139
emb|AF085429|AF085429 Candida parapsilosis ADP/ATP carrier prote... 311 e-134
dbj|D89102|D89102 Schizosaccharomyces pombe mRNA, partial cds, c... 265 e-133
gb|L33797|YSKAAC Kluyveromyces lactis ADP/ATP translocase (AAC) ... 259 e-132
45 emb|AF237675|AF237675 Yarrowia lipolytica ADP/ATP carrier protei... 247 e-132
emb|AJ277099|CUT277099 Candida utilis anc gene for mitochondrial... 253 e-131
emb|AJ277098|CUT277098 Candida utilis anc gene for mitochondrial... 253 e-131
gb|M34075|YSCAAC3 S.cerevisiae ADP/ATP-translocator protein (AAC... 252 e-129
emb|X77291|SCIILDNA S.cerevisiae YBL0421, YBL0438, YBL0418, YBL0... 252 e-129
50 emb|Z35791|SCYBL030C S.cerevisiae chromosome II reading frame OR... 252 e-129
emb|X74427|SCADNUCA S.cerevisiae gene for adenine nucleotide car... 252 e-129
gb|J04021|YSCAAC2 S.cerevisiae ADP/ATP carrier protein (AAC2) ge... 252 e-129
emb|X00363|NCADPATP Neurospora crassa mRNA for mitochondrial ADP... 280 e-126
emb|Z49703|SC9796 S.cerevisiae chromosome XIII cosmid 9796. 248 e-125
55 gb|M12514|YSCPET9 S.cerevisiae ADP/ATP translocator protein (AAC... 248 e-125
emb|Z35954|SCYBR085W S.cerevisiae chromosome II reading frame OR... 247 e-125
gb|M34076|YSCAAC2A S.cerevisiae ADP/ATP-translocator protein (AA... 247 e-125
emb|AW774326|AW774326 EST333477 KV3 Medicago truncatula cDNA clo... 288 e-124
emb|AL111975|CNS019QN Botrytis cinerea strain T4 cDNA library un... 254 e-122
60 emb|AW647699|AW647699 EST307178 tomato germinating seedlings, TA... 299 e-120

- emb|AW349848|AW349848 GM210006A11G9R Gm-r1021 Glycine max cDNA 3... 326 e-118
- emb|AW624842|AW624842 EST313671 tomato radicle, 5 d post-imbibit... 229 e-116
- emb|X95863|TTANT1 T.turgidum ant gene (1549bp). 195 e-114
- 5 emb|AW041186|AW041186 EST284050 tomato mixed elicitor, BTI Lycop... 239 e-114
- emb|X95864|TTANT2 T.turgidum ant gene (1494bp). 191 e-112
- emb|AW706324|AW706324 sj54h05.y1 Gm-cl033 Glycine max cDNA clone... 245 e-110
- emb|AL157416|LMFL6066 Leishmania major Friedlin chromosome 19 co... 233 e-108
- emb|AW160172|AW160172 EST290029 L. pennellii trichome, Cornell U... 328 e-108
- 10 emb|AW928728|AW928728 EST337516 tomato flower buds 8 mm to pre-a... 247 e-107
- emb|AW218544|AW218544 EST303727 tomato radicle, 5 d post-imbibit... 325 e-105
- emb|AW830381|AW830381 sm26a12.y1 Gm-cl028 Glycine max cDNA clone... 268 e-105
- emb|AW201674|AW201674 sf05h11.y1 Gm-cl027 Glycine max cDNA clone... 309 e-104
- emb|AI812944|AI812944 22G12 Pine Lambda Zap Xylem library Pinus ... 251 e-103
- 15 emb|AI777865|AI777865 EST258744 tomato susceptible, Cornell Lyco... 284 e-102
- emb|AW234033|AW234033 sf33d01.y1 Gm-cl028 Glycine max cDNA clone... 237 e-101
- emb|AW831587|AW831587 sm28b02.y1 Gm-cl028 Glycine max cDNA clone... 300 e-101
- emb|AW668198|AW668198 GA__Ea0013C13 Gossypium arboreum 7-10 dpa ... 331 e-100
- emb|AF049130|AF049130 Trypanosoma brucei brucei ADP/ATP carrier ... 238 1e-98
- 20 emb|AI898886|AI898886 EST268329 tomato ovary, TAMU Lycopersicon ... 213 2e-98
- gb|U32987|TBU32987 Trypanosoma brucei rhodesiense ADP/ATP carrie... 238 3e-98
- emb|AW223982|AW223982 EST300793 tomato fruit red ripe, TAMU Lyco... 327 1e-96
- emb|AW624951|AW624951 EST313780 tomato radicle, 5 d post-imbibit... 327 1e-96
- emb|AW348348|AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3... 328 2e-96
- 25 emb|AW441243|AW441243 EST310639 tomato fruit red ripe, TAMU Lyco... 324 1e-95
- emb|AW223973|AW223973 EST300784 tomato fruit red ripe, TAMU Lyco... 321 7e-95
- emb|AW931569|AW931569 EST357412 tomato fruit mature green, TAMU ... 328 2e-94
- emb|AW218871|AW218871 EST301353 tomato root during/after fruit s... 327 8e-94
- 30 emb|AL116444|CNS01D6S Botrytis cinerea strain T4 cDNA library un... 267 4e-93
- emb|AW831561|AW831561 sm34f06.y1 Gm-cl028 Glycine max cDNA clone... 312 2e-92
- emb|AI484151|AI484151 EST248958 tomato resistant, Cornell Lycope... 264 3e-91
- emb|AW925414|AW925414 HVSMEg0001L02 Hordeum vulgare pre-anthesis... 299 6e-91
- emb|AI731594|AI731594 BNLGHi10182 Six-day Cotton fiber Gossypium... 335 7e-91
- 35 emb|AW730597|AW730597 GA__Ea0027H02 Gossypium arboreum 7-10 dpa ... 333 1e-90
- emb|AW647665|AW647665 EST307143 tomato germinating seedlings, TA... 317 1e-90
- emb|AW395111|AW395111 sh40a06.y1 Gm-cl017 Glycine max cDNA clone... 303 6e-90
- emb|AI725588|AI725588 BNLGHi12376 Six-day Cotton fiber Gossypium... 288 1e-89
- emb|AW934656|AW934656 EST353548 tomato flower buds 0-3 mm, Corne... 328 2e-89
- 40 emb|AW757478|AW757478 874001D11.y1 C. reinhardtii CC-1690, Lambd... 202 3e-89
- emb|AW725897|AW725897 GA__Ea0020B06 Gossypium arboreum 7-10 dpa ... 328 8e-89
- emb|AW647757|AW647757 EST326211 tomato germinating seedlings, TA... 301 1e-88
- emb|AW509174|AW509174 sh92b04.y1 Gm-cl016 Glycine max cDNA clone... 297 4e-88
- emb|AW666654|AW666654 GA__Ea0005E11 Gossypium arboreum 7-10 dpa ... 279 7e-88
- 45 emb|AL114553|CNS01BQ9 Botrytis cinerea strain T4 cDNA library un... 231 3e-87
- gb|BE021489|BE021489 sm59b05.y1 Gm-cl028 Glycine max cDNA clone ... 322 5e-87
- emb|AW507801|AW507801 si45c02.y1 Gm-r1030 Glycine max cDNA clone... 259 2e-86
- emb|AW733916|AW733916 sk85a11.y1 Gm-cl035 Glycine max cDNA clone... 306 2e-86
- emb|AW096468|AW096468 EST289648 tomato mixed elicitor, BTI Lycop... 292 6e-86
- 50 emb|AW156741|AW156741 se30b08.y1 Gm-cl015 Glycine max cDNA clone... 184 1e-85
- emb|AI729625|AI729625 BNLGHi13824 Six-day Cotton fiber Gossypium... 276 4e-85
- emb|AW034214|AW034214 EST277785 tomato callus, TAMU Lycopersicon... 304 5e-85
- emb|AJ273864|AJ273864 AJ273864 Metarhizium anisopliae ARSEF 2575... 184 1e-84
- emb|AI775647|AI775647 EST256747 tomato resistant, Cornell Lycope... 297 1e-84
- 55 emb|AI822682|AI822682 L0-1204T3 Ice plant Lambda Uni-Zap XR expr... 314 2e-84
- emb|AW625107|AW625107 EST313924 tomato radicle, 5 d post-imbibit... 314 2e-84
- emb|AI726147|AI726147 BNLGHi5085 Six-day Cotton fiber Gossypium ... 263 6e-83
- emb|AW755396|AW755396 sl03d11.y1 Gm-cl036 Glycine max cDNA clone... 306 3e-82
- emb|AI728088|AI728088 BNLGHi9938 Six-day Cotton fiber Gossypium ... 259 5e-82
- 60 emb|AW979992|AW979992 EST310378 tomato root deficiency, Cornell ... 285 8e-82
- emb|AW333018|AW333018 S16C3 AGS-1 Pneumocystis carinii f. sp. ca... 278 1e-81

- emb|AI780394|AI780394 EST261273 tomato susceptible, Cornell Lyco... 284 2e-81
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 5 emb|AW760027|AW760027 sl57b04.y1 Gm-c1027 Glycine max cDNA clone... 301 1e-80
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 10 emb|AI775628|AI775628 EST256728 tomato resistant, Cornell Lycopers... 295 7e-79
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 emb|AJ273749|AJ273749 AJ273749 Metarhizium anisopliae ARSEF 2575... 256 1e-77
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 20 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14251|/ncgi)
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 (630 letters)
- 25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
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- 30
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 Sequences producing significant alignments: (bits) Value
- emb|X78203|HMGST H.muticus mRNA for glutathione S-transferase. 271 4e-72
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 35 emb|AF002692|AF002692 Solanum commersonii glutathione S-transfer... 264 3e-70
 dbj|D10524|TOBPARB Nicotiana tabacum mRNA for glutathione S-tran... 262 2e-69
 emb|AW731360|AW731360 GA_Ea0030G14 Gossypium arboreum 7-10 dpa ... 142 3e-69
 dbj|D29680|TOBAPI2B Tobacco api2 mRNA (which expression is induc... 261 4e-69
 emb|AW220064|AW220064 EST302547 tomato root during/after fruit s... 260 5e-69
 40 emb|Z71749|NPGSTMR N.plumbaginifolia mRNA for glutathione S-tran... 260 8e-69
 emb|AI774583|AI774583 EST255683 tomato resistant, Cornell Lycopers... 258 3e-68
 emb|AW728413|AW728413 GA_Ea0016J18 Gossypium arboreum 7-10 dpa ... 142 7e-68
 emb|AI725552|AI725552 BNLGHi12077 Six-day Cotton fiber Gossypium... 142 4e-67
 emb|AI728937|AI728937 BNLGHi12090 Six-day Cotton fiber Gossypium... 142 4e-67
 45 gb|BE033971|BE033971 MG02G09 MG Mesembryanthemum crystallinum cD... 228 2e-65
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 50 emb|AW218151|AW218151 EST303332 tomato radicle, 5 d post-imbibit... 232 1e-60
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15 dbj|D49526|TOBPBARBA Tobacco chimeric parB promoter/beta-glucuron... 163 1e-39
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20 emb|Y07721|PHGLSTRAN P.hybrida mRNA for glutathione S-transferase. 151 5e-36
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25 emb|AW926756|AW926756 HVSMEg0008B23 Hordeum vulgare pre-anthesis... 92 3e-35
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30 emb|AW164336|AW164336 se71b09.y1 Gm-cl023 Glycine max cDNA clone... 139 1e-32
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 emb|AW171715|AW171715 N100609e rootphos(-) Medicago truncatula c... 112 3e-24
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 5 emb|AI352728|AI352728 MB47-17 PZ204.BNlib Brassica napus cDNA cl... 110 1e-23
 emb|AW127163|AW127163 M110099 GVN Medicago truncatula cDNA clone... 110 1e-23
 emb|AW924273|AW924273 WS1_51_A04.b1_A002 Water-stressed 1 (WS1) ... 95 1e-23
 emb|AW680779|AW680779 WS1_7_D01.b1_A002 Water-stressed 1 (WS1) S... 97 1e-23
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 10 emb|AW459151|AW459151 sh21c07.y1 Gm-c1016 Glycine max cDNA clone... 66 6e-23

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20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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30	emb AJ007574 RCO7574 Ricinus communis mRNA for amino acid carrier.	410	0.0
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	emb AJ132228 RCO132228 Ricinus communis mRNA for amino acid carr...	342	0.0
	emb AF080543 AF080543 Nepenthes alata amino acid transporter (AA...	641	0.0
	emb Y09826 STAAP2 S.tuberosum mRNA for amino acid transporter AA...	354	0.0
	emb AF080544 AF080544 Nepenthes alata amino acid transporter (AA...	596	0.0
35	emb Y09825 STAAP1 S.tuberosum mRNA for amino acid transporter AA...	288	e-158
	emb Z68759 RCAACMR R.communis mRNA for amino acid carrier.	334	e-155
	emb AF080542 AF080542 Nepenthes alata amino acid transporter (AA...	239	e-145
	emb AF061435 AF061435 Vicia faba amino acid transporter b (AAPB)...	501	e-141
	emb Y11121 RCAACARR Ricinus communis mRNA for amino acid carrier...	264	e-123
40	emb AF061434 AF061434 Vicia faba amino acid transporter a (AAPA)...	290	e-107
	emb AF061436 AF061436 Vicia faba amino acid transporter c (AAPC)...	259	5e-95
	emb AW560155 AW560155 EST315203 DSIR Medicago truncatula cDNA cl...	293	4e-86
	emb AW203255 AW203255 sf27a03.y1 Gm-c1028 Glycine max cDNA clone...	312	4e-84
	emb AI166826 AI166826 xylem.est.62 Poplar xylem Lambda ZAPII lib...	188	2e-68
45	emb AW648039 AW648039 EST326493 tomato germinating seedlings, TA...	226	2e-67
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- emb|AW349599|AW349599 GM210005A21G12R Gm-r1021 Glycine max cDNA ... 140 5e-49
- emb|AI487167|AI487167 EST245489 tomato ovary, TAMU Lycopersicon ... 122 2e-48
- emb|AW737784|AW737784 EST339211 tomato flower buds, anthesis, Co... 192 6e-48
- 5 emb|AW309945|AW309945 sf27a03.x1 Gm-c1028 Glycine max cDNA clone... 149 5e-47
- emb|AW738557|AW738557 EST339984 tomato flower buds, anthesis, Co... 188 8e-47
- emb|AQ842052|AQ842052 T134338 Soybean RFLP probe Glycine max gen... 148 2e-44
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- emb|AW649763|AW649763 EST328217 tomato germinating seedlings, TA... 127 3e-43
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- emb|AW306512|AW306512 se51h04.y1 Gm-c1017 Glycine max cDNA clone... 140 1e-41
- emb|AW395873|AW395873 sh01d01.y1 Gm-c1026 Glycine max cDNA clone... 112 4e-41
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- emb|AW684816|AW684816 NF021D09NR1F1000 Nodulated root Medicago t... 164 2e-39
- emb|AZ051221|AZ051221 Gm_UMb001_166_P11R UMN Soybean BAC Library... 159 7e-38
- emb|AI779305|AI779305 EST260184 tomato susceptible, Cornell Lyco... 155 1e-36
- emb|AI779304|AI779304 EST260183 tomato susceptible, Cornell Lyco... 155 1e-36
- 20 emb|AW830977|AW830977 sm31a10.y1 Gm-c1028 Glycine max cDNA clone... 149 4e-35
- emb|AW096758|AW096758 EST289938 tomato mixed elicitor, BTI Lycop... 147 3e-34
- emb|AJ004829|STAJ4829 Solanum tuberosum fdh3 pseudogene. 110 3e-33
- emb|AQ841805|AQ841805 T134055 Soybean RFLP probe Glycine max gen... 140 2e-32
- emb|AW736648|AW736648 EST333140 KV3 Medicago truncatula cDNA clo... 138 1e-31
- 25 emb|AV418629|AV418629 AV418629 Lotus japonicus young plants (two... 130 3e-29
- emb|AW442349|AW442349 EST311745 tomato fruit red ripe, TAMU Lyco... 130 3e-29
- emb|AW738564|AW738564 EST339991 tomato flower buds, anthesis, Co... 104 7e-29
- emb|AW561095|AW561095 EST316143 DSIR Medicago truncatula cDNA cl... 126 6e-28
- emb|AW234791|AW234791 sf19c06.y1 Gm-c1028 Glycine max cDNA clone... 124 2e-27
- 30 gb|U31932|NSU31932 Nicotiana sylvestris amino acid permease 1 (N... 61 3e-27
- emb|AI441371|AI441371 sa64f02.y1 Gm-c1004 Glycine max cDNA clone... 72 2e-26
- emb|AW438003|AW438003 ST83D04 Pine TriplEx shoot tip library Pin... 111 2e-23
- emb|AW056573|AW056573 ST52G03 Pine TriplEx shoot tip library Pin... 109 8e-23
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- 35 emb|AW924285|AW924285 WS1_52_F10.b1_A002 Water-stressed 1 (WS1) ... 106 5e-22
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- emb|AW620352|AW620352 sj04b02.y1 Gm-c1032 Glycine max cDNA clone... 92 1e-17
- 40 emb|AW288077|AW288077 N100921e rootphos(-) Medicago truncatula c... 84 2e-15
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 5 emb|X87611|SCXCOSM83 S.cerevisiae chromosome X DNA (cosmid 83). 44 0.003
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15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 35 emb|AV428977|AV428977 AV428977 Lotus japonicus young plants (two... 343 7e-94
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 emb|X72928|SC13OLP S.commersonii (pOSML13) gene for osmotin-like... 200 1e-88
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 15 emb|AF109653|AF109653 AF109653 Capsicum annuum root susceptible ... 192 9e-84
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 emb|AW650675|AW650675 EST329129 tomato germinating seedlings, TA... 193 1e-82
 emb|AW034088|AW034088 EST277583 tomato callus, TAMU Lycopersicon... 193 1e-81
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 20 emb|AW034433|AW034433 EST278004 tomato callus, TAMU Lycopersicon... 175 2e-80
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 25 gb|M29279|TOBOSM N.tabacum osmotin mRNA, complete cds. 242 4e-79
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 50 emb|AW031249|AW031249 EST274624 tomato callus, TAMU Lycopersicon... 200 3e-70
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 (357 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	gb U59379 BNU59379 Brassica napus thioredoxin-h-like-1 (THL-1) m...	194	2e-49
	emb AB010434 AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ...	192	9e-49
	emb AW255457 AW255457 ML480 peppermint glandular trichome Mentha...	190	3e-48
20	emb AW569018 AW569018 si74e02.y1 Gm-c1031 Glycine max cDNA clone...	185	1e-46
	emb AI988470 AI988470 sd02f07.y1 Gm-c1020 Glycine max cDNA clone...	185	1e-46
	emb Z70677 RCTHIORXN R.communis mRNA for thioredoxin.	183	5e-46
	emb AI161830 AI161830 A007P52U Hybrid aspen plasmid library Popu...	182	9e-46
	gb BE053835 BE053835 GA_Ea0009P21f Gossypium arboreum 7-10 dpa ...	182	9e-46
25	emb AW677726 AW677726 WS1_10_F03.g1_A002 Water-stressed 1 (WS1) ...	181	2e-45
	emb AW924685 AW924685 WS1_71_B11.b1_A002 Water-stressed 1 (WS1) ...	181	2e-45
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	emb AW671668 AW671668 LG1_349_G02.b1_A002 Light Grown 1 (LG1) So...	181	2e-45
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55 emb|AW681036|AW681036 WS1_8_D05.b1_A002 Water-stressed 1 (WS1) S... 154 2e-37
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 (1896 letters)

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Score E
 Sequences producing significant alignments: (bits) Value

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emb AW349113 AW349113	GM210004B21A1R Gm-r1021 Glycine max cDNA 3...	131	4e-41
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emb AW622684 AW622684	EST306821 tomato flower buds 3-8 mm, Come...	105	7e-38
emb AW217219 AW217219	EST295933 tomato callus, TAMU Lycopersicon...	157	2e-37
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5 emb|AW596402|AW596402 sj12a06.y1 Gm-c1032 Glycine max cDNA clone... 103 9e-35
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10 emb|AV408894|AV408894 AV408894 Lotus japonicus young plants (two... 132 1e-29
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15 emb|AI900868|AI900868 sb95e02.y1 Gm-c1012 Glycine max cDNA clone... 104 1e-26
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emb|AI898974|AI898974 EST268417 tomato ovary, TAMU Lycopersicon ... 99 3e-24
emb|AI778687|AI778687 EST259566 tomato susceptible, Cornell Lyco... 113 5e-24
emb|AW981373|AW981373 EST392526 DSIL Medicago truncatula cDNA cl... 101 1e-23
20 emb|AI441355|AI441355 sa55f08.y1 Gm-c1004 Glycine max cDNA clone... 59 8e-22
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25 emb|AI166806|AI166806 xylem.est.601 Poplar xylem Lambda ZAPII li... 84 9e-20
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45 emb|AI897063|AI897063 EST266506 tomato ovary, TAMU Lycopersicon ... 66 8e-10
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emb|AW683199|AW683199 NF008H01LF1F1014 Developing leaf Medicago ... 63 8e-09
gb|BE059206|BE059206 sn27f04.y1 Gm-c1016 Glycine max cDNA clone ... 62 1e-08
emb|AW616334|AW616334 EST322745 L. hirsutum trichome, Cornell Un... 61 3e-08
50 emb|AI483553|AI483553 EST249402 tomato ovary, TAMU Lycopersicon ... 59 1e-07
emb|AI773748|AI773748 EST254848 tomato resistant, Cornell Lycop... 59 1e-07
emb|AW038769|AW038769 EST280630 tomato mixed elicitor, BTI Lycop... 56 9e-07
gb|L38057|L38057 BNAF0397E Mustard flower buds Brassica rapa cDN... 53 8e-06
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aminotransferase [arabidopsis thaliana] /blast_score 0 /ec_number
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(1582 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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	dbj D88273 D88273 Hordeum vulgare naat-A mRNA for nicotianamine ...	446	e-124
	emb AB005788 AB005788 Hordeum vulgare mRNA for nicotianamine ami...	433	e-120
	emb AB024006 AB024006 Hordeum vulgare naat-B and naat-A genes fo...	184	3e-78
15	emb AW760137 AW760137 sl58e07.y1 Gm-c1027 Glycine max cDNA clone...	270	1e-72
	emb AW508844 AW508844 si41a10.y1 Gm-r1030 Glycine max cDNA clone...	191	7e-61
	emb AW348839 AW348839 GM210003B11G12R Gm-r1021 Glycine max cDNA ...	233	2e-60
	emb AW832427 AW832427 sm10c03.y1 Gm-c1027 Glycine max cDNA clone...	233	3e-60
20	emb AW760284 AW760284 sl48d01.y1 Gm-c1027 Glycine max cDNA clone...	206	6e-55
	emb AW620771 AW620771 sj09d03.y1 Gm-c1032 Glycine max cDNA clone...	209	5e-53
	emb AW568831 AW568831 si61g09.y1 Gm-r1030 Glycine max cDNA clone...	199	5e-50
	emb AW030722 AW030722 EST273977 tomato callus, TAMU Lycopersicon...	198	9e-50
	emb AW306460 AW306460 se51a02.y1 Gm-c1017 Glycine max cDNA clone...	178	8e-44
25	emb AW459166 AW459166 sh21e03.y1 Gm-c1016 Glycine max cDNA clone...	170	3e-41
	emb AW030650 AW030650 EST273905 tomato callus, TAMU Lycopersicon...	96	4e-38
	emb AW202348 AW202348 sf14a04.y1 Gm-c1027 Glycine max cDNA clone...	96	1e-33
	emb AW760709 AW760709 sl36a11.y1 Gm-c1027 Glycine max cDNA clone...	138	8e-32
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30	gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine aminotransf...	97	1e-26
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	emb AI487927 AI487927 EST246249 tomato ovary, TAMU Lycopersicon ...	70	7e-23
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	emb AL096788 SPBC582 S.pombe chromosome II cosmid c582.	57	1e-15
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	gb U53880 YSCL9449 Saccharomyces cerevisiae chromosome XII cosmi...	51	2e-14
50	emb Z73261 SCYLR089C S.cerevisiae chromosome XII reading frame O...	51	2e-14
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 emb|AF083816|AF083816 Antirrhinum majus ACC synthase 3 (ACS3) mR... 46 2e-06
 10 emb|AI080889|AI080889 TENU3747 T. cruzi epimastigote normalized ... 52 9e-06
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 15 emb|AW691076|AW691076 NF041A07ST1F1000 Developing stem Medicago ... 44 2e-05
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 20 emb|AF074931|AF074931 Sinapis arvensis 1-aminocyclopropane-1-car... 46 3e-05
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 35 emb|Z26322|HVALAAT H.vulgare mRNA for alanine aminotransferase. 48 2e-04
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 45 emb|AF052832|AF052832 Trypanosoma cruzi CL Brener cosmid 1b21 ch... 47 4e-04
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 50 emb|AB015624|AB015624 Pyrus pyrifolia mRNA for 1-aminocyclopropan... 41 7e-04
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 (460 letters)

Database: plantfungal
 60 661,018 sequences; 426,114,510 total letters

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	emb AW032485 AW032485	EST276044 tomato callus, TAMU Lycopersicon...	272 1e-72
10	gb M37637 ARCPNC2	A.hypogaea cationic peroxidase mRNA, complete ...	271 2e-72
	emb AF149279 AF149279	Phaseolus vulgaris peroxidase 4 precursor ...	265 1e-70
	emb AI777064 AI777064	EST252031 tomato callus, TAMU Lycopersicon...	261 3e-69
	emb AW216562 AW216562	EST295276 tomato callus, TAMU Lycopersicon...	259 9e-69
	emb AW035446 AW035446	EST281184 tomato callus, TAMU Lycopersicon...	258 2e-68
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	emb AW216873 AW216873	EST295587 tomato callus, TAMU Lycopersicon...	251 2e-66
	emb AV414074 AV414074	AV414074 Lotus japonicus young plants (two...	250 5e-66
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	gb L36112 SSNPEROXIC	Stylosanthes humilis peroxidase mRNA.	193 3e-64
20	emb Y10468 SOPR XR7	S.oleracea mRNA for peroxidase, clone PC36.	242 8e-64
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	emb AW224631 AW224631	EST303074 tomato root, plants pre-anthesis...	235 2e-61
25	emb AW219926 AW219926	EST302409 tomato root during/after fruit s...	235 2e-61
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30	emb AW219112 AW219112	EST301594 tomato root during/after fruit s...	227 3e-59
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	emb AW035660 AW035660	EST281492 tomato callus, TAMU Lycopersicon...	223 7e-58
	emb AW035872 AW035872	EST282181 tomato callus, TAMU Lycopersicon...	221 4e-57
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35	emb AW666030 AW666030	sk31c04.y1 Gm-c1028 Glycine max cDNA clone...	216 8e-56
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	emb AW030052 AW030052	EST273307 tomato callus, TAMU Lycopersicon...	186 8e-47
45	emb AF145349 AF145349	Glycine max peroxidase (Prx3) mRNA, partia...	143 2e-46
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	emb X57564 ARNEUPERO	A.rusticana mRNA for neutral peroxidase.	129 2e-45
	emb AW220442 AW220442	EST302925 tomato root during/after fruit s...	108 3e-44
	emb AW625509 AW625509	EST319416 tomato radicle, 5 d post-imbibit...	106 7e-44
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	emb AW621545 AW621545	EST312343 tomato root during/after fruit s...	108 2e-43
	emb AW694946 AW694946	NF081G11ST1F1087 Developing stem Medicago ...	142 4e-43
	emb AW132575 AW132575	se05h10.y1 Gm-c1013 Glycine max cDNA clone...	138 5e-43
	emb AF109663 AF109663	AF109663 Capsicum annuum root susceptible ...	161 2e-42
55	emb AW622066 AW622066	EST312864 tomato root during/after fruit s...	111 4e-42
	gb U51194 GMU51194	Glycine max peroxidase (sEPb2) mRNA, partial ...	138 4e-42
	gb L13654 TOMTPX1A	Lycopersicon esculentum peroxidase (TPX1) mRN...	112 5e-42
	gb U51193 GMU51193	Glycine max peroxidase (sEPb1) mRNA, partial ...	133 2e-41
	emb AW219925 AW219925	EST302408 tomato root during/after fruit s...	168 2e-41
60	emb AW622012 AW622012	EST312810 tomato root during/after fruit s...	111 2e-41
	emb AW621198 AW621198	EST311996 tomato root during/after fruit s...	111 2e-41

emb|AW626302|AW626302 EST320209 tomato radicle, 5 d post-imbibit... 111 2e-41
emb|AW720673|AW720673 LjNEST4b2rc Lotus japonicus nodule library... 123 2e-41
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5 emb|AW621449|AW621449 EST312247 tomato root during/after fruit s... 110 5e-41
emb|AW928514|AW928514 EST337302 tomato flower buds 8 mm to pre-a... 95 5e-41
emb|AW220017|AW220017 EST302500 tomato root during/after fruit s... 111 1e-40
emb|AI771103|AI771103 EST252203 tomato ovary, TAMU Lycopersicon ... 111 1e-40
emb|AW649146|AW649146 EST327600 tomato germinating seedlings, TA... 111 1e-40
10 emb|AW219955|AW219955 EST302438 tomato root during/after fruit s... 111 1e-40
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gb|L13653|TOMTPX2A Lycopersicon esculentum peroxidase (TPX2) mRN... 107 2e-40
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15 emb|AI725603|AI725603 BNLGH112435 Six-day Cotton fiber Gossypium... 153 5e-40
emb|AF155124|AF155124 Gossypium hirsutum bacterial-induced perox... 94 8e-40
emb|AV426241|AV426241 AV426241 Lotus japonicus young plants (two... 163 9e-40
emb|AW034987|AW034987 EST279216 tomato callus, TAMU Lycopersicon... 163 9e-40
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20 emb|Y10470|SOPR XR9 S.oleracea mRNA for peroxidase, clone PC56. 151 1e-39
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emb|AW671673|AW671673 LG1_349_F09.b1_A002 Light Grown 1 (LG1) So... 147 2e-39
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25 emb|AW625780|AW625780 EST319687 tomato radicle, 5 d post-imbibit... 105 2e-39
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emb|Y16778|SPY16778 Spinacia oleracea mRNA for peroxidase, prx11... 130 3e-39
emb|AI522935|AI522935 sa92c07.y1 Gm-c1004 Glycine max cDNA clone... 126 3e-39
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30 emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase. 121 9e-39
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emb|AW220074|AW220074 EST302557 tomato root during/after fruit s... 113 1e-38
emb|AW219160|AW219160 EST301642 tomato root during/after fruit s... 107 1e-38
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35 emb|AW625860|AW625860 EST319767 tomato radicle, 5 d post-imbibit... 105 1e-38
emb|AW219258|AW219258 EST301740 tomato root during/after fruit s... 112 2e-38
emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidase... 101 3e-38
emb|AW647641|AW647641 EST307119 tomato germinating seedlings, TA... 107 3e-38
emb|AI895098|AI895098 EST264541 tomato callus, TAMU Lycopersicon... 111 6e-38
40 emb|AW032353|AW032353 EST275807 tomato callus, TAMU Lycopersicon... 156 7e-38
emb|AW719266|AW719266 LjNEST1h8r Lotus japonicus nodule library,... 111 1e-37
emb|AI055188|AI055188 coau0003E18 Cotton Boll Abscission Zone cD... 99 2e-37
emb|AW689722|AW689722 NF023F03ST1F1000 Developing stem Medicago ... 123 2e-37
emb|AW686882|AW686882 NF003E08RT1F1000 Developing root Medicago ... 105 3e-37
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(2766 letters)

55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

60 Searching.....done

Score E

Sequences producing significant alignments:

(bits) Value

	emb AF053127 AF053127 Malus domestica leucine-rich receptor-like...	333	2e-91
	emb AW036763 AW036763 EST252152 tomato ovary, TAMU Lycopersicon ...	175	3e-77
5	emb AW036762 AW036762 EST252151 tomato ovary, TAMU Lycopersicon ...	173	3e-76
	gb U42444 U42444 Lycopersicon pimpinellifolium leucine rich repe...	198	1e-70
	emb A57130 A57130 Sequence 1 from Patent WO9531564.	198	1e-70
	gb U42445 U42445 Lycopersicon pimpinellifolium leucine rich repe...	198	1e-70
	emb A57133 A57133 Sequence 4 from Patent WO9531564.	198	1e-70
10	emb AF053998 AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ...	194	3e-68
	emb A67434 A67434 Sequence 7 from Patent WO9743429.	194	3e-68
	gb U77888 INU77888 Ipomoea nil receptor-like protein kinase (inr...	174	2e-66
	emb AF053995 AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ...	195	1e-65
	emb AF053993 AF053993 Lycopersicon esculentum disease resistance...	198	2e-65
15	emb A67429 A67429 Sequence 2 from Patent WO9743429.	198	2e-65
	emb A67428 A67428 Sequence 1 from Patent WO9743429.	198	2e-65
	emb AI485090 AI485090 EST243394 tomato ovary, TAMU Lycopersicon ...	177	9e-64
	emb AF053996 AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr...	180	8e-62
20	gb BE034258 BE034258 MH02C02 MH Mesembryanthemum crystallinum cD...	239	9e-62
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25	emb AF197947 AF197947 Glycine max receptor protein kinase-like p...	144	2e-59
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30	emb AW224642 AW224642 EST303085 tomato root, plants pre-anthesis...	123	6e-54
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	emb AW727470 AW727470 GA_Ea0012H16 Gossypium arboreum 7-10 dpa ...	86	5e-41
35	emb AW979740 AW979740 EST341365 tomato root deficiency, Cornell ...	151	2e-39
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45	emb AW267958 AW267958 EST306300 DSIR Medicago truncatula cDNA cl...	125	2e-34
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	emb AW156187 AW156187 se20f08.y1 Gm-cl015 Glycine max cDNA clone...	137	5e-31
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	emb AW224303 AW224303 EST301030 tomato fruit red ripe, TAMU Lyco...	128	1e-30
	emb AW035394 AW035394 EST281132 tomato callus, TAMU Lycopersicon...	136	1e-30
	emb AW930866 AW930866 EST356709 tomato fruit mature green, TAMU ...	84	1e-30
	emb AW932515 AW932515 EST358358 tomato fruit mature green, TAMU ...	78	1e-30
60	emb AI166936 AI166936 xylem.est.719 Poplar xylem Lambda ZAPII li...	85	1e-30
	emb AV419736 AV419736 AV419736 Lotus japonicus young plants (two...	135	1e-30

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 5 gb|BE060551|BE060551 HVSMEg0012J19f Hordeum vulgare pre-anthesis... 88 1e-29
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 85 3e-29
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 10 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 129 8e-29
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 20 emb|AI727547|AI727547 BNLGHi8389 Six-day Cotton fiber Gossypium ... 75 9e-28
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 25 emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7... 73 2e-27
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 (921 letters)

50 Database: plantfungal
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Searching.....done

55 Score E
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60 gb|U22147|HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1)... 279 e-123
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 emb|A26449|A26449 Soya mutant beta-1,3-glucanase cDNA. 259 e-117

- emb|A26447|A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f... 259 e-117
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 5 emb|X07280|NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca... 245 e-108
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 gb|L02212|PEABETAGLU Pea beta-1,3-glucanase gene, complete cds. 246 e-106
 gb|S51479|S51479 beta-1,3-glucanase [Pisum sativum=peas, cultiva... 246 e-106
 10 gb|U27179|MSU27179 Medicago sativa acidic glucanase mRNA, comple... 232 e-104
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 gb|M60403|TOBGLB13B Nicotiana tabacum glucan beta-1,3-glucosidas... 238 2e-94
 emb|AF034117|AF034117 Glycine max beta-1,3-glucanase 12 (SGlu12)... 180 3e-94
 gb|M59442|TOBGLUCA N.tabacum basic-1,3-glucanase gene, complete cds. 236 7e-94
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 25 gb|M59443|TOBGLUCB N.tabacum acidic beta-1,3-glucanase gene, com... 150 2e-92
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 gb|M60460|TOBPR2A Tobacco PR2 protein mRNA, complete cds. 149 4e-91
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 30 gb|U49454|PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene... 211 2e-89
 emb|AF227953|AF227953 Capsicum annuum basic beta-1,3-glucanase (... 224 4e-89
 emb|AF034106|AF034106 Glycine max beta-1,3-glucanase 1 (SGlu1) g... 221 2e-88
 emb|AF141654|AF141654 Nicotiana tabacum beta-1,3-glucanase (GGL4... 139 3e-88
 gb|M60463|TOBGL153A Tobacco GL153 protein mRNA, complete cds. 139 3e-88
 35 gb|M20620|TOBGLUBC N.tabacum beta-1,3-glucanase mRNA, clone pGL43. 238 4e-88
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 emb|X54431|NTSP41B Tobacco sp41b mRNA for (1-3)-beta-glucanase. 136 6e-87
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 gb|M60464|TOBB13G Tobacco beta-1,3-glucanase mRNA, complete cds. 136 1e-86
 40 emb|AJ000081|CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase. 113 2e-86
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 emb|X54430|NTSP41A Tobacco sp41a mRNA for (1-3)-beta-glucanase. 135 8e-86
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 dbj|E02108|E02108 cDNA sequence coding for beta-1,3-endoglucanase. 167 3e-84
 45 gb|M37753|SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple... 167 3e-84
 emb|AJ009932|STAJ9932 Solanum tuberosum mRNA for beta-1,3-glucan... 144 4e-84
 emb|AW034632|AW034632 EST278316 tomato callus, TAMU Lycopersicon... 188 1e-82
 gb|U41323|GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c... 169 3e-82
 emb|AW033770|AW033770 EST277341 tomato callus, TAMU Lycopersicon... 186 5e-82
 50 gb|M80604|TOMB13GLUA Lycopersicon esculentum beta-1,3-glucanase ... 142 5e-82
 emb|X74905|LEQA L.esculentum TomQ'a mRNA for beta(1,3)glucanase. 128 4e-79
 emb|AI896001|AI896001 EST265444 tomato callus, TAMU Lycopersicon... 175 9e-79
 emb|AW034584|AW034584 EST278268 tomato callus, TAMU Lycopersicon... 226 9e-79
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- emb|AW216637|AW216637 EST295351 tomato callus, TAMU Lycopersicon... 164 2e-75
 emb|AW032447|AW032447 EST276006 tomato callus, TAMU Lycopersicon... 227 2e-74
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 5 gb|M63634|TOBGCBREG Nicotiana plumbaginifolia beta(1,3)-glucanas... 250 9e-73
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 gb|M13237|BLYGLUCB Barley beta glucanase mRNA. 158 7e-68
 25 emb|Z15131|ASBGLUCAN A.sativa mRNA for beta glucanase. 158 9e-68
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 30 emb|AW032451|AW032451 EST276010 tomato callus, TAMU Lycopersicon... 136 3e-67
 emb|AW031353|AW031353 EST274807 tomato callus, TAMU Lycopersicon... 136 3e-67
 emb|AI895981|AI895981 EST265424 tomato callus, TAMU Lycopersicon... 136 3e-67
 gb|U73709|VVU73709 Vitis vinifera beta-1,3-glucanase mRNA, parti... 244 3e-67
 emb|Z22874|TABETGLUB T.aestivum (1,3;1,4) beta glucanase mRNA, c... 160 3e-67
 35 emb|AF034114|AF034114 Glycine max beta-1,3-glucanase 9 (SGlu9) p... 119 7e-67

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 gb|aac49117.1|(u18993) tryptophan synthase alpha chain [arabidopsis
 40 thaliana] /blast_score 1.00e-158 /ec_number /family /chip nova
 /gb_link /ncgi
 (939 letters)

Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 50 Sequences producing significant alignments: (bits) Value

- emb|AW730233|AW730233 GA_Ea0014B16 Gossypium arboreum 7-10 dpa ... 352 5e-98
 emb|AW649960|AW649960 EST328414 tomato germinating seedlings, TA... 308 4e-83
 emb|AW621664|AW621664 EST312462 tomato root during/after fruit s... 290 1e-77
 55 emb|AW031327|AW031327 EST274781 tomato callus, TAMU Lycopersicon... 282 3e-75
 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 271 4e-72
 emb|AW775853|AW775853 EST334918 DSIL Medicago truncatula cDNA cl... 264 9e-70
 emb|Z21642|CHASTRNAA Antithamnion sp. Chloroplast trnK, trnE, trpA... 255 4e-67
 gb|BE124387|BE124387 EST393422 GVN Medicago truncatula cDNA clon... 227 9e-59
 60 gb|BE121873|BE121873 894015F07.y1 C. reinhardtii CC-1690, normal... 227 1e-58
 emb|AF022186|AF022186 Cyanidium caldarium strain RK1 chloroplast... 220 1e-56

- emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53
emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49
dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49
emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49
5 emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47
dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46
emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46
dbj|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45
gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43
10 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42
emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42
emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38
emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38
emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32
15 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycopersicon... 138 5e-32
emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 74 3e-30
emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26
emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21
emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19
20 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17
emb|AF084886|AF084886 Neurospora crassa 314-448A mutant tryptoph... 68 9e-11
emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptop... 53 4e-10
emb|AF084880|AF084880 Neurospora crassa EMSG9-9A mutant tryptoph... 66 5e-10
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25 emb|AF084884|AF084884 Neurospora crassa 314-722A mutant tryptoph... 64 1e-09
emb|AF084883|AF084883 Neurospora crassa 314-709A mutant tryptoph... 64 1e-09
emb|AF084882|AF084882 Neurospora crassa 314-682A mutant tryptoph... 64 1e-09
emb|AF084881|AF084881 Neurospora crassa 314-693A mutant tryptoph... 64 2e-09
emb|AF084889|AF084889 Neurospora crassa 314-492-2A mutant trypto... 53 3e-09
30 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08
emb|AU011013|AU011013 AU011013 Schizosaccharomyces pombe late lo... 54 2e-06
emb|AW693052|AW693052 NF059C08ST1F1065 Developing stem Medicago ... 51 1e-05
emb|AV390244|AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla... 49 4e-05
emb|AW616467|AW616467 EST322878 L. hirsutum trichome, Cornell Un... 48 7e-05
35 emb|AL354022|P761R Leishmania major Friedlin PAC P761 right end-... 44 0.002
gb|M91656|CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1... 43 0.005
emb|AQ903789|AQ903789 GSSTc04230 Trypanosome cruzi random genomi... 35 0.24
emb|AW727215|AW727215 GA_Ea0023N23 Gossypium arboreum 7-10 dpa ... 36 0.52
gb|M91654|CCITRP03 Coprinus cinereus tryptophan synthetase (TRP1... 36 0.52
40 emb|AW728975|AW728975 GA_Ea0018P19 Gossypium arboreum 7-10 dpa ... 35 0.64
emb|AL139794|LMFP1105 Leishmania major Friedlin chromosome 4 PAC... 35 0.87
emb|AW926438|AW926438 HVSMEg0007D14 Hordeum vulgare pre-anthesis... 34 1.2
emb|AA965348|AA965348 e9d04a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
gb|U12630|ENU12630 Emericella nidulans R153 core histone H3 (H3)... 34 1.3
45 emb|AI007494|AI007494 e9c09a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
emb|AA787433|AA787433 n3d04a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
emb|X55548|ANH3GENE A.nidulans gene for core histone for H3. 34 1.3
emb|AQ396426|AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P... 34 1.6
emb|AF262997|AF262997 Ricinus communis NADP-dependent malic prot... 34 1.6
50 gb|M19025|CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c... 34 1.6
emb|AF084888|AF084888 Neurospora crassa 656-2A mutant tryptophan... 31 1.7
emb|AF084887|AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta... 31 1.7
emb|AW694774|AW694774 NF080A05ST1F1036 Developing stem Medicago ... 34 1.8
emb|Y18012|TVE18012 Trametes versicolor mRNA for laccase. 33 2.3
55 emb|AQ500614|AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc... 33 2.5
emb|AW187498|AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium ... 33 3.1
emb|AW187530|AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium ... 33 3.1
emb|AW694072|AW694072 NF072B12ST1F1096 Developing stem Medicago ... 33 3.1
emb|AW186883|AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium ... 33 3.1
60 emb|AW187537|AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ... 33 3.1
emb|AW187474|AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium ... 33 3.1

emb|AA167859|AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor... 33 3.5
 emb|AV421993|AV421993 AV421993 Lotus japonicus young plants (two... 33 4.3
 emb|AF129874|AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp... 33 4.3
 emb|AL112679|CNS01AA7 Botrytis cinerea strain T4 cDNA library un... 33 4.7
 5 gb|BE028433|BE028433 EtESTea78d07.y1 Eimeria M5-6 Merozoite stag... 32 5.9
 emb|AI166784|AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li... 32 5.9
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 10 emb|AI757375|AI757375 EtESTea32d03.y1 Eimeria S5-2 Sporozoite st... 32 5.9
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 emb|AI973878|AI973878 sd13a09.y1 Gm-c1020 Glycine max cDNA clone... 32 5.9
 dbj|D85261|D85261 Plasmodium vivax clone TD439B DNA for merozoit... 32 5.9
 dbj|D85251|D85251 Plasmodium vivax clone TD207B DNA for merozoit... 32 5.9
 15 emb|Z69381|SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom... 32 6.5
 emb|Z71509|SCYNL233W S.cerevisiae chromosome XIV reading frame O... 32 6.5
 emb|AW707662|AW707662 832011E08.y1 C. reinhardtii CC-125 nutrien... 28 7.3
 emb|AF083075|AF083075 Fusarium oxysporum f. sp. lycopersici exop... 32 8.1
 emb|AV411934|AV411934 AV411934 Lotus japonicus young plants (two... 32 8.1
 20 emb|AW703740|AW703740 sk23g09.y1 Gm-c1028 Glycine max cDNA clone... 32 8.1
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 emb|AV419698|AV419698 AV419698 Lotus japonicus young plants (two... 32 8.1
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 25 emb|AV408860|AV408860 AV408860 Lotus japonicus young plants (two... 32 8.1
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 emb|AW720540|AW720540 LjNEST18h4r Lotus japonicus nodule library... 32 8.1
 emb|X77895|CPGPRNL28 G.pyrenaica chloroplast trnL gene intron. 32 8.1
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 /blast_score 5.00e-55 /ec_number /family /chip nova /gb_link
 35 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|z97339|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|z97339|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|z97339|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?z97339>
 (441 letters)

40 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

45 Score E
 Sequences producing significant alignments: (bits) Value

emb|AW685774|AW685774 NF035A03NR1F1000 Nodulated root Medicago t... 123 6e-28
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 50 emb|AW687794|AW687794 NF013E08RT1F1066 Developing root Medicago ... 89 3e-23
 emb|AW310121|AW310121 sf31d07.x1 Gm-c1028 Glycine max cDNA clone... 68 3e-19
 emb|AW704640|AW704640 sk54f05.y1 Gm-c1019 Glycine max cDNA clone... 68 3e-19
 emb|AW395252|AW395252 sh45g06.y1 Gm-c1017 Glycine max cDNA clone... 68 3e-19
 emb|AW704612|AW704612 sk54c11.y1 Gm-c1019 Glycine max cDNA clone... 68 3e-19
 55 emb|AT000508|AT000508 AT000508 Brassica rapa guard cell Brassica... 50 2e-18
 emb|AW704218|AW704218 sk17c12.y1 Gm-c1028 Glycine max cDNA clone... 63 3e-17
 emb|AW423428|AW423428 sh66f08.y1 Gm-c1015 Glycine max cDNA clone... 63 1e-16
 emb|AW687188|AW687188 NF006H09RT1F1079 Developing root Medicago ... 82 3e-15
 emb|AW684973|AW684973 NF023G04NR1F1000 Nodulated root Medicago t... 68 1e-13
 60 emb|AW233878|AW233878 sf31d07.y1 Gm-c1028 Glycine max cDNA clone... 69 3e-13
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	emb AI437669 AI437669 sa38a11.y1 Gm-cl004 Glycine max cDNA clone...	48	1e-11
	emb AW348644 AW348644 GM210003A11A8R Gm-r1021 Glycine max cDNA 3...	48	2e-11
	emb AW687565 AW687565 NF011A04RT1F1024 Developing root Medicago ...	48	2e-11
5	gb BE033951 BE033951 MG02E05 MG Mesembryanthemum crystallinum cD...	44	3e-10
	emb AW185776 AW185776 se59e03.y1 Gm-cl019 Glycine max cDNA clone...	51	2e-08
	emb AI930953 AI930953 sb45c07.y1 Gm-cl015 Glycine max cDNA clone...	48	4e-08
	emb AI440599 AI440599 sa68c05.y1 Gm-cl004 Glycine max cDNA clone...	48	6e-08
	emb AW394608 AW394608 sh33e11.y1 Gm-cl017 Glycine max cDNA clone...	46	2e-07
10	emb AW284126 AW284126 LG1_262_A05.g1_A002 Light Grown 1 (LG1) So...	55	3e-07
	emb AI960446 AI960446 sc84a10.y1 Gm-cl018 Glycine max cDNA clone...	48	4e-06
	emb AI794716 AI794716 sb68b06.y1 Gm-cl019 Glycine max cDNA clone...	48	5e-06
	gb BE024111 BE024111 sm96h03.y1 Gm-cl015 Glycine max cDNA clone ...	48	9e-06
	emb Z99969 MAZ99969 Musa acuminata mRNA for putative beta-1,3-gl...	41	6e-05
15	emb AV412437 AV412437 AV412437 Lotus japonicus young plants (two...	47	9e-05
	emb AV427297 AV427297 AV427297 Lotus japonicus young plants (two...	46	2e-04
	emb AW666090 AW666090 sk32a11.y1 Gm-cl028 Glycine max cDNA clone...	42	2e-04
	emb AW277478 AW277478 sf82e11.y1 Gm-cl019 Glycine max cDNA clone...	37	4e-04
	emb AW775954 AW775954 EST335019 DSIL Medicago truncatula cDNA cl...	42	7e-04
20	gb BE122569 BE122569 Ljimpest29-344-g6 Ljirnp Lambda HybriZap t...	43	0.001
	emb AW299135 AW299135 EST305809 KV2 Medicago truncatula cDNA clo...	43	0.002
	emb AW423359 AW423359 sh06g04.y1 Gm-cl016 Glycine max cDNA clone...	41	0.004
	emb AW171748 AW171748 N100642e rootphos(-) Medicago truncatula c...	40	0.014
	emb AW285241 AW285241 LG1_236_C10.g1_A002 Light Grown 1 (LG1) So...	39	0.026
25	emb AW747074 AW747074 WS1_65_A07.g1_A002 Water-stressed 1 (WS1) ...	39	0.026
	emb AW649685 AW649685 EST328139 tomato germinating seedlings, TA...	38	0.036
	emb AW299176 AW299176 EST305986 KV2 Medicago truncatula cDNA clo...	38	0.036
	emb AW220014 AW220014 EST302497 tomato root during/after fruit s...	38	0.050
	gb C96140 C96140 C96140 Marchantia polymorpha immature sex organ...	38	0.050
30	emb AW625648 AW625648 EST319555 tomato radicle, 5 d post-imbibit...	38	0.050
	emb AW926780 AW926780 HVSMEg0008D23 Hordeum vulgare pre-anthesis...	37	0.094
	gb L05906 PMCMMSGF Pneumocystis carinii (clone GP3) major surface...	36	0.18
	emb AW333354 AW333354 S20F5 AGS-1 Pneumocystis carinii f. sp. ca...	36	0.18
	emb Z98595 SPAC11E3 S.pombe chromosome I cosmid c11E3.	35	0.24
35	emb AW725520 AW725520 GA_Ea0018G22 Gossypium arboreum 7-10 dpa ...	35	0.46
	gb BE052896 BE052896 GA_Ea0025I06f Gossypium arboreum 7-10 dpa ...	35	0.46
	emb AW309936 AW309936 sf26g12.x1 Gm-cl028 Glycine max cDNA clone...	35	0.46
	emb AW310120 AW310120 sf31d06.x1 Gm-cl028 Glycine max cDNA clone...	35	0.46
	emb AW233798 AW233798 sf26g12.y1 Gm-cl028 Glycine max cDNA clone...	35	0.46
40	gb BE053040 BE053040 GA_Ea0015D14f Gossypium arboreum 7-10 dpa ...	35	0.46
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	emb AI731906 AI731906 BNLGHi11249 Six-day Cotton fiber Gossypium...	35	0.46
	gb BE054609 BE054609 GA_Ea0006A14f Gossypium arboreum 7-10 dpa ...	35	0.46
	emb AW278505 AW278505 sf45c08.y1 Gm-cl009 Glycine max cDNA clone...	35	0.46
45	emb AC013353 AC013353 Trypanosoma brucei chromosome VI clone RPC...	34	0.63
	emb AI728996 AI728996 BNLGHi12315 Six-day Cotton fiber Gossypium...	34	0.63
	emb AW691828 AW691828 NF044F04ST1F1000 Developing stem Medicago ...	34	0.63
	emb AI729057 AI729057 BNLGHi12476 Six-day Cotton fiber Gossypium...	34	0.63
	emb AI731500 AI731500 BNLGHi9982 Six-day Cotton fiber Gossypium ...	34	0.63
50	emb AQ660279 AQ660279 Sheared DNA-3L23.TF Sheared DNA Trypanosom...	34	0.63
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	emb AI725456 AI725456 BNLGHi12219 Six-day Cotton fiber Gossypium...	34	0.63
	emb AQ656131 AQ656131 Sheared DNA-27G20.TF Sheared DNA Trypanoso...	34	0.63
	emb AI731231 AI731231 BNLGHi8954 Six-day Cotton fiber Gossypium ...	34	0.87
55	emb AL035477 PFMAL4P4 Plasmodium falciparum chromosome 4 strain ...	34	0.87
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	emb AI727451 AI727451 BNLGHi8020 Six-day Cotton fiber Gossypium ...	34	0.87
60	emb AW620830 AW620830 sj47b03.y1 Gm-cl033 Glycine max cDNA clone...	28	1.1
	dbj D63449 YSCATF1A Yeast ATF1 gene for alcohol acetyltransferas...	33	1.2

dbj|E08050|E08050 cDNA encoding beer yeast alcohol acetyltransfe... 33 1.2
 dbj|E06817|E06817 DNA encoding alcohol acetyltransferase 1. 33 1.2
 dbj|D26554|YSCATF1 Yeast ATF1 gene for alcohol acetyltransferase... 33 1.2
 dbj|E08049|E08049 cDNA encoding sake yeast alcohol acetyltransfe... 33 1.2
 5 dbj|E06816|E06816 DNA encoding alcohol acetyltransferase 1. 33 1.2
 emb|Z75285|SCYOR377W *S.cerevisiae* chromosome XV reading frame OR... 33 1.2
 emb|AW725476|AW725476 GA_Ea0018C14 *Gossypium arboreum* 7-10 dpa ... 33 1.6
 emb|AI812453|AI812453 11C3 Pine Lambda Zap Xylem library *Pinus t...* 33 1.6
 emb|AW459992|AW459992 si07c04.y1 *Gm-c1029* Glycine max cDNA clone... 33 1.6
 10 emb|X01777|HVB3HORD Barley mRNA fragment for B3-hordein. 33 1.6
 emb|AQ449927|AQ449927 500006A04.x1 CpIOWAM13mp18gDNA1 *Cryptospor...* 33 1.6
 emb|AE001274|AE001274 *Leishmania major* chromosome 1, complete se... 30 2.2
 emb|AL031261|SPBC3H7 *S.pombe* chromosome II cosmid c3H7. 32 2.2
 emb|AI812374|AI812374 1F12 Pine Lambda Zap Xylem library *Pinus t...* 32 2.2
 15 emb|AI728744|AI728744 BNLGHi11492 Six-day Cotton fiber *Gossypium...* 32 2.2
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 emb|AW925749|AW925749 HVSMEg0005G16 *Hordeum vulgare* pre-anthesis... 32 3.1
 emb|AQ411951|AQ411951 CpG0926A CpIOWAgDNA1 *Cryptosporidium parvu...* 32 3.1
 emb|AQ935548|AQ935548 CpG2528A CpIOWAgDNA1 *Cryptosporidium parvu...* 32 3.1
 20 emb|AQ411952|AQ411952 CpG0926B CpIOWAgDNA1 *Cryptosporidium parvu...* 32 3.1
 gb|B67221|B67221 CpG0036A CpIOWAgDNA1 *Cryptosporidium parvum* gen... 32 3.1
 emb|AW030301|AW030301 EST273556 tomato callus, TAMU *Lycopersicon...* 31 4.2
 emb|AL160371|LMFLCHR15 *Leishmania major* Friedlin assembled chrom... 31 4.2
 emb|AL122012|LMFL8342 *Leishmania major* Friedlin chromosome 23 co... 31 4.2
 25 emb|X60772|GMOLEOA *G.max* mRNA for 24 kDa oleosin isoform (partia... 31 4.2

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 30 /blast_score 1.00e-111 /ec_number /family /chip nova /gb_link /ncgi

(592 letters)

Database: plantfungal
 35 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 40 Sequences producing significant alignments: (bits) Value

emb|X90695|MSRNAPE02 *M.sativa* mRNA for peroxidase 2. 339 1e-92
 emb|AJ011939|TRE011939 *Trifolium repens* mRNA for peroxidase. 335 2e-91
 emb|Y10469|SOPR XR8 *S.oleracea* mRNA for peroxidase, clone PC55. 332 2e-90
 45 emb|AI487510|AI487510 EST245832 tomato ovary, TAMU *Lycopersicon ...* 327 5e-89
 emb|AI486784|AI486784 EST245106 tomato ovary, TAMU *Lycopersicon ...* 327 5e-89
 emb|AI895842|AI895842 EST265285 tomato callus, TAMU *Lycopersicon...* 325 1e-88
 emb|AW032442|AW032442 EST276001 tomato callus, TAMU *Lycopersicon...* 325 2e-88
 gb|L36158|ALFPXDD *Medicago sativa* peroxidase (pxdD) mRNA, 3' end. 320 6e-87
 50 emb|AW216351|AW216351 EST295095 tomato callus, TAMU *Lycopersicon...* 319 1e-86
 emb|AW691003|AW691003 NF040C11ST1F1000 Developing stem *Medicago ...* 319 2e-86
 emb|AW625601|AW625601 EST319508 tomato radicle, 5 d post-imbibit... 318 3e-86
 gb|BE124281|BE124281 EST394406 DSIL *Medicago truncatula* cDNA clo... 314 4e-85
 emb|AI894487|AI894487 EST263930 tomato callus, TAMU *Lycopersicon...* 307 4e-83
 55 emb|AW666274|AW666274 sk34e11.y1 *Gm-c1028* Glycine max cDNA clone... 304 4e-82
 emb|AI897419|AI897419 EST266862 tomato ovary, TAMU *Lycopersicon ...* 295 2e-79
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 emb|AW666298|AW666298 sk34h04.y1 *Gm-c1028* Glycine max cDNA clone... 292 2e-78
 emb|AW030788|AW030788 EST274043 tomato callus, TAMU *Lycopersicon...* 292 2e-78
 60 emb|AW031625|AW031625 EST275079 tomato callus, TAMU *Lycopersicon...* 291 3e-78
 emb|AW278809|AW278809 sf98g02.y1 *Gm-c1019* Glycine max cDNA clone... 200 3e-78

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	emb AW216725 AW216725 EST295439 tomato callus, TAMU Lycopersicon...	287	4e-77
	emb AW035689 AW035689 EST281843 tomato callus, TAMU Lycopersicon...	286	1e-76
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(940 letters)

Database: plantfungal

30 661,018 sequences; 426,114,510 total letters

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35 Sequences producing significant alignments: (bits) Value

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(940 letters)

Database: plantfungal

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	emb AW033257 AW033257 EST276828 tomato callus, TAMU Lycopersicon...	61 1e-18
	emb AI771191 AI771191 EST252387 tomato ovary, TAMU Lycopersicon ...	61 1e-18
30	emb AV424248 AV424248 AV424248 Lotus japonicus young plants (two...	73 1e-18
	emb AW032357 AW032357 EST275811 tomato callus, TAMU Lycopersicon...	61 1e-18
	emb AW706014 AW706014 sk64g01.y1 Gm-c1016 Glycine max cDNA clone...	66 3e-18
	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA...	62 4e-18
	emb AW622660 AW622660 EST313460 tomato root during/after fruit s...	62 5e-18
35	emb AV411226 AV411226 AV411226 Lotus japonicus young plants (two...	71 6e-18
	emb AV419929 AV419929 AV419929 Lotus japonicus young plants (two...	71 6e-18
	gb BE058334 BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone ...	72 8e-18
	emb AI894999 AI894999 EST264442 tomato callus, TAMU Lycopersicon...	62 2e-17
	emb AV423254 AV423254 AV423254 Lotus japonicus young plants (two...	76 3e-17
40	emb AW755973 AW755973 sl11h06.y1 Gm-c1036 Glycine max cDNA clone...	70 4e-17
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	emb AV413163 AV413163 AV413163 Lotus japonicus young plants (two...	68 7e-17
45	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon...	54 3e-16
	emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t...	70 3e-16
	emb AV422432 AV422432 AV422432 Lotus japonicus young plants (two...	70 3e-16
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50	emb AI736394 AI736394 sb28a06.y1 Gm-c1009 Glycine max cDNA clone...	64 7e-16
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	emb AV411832 AV411832 AV411832 Lotus japonicus young plants (two...	64 9e-16
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55	emb AV416264 AV416264 AV416264 Lotus japonicus young plants (two...	62 4e-15
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5 emb|AV423498|AV423498 AV423498 Lotus japonicus young plants (two... 58 5e-14
emb|AV428398|AV428398 AV428398 Lotus japonicus young plants (two... 58 5e-14
emb|AI484099|AI484099 EST249970 tomato ovary, TAMU Lycopersicon ... 62 5e-14
emb|AW738399|AW738399 EST339826 tomato flower buds, anthesis, Co... 62 5e-14

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emb|caal7150.1| (al021890) putative protein [arabidopsis thaliana]
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(426 letters)

15
Database: plantfungal
661,018 sequences; 426,114,510 total letters

20
Searching.....done

Score E
Sequences producing significant alignments: (bits) Value

25 emb|AW667752|AW667752 GA_Ea0010I06 Gossypium arboreum 7-10 dpa ... 247 4e-65
emb|AW224013|AW224013 EST300824 tomato fruit red ripe, TAMU Lyco... 244 3e-64
emb|AW223703|AW223703 EST300514 tomato fruit red ripe, TAMU Lyco... 244 3e-64
emb|AW441269|AW441269 EST310665 tomato fruit red ripe, TAMU Lyco... 244 3e-64
emb|AW034892|AW034892 EST279121 tomato callus, TAMU Lycopersicon... 244 3e-64
30 gb|BE124622|BE124622 EST393657 GVN Medicago truncatula cDNA clon... 243 5e-64
emb|AW747419|AW747419 WS1_68_E10.b1_A002 Water-stressed 1 (WS1) ... 242 1e-63
gb|BE033541|BE033541 MF02E10 MF Mesembryanthemum crystallinum cD... 242 1e-63
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emb|AW730496|AW730496 GA_Ea0026O23 Gossypium arboreum 7-10 dpa ... 242 1e-63
emb|AI960575|AI960575 sc86c01.y1 Gm-c1018 Glycine max cDNA clone... 240 4e-63
35 emb|AW706639|AW706639 sj62h07.y1 Gm-c1033 Glycine max cDNA clone... 240 4e-63
emb|AW568285|AW568285 si69g11.y1 Gm-r1030 Glycine max cDNA clone... 240 5e-63
emb|AW186193|AW186193 se64g04.y1 Gm-c1019 Glycine max cDNA clone... 240 5e-63
gb|BE020351|BE020351 sm43b05.y1 Gm-c1028 Glycine max cDNA clone ... 240 5e-63
40 emb|AW981480|AW981480 EST392633 DSIL Medicago truncatula cDNA cl... 239 1e-62
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emb|AI855496|AI855496 sc16h05.y1 Gm-c1013 Glycine max cDNA clone... 232 8e-61
emb|AW132618|AW132618 se06f04.y1 Gm-c1013 Glycine max cDNA clone... 222 9e-58
emb|AW760599|AW760599 sl52d09.y1 Gm-c1027 Glycine max cDNA clone... 217 3e-56
45 emb|AI965929|AI965929 sc79h07.y1 Gm-c1018 Glycine max cDNA clone... 199 1e-50
emb|AV398027|AV398027 AV398027 Chlamydomonas reinhardtii C9 Chla... 127 9e-50
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emb|AW738874|AW738874 gb03e09.y1 Moss EST library PPN Physcomitr... 184 2e-46
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50 emb|AW739119|AW739119 gb26a12.y1 Moss EST library PPN Physcomitr... 173 7e-43
emb|AL049558|SPBC216 S.pombe chromosome II cosmid c216. 84 1e-38
emb|AV408412|AV408412 AV408412 Lotus japonicus young plants (two... 157 5e-38
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55 emb|AI495735|AI495735 sb15f07.y1 Gm-c1004 Glycine max cDNA clone... 154 4e-37
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emb|AI777814|AI777814 EST258693 tomato susceptible, Cornell Lyco... 143 8e-36
emb|AI166395|AI166395 xylem.est.231 Poplar xylem Lambda ZAPII li... 148 3e-35
emb|AW335287|AW335287 S45D10 AGS-1 Pneumocystis carinii f. sp. c... 76 5e-35
60 emb|AI026521|AI026521 TENU0733 T. cruzi epimastigote normalized ... 124 3e-31
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- emb|AA740047|AA740047 812 PtIFG2 Pinus taeda cDNA clone 9275M 3'... 126 1e-28
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 emb|AW222361|AW222361 EST299172 tomato fruit red ripe, TAMU Lyco... 89 7e-25
 5 emb|X59720|SCCHRIII S.cerevisiae chromosome III complete DNA seq... 80 8e-25
 emb|AW617209|AW617209 EST323620 L. hirsutum trichome, Cornell Un... 89 1e-24
 emb|AW775277|AW775277 EST334342 DSIL Medicago truncatula cDNA cl... 85 3e-24
 emb|AI730110|AI730110 BNLGHi6160 Six-day Cotton fiber Gossypium ... 90 3e-23
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 10 emb|AW222638|AW222638 EST299449 tomato fruit red ripe, TAMU Lyco... 89 2e-22
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 emb|AL160493|LMFLCHR26 Leishmania major Friedlin assembled chrom... 94 5e-19
 emb|AW222387|AW222387 EST299198 tomato fruit red ripe, TAMU Lyco... 91 3e-18
 emb|AW476911|AW476911 ga38h10.y1 Moss EST library PPU Physcomitr... 91 3e-18
 20 emb|AW220746|AW220746 EST297215 tomato fruit mature green, TAMU ... 89 2e-17
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 emb|AW650769|AW650769 EST329223 tomato germinating seedlings, TA... 72 3e-12
 25 emb|AT000681|AT000681 AT000681 Brassica rapa guard cell Brassica... 61 3e-12
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 emb|AW907238|AW907238 EST343361 potato stolon, Cornell Universit... 63 9e-10
 30 emb|AZ215418|AZ215418 Sheared DNA-79B7.TF Sheared DNA Trypanosom... 54 2e-09
 emb|AA842826|AA842826 CFB57 Floral bud cDNA library of Hot peppe... 59 2e-08
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 35 emb|Z72847|SCYGR062C S.cerevisiae chromosome VII reading frame O... 35 0.23
 emb|AW156147|AW156147 se20b05.y1 Gm-cl015 Glycine max cDNA clone... 35 0.23
 gb|M83672|YSCSPT4A Saccharomyces cerevisiae zinc finger protein ... 35 0.23
 gb|U59742|SCU59742 Saccharomyces cerevisiae Cox18p (COX18) gene,... 35 0.23
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 40 emb|AQ945483|AQ945483 Sheared DNA-44G3.TR Sheared DNA Trypanosom... 32 2.1
 emb|AI374297|AI374297 T6531 MVAT4 bloodstream form of serodeme W... 26 2.3
 emb|AW030467|AW030467 EST273722 tomato callus, TAMU Lycopersicon... 31 4.0
 emb|AW624450|AW624450 EST322395 tomato flower buds 3-8 mm, Corne... 31 4.0
 emb|AW979733|AW979733 EST341357 tomato root deficiency, Cornell ... 31 4.0
 45 emb|AW737565|AW737565 EST338992 tomato flower buds, anthesis, Co... 31 4.0
 emb|AW679327|AW679327 WS1_23_A02.g1_A002 Water-stressed 1 (WS1) ... 31 5.5
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 emb|AF077352|AF077352 Chlamydomonas reinhardtii myosin heavy cha... 30 7.6
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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002391|/ncgi)
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Score E

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	emb AB022732 AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy...	334	e-148
	emb AJ012581 CAR012581 Cicer arietinum mRNA for cytochrome P450.	333	e-147
	emb AB025016 AB025016 Lotus japonicus mRNA for cytochrome P450, ...	309	e-145
	emb AJ000478 HTCYP81L Helianthus tuberosus mRNA for cytochrome P...	227	e-136
15	emb AJ000477 HTCYP81C Helianthus tuberosus mRNA for cytochrome P...	227	e-135
	emb AJ239051 CAR239051 Cicer arietinum mRNA for cytochrome P450 ...	236	7e-85
	emb AJ249800 CAR249800 Cicer arietinum partial mRNA for cytochro...	299	3e-80
	emb AW185361 AW185361 se90e02.y1 Gm-c1027 Glycine max cDNA clone...	272	4e-72
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25	emb AW171738 AW171738 N100632e rootphos(-) Medicago truncatula c...	245	6e-64
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	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber Gossypium...	183	4e-58
	emb AI725744 AI725744 BNLGHi12803 Six-day Cotton fiber Gossypium...	182	1e-57
	emb AW257188 AW257188 EST305325 KV2 Medicago truncatula cDNA clo...	189	1e-56
30	emb AW329224 AW329224 N200436e rootphos(-) Medicago truncatula c...	220	2e-56
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	emb AI776121 AI776121 EST257209 tomato resistant, Cornell Lycopersicon...	106	3e-44
	emb AW687247 AW687247 NF007E11RT1F1086 Developing root Medicago ...	178	8e-44
	emb AW616086 AW616086 EST296847 L. hirsutum trichome, Cornell Un...	142	1e-43
	emb AW617900 AW617900 EST324311 L. hirsutum trichome, Cornell Un...	142	1e-43
60	emb AW031264 AW031264 EST274639 tomato callus, TAMU Lycopersicon...	143	5e-43
	emb AW309826 AW309826 sf25c03.x1 Gm-c1028 Glycine max cDNA clone...	175	8e-43

- dbj|E13663|E13663 cDNA encoding cytochrome P450 which is induced... 103 8e-43
 dbj|D83968|SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... 103 8e-43
 emb|AW617323|AW617323 EST323734 *L. hirsutum* trichome, Cornell Un... 138 1e-42
 emb|AW617605|AW617605 EST324016 *L. hirsutum* trichome, Cornell Un... 138 1e-42
 5 emb|Y10492|GMC450CP5 *G.max* mRNA for putative cytochrome P450, cl... 105 2e-42
 emb|AF195809|AF195809 *Vigna radiata* isoflavone synthase 4 (ifs4)... 100 3e-42
 emb|AF155332|AF155332 *Petunia x hybrida* flavonoid 3'-hydroxylase... 155 3e-42
 emb|AF135484|AF135484 *Glycine max* cytochrome P450 monooxygenase ... 100 4e-42
 emb|AF195807|AF195807 *Vigna radiata* isoflavone synthase 2 (ifs2)... 100 4e-42
 10 emb|AW616809|AW616809 EST323220 *L. hirsutum* trichome, Cornell Un... 137 4e-42
 emb|AF195811|AF195811 *Trifolium pratense* isoflavone synthase 2 (... 100 5e-42
 emb|AF195810|AF195810 *Trifolium pratense* isoflavone synthase 1 (... 100 5e-42
 emb|AF195808|AF195808 *Vigna radiata* isoflavone synthase 3 (ifs3)... 100 5e-42
 emb|AF195817|AF195817 *Beta vulgaris* isoflavone synthase 2 (ifs2)... 100 5e-42
 15 emb|AF195800|AF195800 *Medicago sativa* isoflavone synthase 1 (ifs... 100 5e-42
 emb|AF195802|AF195802 *Medicago sativa* isoflavone synthase 3 (ifs... 100 5e-42
 emb|AI973839|AI973839 sd11c06.y1 *Gm-c1020* *Glycine max* cDNA clone... 103 5e-42
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 20 emb|Y10491|GMC450CP4 *G.max* mRNA for putative cytochrome P450, cl... 144 8e-42
 emb|AB015762|AB015762 *Nicotiana tabacum* mRNA for cytochrome P450... 155 8e-42
 emb|AF124372|AF124372 *Nicotiana tabacum* NT7 mRNA, partial cds. 135 8e-42
 emb|AF195798|AF195798 *Glycine max* isoflavone synthase 1 (ifs1) m... 100 1e-41
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 emb|AF195812|AF195812 *Pisum sativum* isoflavone synthase 1 (ifs1)... 100 2e-41
 emb|AW728802|AW728802 GA_Ea0028112 *Gossypium arboreum* 7-10 dpa ... 153 3e-41
 emb|AW617833|AW617833 EST324232 *L. hirsutum* trichome, Cornell Un... 142 3e-41
 30 emb|AW617284|AW617284 EST323695 *L. hirsutum* trichome, Cornell Un... 142 3e-41
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 40 emb|AF195805|AF195805 *Lens culinaris* isoflavone synthase 2 (ifs2... 100 2e-40
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 emb|Y10982|GMP450CP6 *Glycine max* mRNA for cytochrome P450-like p... 150 4e-40
 emb|AW255096|AW255096 ML139 peppermint glandular trichome *Mentha*... 154 5e-40
 45 emb|AF195804|AF195804 *Lens culinaris* isoflavone synthase 1 (ifs1... 96 6e-40
 emb|AF195816|AF195816 *Beta vulgaris* isoflavone synthase 1 (ifs1)... 99 6e-40
 emb|AJ243804|CAR243804 *Cicer arietinum* mRNA for cytochrome P450 ... 96 8e-40

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 thaliana] /blast_score 1.00e-133 /ec_number /family dehydrogenase
 /chip nova /gb_link
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 55 [post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004411|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004411|/ncgi)
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Database: plantfungal

- 60 661,018 sequences; 426,114,510 total letters

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	gb U21801 LEU21801	Lycopersicon esculentum alcohol dehydrogenase...	111 1e-64
	emb AW729170 AW729170	GA_Ea0024E17 Gossypium arboreum 7-10 dpa ...	126 3e-59
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	emb AW625848 AW625848	EST319755 tomato radicle, 5 d post-imbibit...	125 2e-54
	emb AW096560 AW096560	EST289740 tomato mixed elicitor, BTI Lycop...	117 5e-52
	emb AI494929 AI494929	sa92g06.y1 Gm-c1004 Glycine max cDNA clone...	203 1e-51
	emb AB018559 AB018559	Citrullus lanatus mRNA for wts2L, complete...	74 1e-50
	emb AF053638 AF053638	Pisum sativum short-chain alcohol dehydrog...	103 3e-50
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	emb AF097651 AF097651	Pisum sativum short-chain alcohol dehydrog...	103 8e-50
	emb AF053639 AF053639	Pisum sativum short-chain alcohol dehydrog...	103 2e-49
	emb AW092874 AW092874	EST286054 tomato mixed elicitor, BTI Lycop...	112 3e-49
	emb AJ223178 NTAJ3178	Nicotiana tabacum SCANT gene.	93 7e-49
	emb AJ223177 NTAJ3177	Nicotiana tabacum mRNA for short chain alc...	93 7e-49
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	emb AW350415 AW350415	GM210008B10E12R Gm-r1021 Glycine max cDNA ...	155 2e-47
	gb U53828 SLU53828	Silene latifolia ssp. alba STA1-12 (STA1-12) ...	140 8e-47
	emb AW682978 AW682978	NF005G04LF1F1035 Developing leaf Medicago ...	107 8e-47
	emb AW093147 AW093147	EST286327 tomato mixed elicitor, BTI Lycop...	118 8e-47
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	emb AF072448 AF072448	Ipomoea trifida short-chain alcohol dehydr...	94 4e-44
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(1056 letters)

55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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60 Score E
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	emb AI488099 AI488099 EST246421 tomato ovary, TAMU Lycopersicon ...	341	5e-93
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	emb AI898058 AI898058 EST267501 tomato ovary, TAMU Lycopersicon ...	336	2e-91
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(1216 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
Sequences producing significant alignments: (bits) Value

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20 emb|AI484813|AI484813 EST243074 tomato ovary, TAMU Lycopersicon ... 150 2e-54
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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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60 emb|AW695003|AW695003 NF082C07ST1F1053 Developing stem Medicago ... 88 2e-16
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 (2403 letters)

40 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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45 Score E
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 50 emb|Y18932|LES18932 Lycopersicon esculentum p69F gene. 142 e-152
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 emb|AJ005173|LEAJ5173 Lycopersicon esculentum p69f gene, complet.. 141 e-146
 emb|AJ005172|LEAJ5172 Lycopersicon esculentum p69e gene, complet... 142 e-146
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 55 emb|AJ006379|LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142
 emb|X98930|LESBT2 L.esculentum mRNA for serine protease, SBT2. 163 e-142
 emb|AJ006786|LES6786 Lycopersicon esculentum p69d gene. 141 e-136
 emb|AJ005171|LEAJ517 Lycopersicon esculentum p69c gene, complete... 142 e-136
 emb|Y17276|LES17276 Lycopersicon esculentum p69b gene, complete ... 138 e-130
 60 emb|Y10149|LESUBTIL1 L.esculentum mRNA for subtilisin-like protein. 138 e-130
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- emb|X95270|LESUBENDO *L.esculentum* mRNA for subtilisin-like endop... 138 e-126
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 5 emb|AW218382|AW218382 EST303565 tomato radicle, 5 d post-imbibit... 322 6e-87
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 10 emb|AJ006376|LES6376 *Lycopersicon esculentum* mRNA for serine pro... 102 3e-68
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	emb Y17276 LES17276 Lycopersicon esculentum p69b gene, complete ...	138	e-130
55	emb Y10149 LESUBTILI L.esculentum mRNA for subtilisin-like protein.	138	e-130
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60	emb AI960990 AI960990 sc93f09.y1 Gm-c1019 Glycine max cDNA clone...	338	9e-92
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30 (2002 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	gb U45243 NTU45243 Nicotiana tabacum diphenol oxidase mRNA, part...	232	e-124
	emb Y13769 PTY13769 Populus trichocarpa mRNA for laccase, lac1 g...	237	e-121
45	emb AW774748 AW774748 EST333899 KV3 Medicago truncatula cDNA clo...	419	e-116
	gb BE033690 BE033690 MF07A08 MF Mesembryanthemum crystallinum cD...	408	e-113
	gb U43542 NTU43542 Nicotiana tabacum diphenol oxidase mRNA, comp...	379	e-104
	gb U73103 LTU73103 Liriodendron tulipifera high-pl laccase (LAC2...	363	e-103
	gb U12757 APU12757 Acer pseudoplatanus laccase mRNA, complete cds.	368	e-100
50	gb U73104 LTU73104 Liriodendron tulipifera high-pl laccase (LAC2...	353	3e-99
	emb Y13773 PTY13773 Populus trichocarpa mRNA for laccase, lac110...	355	4e-99
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35 emb|AI167003|AI167003 xylem.est.78 Poplar xylem Lambda ZAPII lib... 204 3e-51
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Database: plantfungal
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20 emb|X56011|TAPERO Wheat mRNA for peroxidase. 102 2e-48
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(1025 letters)

25 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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30 Score E
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20 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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25 Score E
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 55 emb|AI489200|AI489200 EST247539 tomato ovary, TAMU Lycopersicon ... 274 2e-85
 emb|AI726805|AI726805 BNLGHi6594 Six-day Cotton fiber Gossypium ... 315 3e-85
 emb|AI729066|AI729066 BNLGHi12528 Six-day Cotton fiber Gossypium... 315 4e-85
 dbj|D16456|TOMEXT3 Tomato mRNA for endo-xyloglucan transferase, ... 295 4e-85
 dbj|E06971|E06971 DNA encoding xyloglucan endotransferase. 295 4e-85
 60 dbj|E06966|E06966 Anti-sense RNA of xyloglucan endotransferase g... 295 4e-85
 dbj|E06961|E06961 Anti-sense DNA of xyloglucan endotransferase g... 295 4e-85

emb|AW934469|AW934469 EST353373 tomato flower buds 0-3 mm, Corne... 314 7e-85
 emb|AW185234|AW185234 se88f12.y1 Gm-c1023 Glycine max cDNA clone... 314 1e-84
 emb|AI487776|AI487776 EST246098 tomato ovary, TAMU Lycopersicon ... 266 2e-84
 emb|AW216790|AW216790 EST295504 tomato callus, TAMU Lycopersicon... 312 3e-84
 5 emb|AI895031|AI895031 EST264474 tomato callus, TAMU Lycopersicon... 312 4e-84

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AW980826 AW980826	EST391979	GVN Medicago truncatula cDNA clo... 95 2e-22
	emb AW980547 AW980547	EST391700	GVN Medicago truncatula cDNA clo... 95 2e-22
	emb AW685869 AW685869	NF031B09NR1F1000	Nodulated root Medicago t... 95 2e-22
25	gb BE124445 BE124445	EST393480	GVN Medicago truncatula cDNA clon... 95 2e-22
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	emb AW684629 AW684629	NF019B05NR1F1000	Nodulated root Medicago t... 95 2e-22
	emb AW329233 AW329233	N200445e	rootphos(-) Medicago truncatula c... 95 2e-22
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30	emb AW125962 AW125962	N100157e	rootphos(-) Medicago truncatula c... 92 2e-21
	emb AW622601 AW622601	EST313401	tomato root during/after fruit s... 101 2e-21
	emb AW624937 AW624937	EST313766	tomato radicle, 5 d post-imbibit... 101 2e-21
	emb AW560894 AW560894	EST315942	DSIR Medicago truncatula cDNA cl... 95 3e-21
	emb AW621250 AW621250	EST312048	tomato root during/after fruit s... 98 9e-21
35	emb AW626221 AW626221	EST320128	tomato radicle, 5 d post-imbibit... 98 9e-21
	emb AW035571 AW035571	EST281309	tomato callus, TAMU Lycopersicon... 98 1e-20
	emb AW217082 AW217082	EST295796	tomato callus, TAMU Lycopersicon... 98 1e-20
	emb AW032764 AW032764	EST276323	tomato callus, TAMU Lycopersicon... 98 1e-20
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55	emb AW725519 AW725519	GA_Ea0018G20	Gossypium arboreum 7-10 dpa ... 94 4e-19
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	emb X71618 BNPRPPDA	B.napus	proline-rich mRNA accumulating durin... 94 4e-19
	emb AF026382 AF026382	Fragaria x ananassa	HyPRP mRNA, complete cds. 94 4e-19
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60	emb AV413531 AV413531	AV413531	Lotus japonicus young plants (two... 93 1e-18
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15	emb AW306872 AW306872 sf49g05.y1 Gm-c1009 Glycine max cDNA clone...	62	3e-15
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55	emb AI736269 AI736269 sb26b02.y1 Gm-c1008 Glycine max cDNA clone...	69	3e-13
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 5 http://www.ncgr.org/cgi-bin/ff?x95738
 (1579 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 Sequences producing significant alignments: (bits) Value

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 emb|AJ054471|AJ054471 coau0001B09 Cotton Boll Abscission Zone cD... 168 3e-53
 emb|AI895644|AI895644 EST265087 tomato callus, TAMU Lycopersicon... 206 3e-52
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 25 emb|AW672225|AW672225 LG1_358_C11.b1_A002 Light Grown 1 (LG1) So... 192 6e-48
 emb|AW102341|AW102341 sd86d12.y1 Gm-c1009 Glycine max cDNA clone... 186 4e-46
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	emb AW649841 AW649841 EST328295 tomato germinating seedlings, TA...	36	0.86
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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30	emb Z38058 LMCLPB L.major (MHOM/SU/5ASKH) DNA for 100 kDa heat s...	32	3.2
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	emb AF263283 AF263283 Filobasidiella neoformans var. neoformans ...	32	3.2
35	emb X95256 HVXYLISOG H.vulgare xylose isomerase gene.	32	3.2
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45	emb AW185756 AW185756 se59c04.y1 Gm-c1019 Glycine max cDNA clone...	31	4.4
	emb AW119645 AW119645 sd50d05.y1 Gm-c1016 Glycine max cDNA clone...	31	4.4
	emb AI522947 AI522947 sa92d09.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4
	gb L38627 GYNRGNA Gymnodinium catenatum 24S ribosomal RNA (24S r...	31	4.4
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50	emb AW307483 AW307483 sf57e09.y1 Gm-c1009 Glycine max cDNA clone...	31	4.4
	emb AW307220 AW307220 sf54c09.y1 Gm-c1009 Glycine max cDNA clone...	31	4.4
	emb AI437852 AI437852 sa40e07.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4
	emb AW733531 AW733531 sk74g09.y1 Gm-c1016 Glycine max cDNA clone...	31	4.4
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	dbj D87895 D87895 Aspergillus nidulans chiA gene for chitinase, ...	30	8.3
	emb AQ162420 AQ162420 mgxb0012N11r CUGI Rice Blast BAC Library P...	30	8.3
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	emb AW980894 AW980894 EST392047 GVN Medicago truncatula cDNA clo...	30	8.3
	emb AQ447068 AQ447068 mgxb0004O05f CUGI Rice Blast BAC Library P...	30	8.3
	emb AW727134 AW727134 GA_Ea0023J07 Gossypium arboreum 7-10 dpa ...	26	8.7
30	gb BE053868 BE053868 GA_Ea0013O20f Gossypium arboreum 7-10 dpa ...	27	8.9

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(1710 letters)

40 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	emb AF149917 AF149917 Simmondsia chinensis acyl CoA reductase mR...	158 e-144
	emb X99922 BNMS2PROT B.napus mRNA for male sterility protein 2.	137 2e-74
50	emb A45743 A45743 Sequence 22 from Patent WO9520668.	137 2e-74
	emb AW615992 AW615992 EST325442 tomato flower buds 0-3 mm, Corne...	277 2e-73
	emb AI730540 AI730540 BNLGHi7015 Six-day Cotton fiber Gossypium ...	153 4e-59
	emb AW738637 AW738637 EST340064 tomato flower buds, anthesis, Co...	158 3e-51
	emb AW931162 AW931162 EST357005 tomato fruit mature green, TAMU ...	201 1e-50
55	emb AW616784 AW616784 EST323195 L. hirsutum trichome, Cornell Un...	200 3e-50
	emb AW308800 AW308800 sf72b03.y1 Gm-c1013 Glycine max cDNA clone...	141 7e-50
	emb AW278653 AW278653 sf63e03.y1 Gm-c1013 Glycine max cDNA clone...	110 1e-46
	emb AI727421 AI727421 BNLGHi7945 Six-day Cotton fiber Gossypium ...	106 3e-46
	emb AI901240 AI901240 sc22e07.y1 Gm-c1013 Glycine max cDNA clone...	166 3e-40
60	emb AW306151 AW306151 se46e08.y1 Gm-c1017 Glycine max cDNA clone...	145 2e-39
	emb AW688482 AW688482 NF008B06ST1F1000 Developing stem Medicago ...	127 6e-38

	emb AW648210 AW648210 EST326664 tomato germinating seedlings, TA...	107	1e-37
	emb AW279265 AW279265 sf68h11.y1 Gm-c1013 Glycine max cDNA clone...	123	3e-37
	emb AW671408 AW671408 LG1_343_A01.b1_A002 Light Grown 1 (LG1) So...	156	4e-37
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5	emb AW624291 AW624291 EST322152 tomato flower buds 3-8 mm, Corne...	121	1e-32
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	emb AW622996 AW622996 EST320941 tomato flower buds 3-8 mm, Corne...	128	1e-28
	emb AI055562 AI055562 coau0004F11 Cotton Boll Abscission Zone cD...	98	1e-27
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	emb AW649410 AW649410 EST327864 tomato germinating seedlings, TA...	115	1e-24
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15	emb AW217788 AW217788 EST296502 tomato flower buds 8 mm to pre-a...	91	8e-18
	emb AW217787 AW217787 EST296501 tomato flower buds 8 mm to pre-a...	91	3e-17
	emb AW928598 AW928598 EST337386 tomato flower buds 8 mm to pre-a...	86	1e-16
	emb Z11889 MITTARRNG T.aestivum mitochondrion rm26 gene for rRN...	88	2e-16
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	emb AW056631 AW056631 ST53H08 Pine TriplEx shoot tip library Pin...	36	7e-05
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	emb AW929360 AW929360 EST338148 tomato flower buds 8 mm to pre-a...	40	0.074
35	emb AW564691 AW564691 LG1_300_C05.b1_A002 Light Grown 1 (LG1) So...	37	0.50
	emb AF114171 AF114171 Sorghum bicolor BAC clone 25.M18, complete...	37	0.50
	gb BE033566 BE033566 MF03E04 MF Mesembryanthemum crystallinum cD...	36	0.69
	emb AI488290 AI488290 EST246612 tomato ovary, TAMU Lycopersicon ...	36	0.94
	emb AW932683 AW932683 EST358526 tomato fruit mature green, TAMU ...	36	0.94
40	emb AW932440 AW932440 EST358283 tomato fruit mature green, TAMU ...	36	0.94
	emb AQ874417 AQ874417 V108D3 mTn-3xHA/lacZ Insertion Library, st...	35	1.3
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45	emb AV409049 AV409049 AV409049 Lotus japonicus young plants (two...	35	1.8
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50	emb AW694067 AW694067 NF072D11ST1F1093 Developing stem Medicago ...	35	2.4
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 20 emb|AB012945|AB012945 Aspergillus oryzae gene for amyRp, complet... 33 8.7
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 dbj|D29761|YSACSI Candida maltosa gene for chitin synthase 2, p... 33 8.7
 emb|AJ273086|AJ273086 AJ273086 Metarhizium anisopliae ARSEF 2575... 33 8.7
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 25 dbj|D50617|YSCCHRVIN Saccharomyces cerevisiae chromosome VI comp... 33 8.7

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 (1467 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

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emb AI896184 AI896184 EST265627 tomato callus, TAMU Lycopersicon...	282	5e-75
emb AI896887 AI896887 EST266330 tomato callus, TAMU Lycopersicon...	178	1e-72
emb AW030421 AW030421 EST273676 tomato callus, TAMU Lycopersicon...	254	1e-66
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emb AI166722 AI166722 xylem.est.526 Poplar xylem Lambda ZAPII li...	103	3e-29
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emb|AW687571|AW687571 NF011A10RT1F1072 Developing root Medicago ... 90 3e-17
emb|AT000935|AT000935 AT000935 Brassica rapa guard cell Brassica... 89 1e-16
emb|AW684018|AW684018 NF011C08NR1F1000 Nodulated root Medicago t... 68 6e-16
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emb|AW699630|AW699630 gb29d11.y1 Moss EST library PPN Physcomitr... 83 7e-15
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20 emb|AW687218|AW687218 NF007C06RT1F1049 Developing root Medicago ... 78 2e-13
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25 emb|AI485751|AI485751 EST244072 tomato ovary, TAMU Lycopersicon ... 64 2e-09
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emb|AI486383|AI486383 EST244704 tomato ovary, TAMU Lycopersicon ... 58 2e-07
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emb|AW672524|AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So... 49 8e-05
emb|AW348926|AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3... 47 3e-04
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emb|X14399|TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su... 37 0.42
gb|M27164|TRBPOL1 Trypanosoma brucei RNA polymerase I largest su... 37 0.42
emb|AW401287|AW401287 LamdiGest487est L.digitata gametophyte Lam... 36 0.58
emb|AJ276509|TAE276509 Triticum aestivum grp1 gene for glycine-r... 36 0.79
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 (1743 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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10 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 Sequences producing significant alignments: (bits) Value

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5 emb|AW622057|AW622057 EST312855 tomato root during/after fruit s... 182 2e-83
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20 emb|AI771103|AI771103 EST252203 tomato ovary, TAMU Lycopersicon ... 190 8e-75
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gb|BE020787|BE020787 sm52h01.y1 Gm-c1028 Glycine max cDNA clone ... 274 1e-72
25 emb|AW649146|AW649146 EST327600 tomato germinating seedlings, TA... 178 3e-71
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35 emb|AW625509|AW625509 EST319416 tomato radicle, 5 d post-imbibit... 167 2e-65
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40 emb|AW621545|AW621545 EST312343 tomato root during/after fruit s... 166 8e-65
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gb|M37637|ARCPNC2 A.hypogaea cationic peroxidase mRNA, complete ... 100 2e-63
emb|X90694|MSRNAPE1C M.sativa mRNA for peroxidase 1C. 164 3e-63
emb|AW621842|AW621842 EST312640 tomato root during/after fruit s... 151 4e-63
45 emb|X94943|LECEVI16G L.esculentum mRNA for peroxidase. 104 4e-63
emb|AI487546|AI487546 EST245868 tomato ovary, TAMU Lycopersicon ... 150 5e-63
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emb|AF149279|AF149279 Phaseolus vulgaris peroxidase 4 precursor ... 100 2e-62
emb|AW621971|AW621971 EST312769 tomato root during/after fruit s... 147 6e-62
50 emb|AW218589|AW218589 EST303772 tomato radicle, 5 d post-imbibit... 147 6e-62
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	emb X91232 MARNAPRX M.annua mRNA for peroxidase.	163	4e-55
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	emb Y10468 SOPRXX7 S.oleracea mRNA for peroxidase, clone PC36.	96	2e-54
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	emb AW569900 AW569900 si83a10.y1 Gm-c1031 Glycine max cDNA clone...	89 2e-35
	emb AW423852 AW423852 sh52g05.y1 Gm-c1017 Glycine max cDNA clone...	86 4e-35
5	gb U20809 VRU20809 Vigna radiata clone MII-4 auxin-induced prote...	75 4e-35
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	emb AW394813 AW394813 sh35f08.y1 Gm-c1017 Glycine max cDNA clone...	81 1e-28
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	emb AF242503 AF242503 Thuja plicata clone 1 pinoresinol-laricire...	120 7e-76
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 5 emb|Y12689|CPIRLP C.paradisi mRNA isoflavone reductase-like prot... 123 1e-68
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 (734 letters)

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

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	emb AI771755 AI771755 EST252855 tomato ovary, TAMU Lycopersicon ...	122	4e-27
	emb AI490296 AI490296 EST248622 tomato ovary, TAMU Lycopersicon ...	122	4e-27
	emb AI486929 AI486929 EST245251 tomato ovary, TAMU Lycopersicon ...	122	4e-27
	emb AI899397 AI899397 EST268840 tomato ovary, TAMU Lycopersicon ...	122	4e-27
55	emb AI897787 AI897787 EST267230 tomato ovary, TAMU Lycopersicon ...	122	4e-27
	emb AI483636 AI483636 EST249507 tomato ovary, TAMU Lycopersicon ...	122	4e-27
	emb AI485460 AI485460 EST243781 tomato ovary, TAMU Lycopersicon ...	122	4e-27
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	emb AI489199 AI489199 EST247538 tomato ovary, TAMU Lycopersicon ...	122	4e-27
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 (378 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

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	gb J05094 TOMP II L.peruvianum proteinase inhibitor I mRNA, compl...	50 2e-10
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	emb Z12619 NTPII4PI N.tabacum PI-Ia gene encoding pre-pro-protei...	50 8e-10
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	emb X67076 NTTIMPA N.tabacum TIMPA mRNA for inhibitor of microbi...	50 9e-10
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	emb AW093975 AW093975 EST287155 tomato mixed elicitor, BTI Lycop...	35	4e-06
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	emb AW092485 AW092485 EST285665 tomato mixed elicitor, BTI Lycop...	35	4e-06
10	emb AI772725 AI772725 EST253825 tomato resistant, Cornell Lycop...	35	5e-06
	emb AI778944 AI778944 EST259823 tomato susceptible, Cornell Lyco...	35	5e-06
	emb AI774403 AI774403 EST255503 tomato resistant, Cornell Lycop...	35	5e-06
	emb AI772154 AI772154 EST253254 tomato resistant, Cornell Lycop...	35	5e-06
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	emb AW093509 AW093509 EST286689 tomato mixed elicitor, BTI Lycop...	35	5e-06
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40	emb AL132984 SPAC1556 S.pombe chromosome I cosmid c1556.	637	0.0
	emb Z26877 SCDCHR11 S.cerevisiae (S288C) 36.2kb DNA fragment fro...	408	0.0
	emb Z49320 SCYJL045W S.cerevisiae chromosome X reading frame ORF...	403	0.0
	gb M86909 YSCSDH1A Saccharomyces cerevisiae succinate dehydrogen...	408	0.0
45	gb M94874 YSCSDH1B Saccharomyces cerevisiae succinate dehydrogen...	408	0.0
	emb Z28148 SCYKL148C S.cerevisiae chromosome XI reading frame OR...	408	0.0
	gb M86746 YSCSDHA Saccharomyces cerevisiae succinate dehydrogena...	408	0.0
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50	dbj D89263 D89263 Schizosaccharomyces pombe mRNA, partial cds, c...	637	0.0
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55	emb AI727777 AI727777 BNLGHi9047 Six-day Cotton fiber Gossypium ...	391	e-114
	emb AW775119 AW775119 EST334270 KV3 Medicago truncatula cDNA clo...	407	e-112
	emb AL110721 CNS018RU Botrytis cinerea strain T4 cDNA library un...	323	e-110
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	emb AW687411 AW687411 NF009C11RT1F1085 Developing root Medicago ...	208	2e-85
60	emb AW180257 AW180257 MgA0347fMgA Library Mycosphaerella gramin...	309	4e-83
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10 emb|AW667947|AW667947 GA_Ea0012A06 Gossypium arboreum 7-10 dpa ... 250 4e-65
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35 emb|AW736633|AW736633 EST333125 KV3 Medicago truncatula cDNA clo... 128 6e-32
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40 emb|AW991033|AW991033 SsS0224 Suaeda salsa ZAP cDNA library Suae... 95 9e-28
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45 emb|AW830714|AW830714 sm35c05.y1 Gm-cl028 Glycine max cDNA clone... 81 3e-18
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55 gb|L36344|YSCTGGMS Saccharomyces cerevisiae tRNA-Met, tRNA-Ser, ... 47 1e-06
gb|L26347|YSCSEQA Saccharomyces cerevisiae COR gene cluster, iso... 47 1e-06
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60 emb|AC011017|AC011017 Leishmania major chromosome 35 clone L3184... 45 1e-05
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30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 Sequences producing significant alignments: (bits) Value

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 40 emb|AI782064|AI782064 EST262943 tomato susceptible, Cornell Lyco... 220 4e-56
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 emb|AA856223|AA856223 L30-246T3 Ice plant Lambda Uni-Zap XR expr... 182 1e-45
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 60 emb|AW698260|AW698260 NXNV_070_G09_F Nsf Xylem Normal wood Verti... 81 3e-14
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15 emb|AI726381|AI726381 BNLGHi5700 Six-day Cotton fiber Gossypium ... 44 7e-11
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gb|BE053500|BE053500 GA_Ea0001P09f Gossypium arboreum 7-10 dpa ... 53 1e-09
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emb|AW030242|AW030242 EST273497 tomato callus, TAMU Lycopersicon... 38 2e-08
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25 emb|AI897759|AI897759 EST267202 tomato ovary, TAMU Lycopersicon ... 54 6e-07
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30 emb|AI898184|AI898184 EST267627 tomato ovary, TAMU Lycopersicon ... 54 3e-06
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 (938 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

30 Searching.....done

Score E
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gb|BE036593|BE036593 MP01G10 MP Mesembryanthemum crystallinum cD... 387 e-119
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 emb|AW329378|AW329378 N200608e rootphos(-) Medicago truncatula c... 386 e-107
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 40 emb|AW442228|AW442228 EST311624 tomato fruit red ripe, TAMU Lyco... 308 5e-95
 emb|AW255529|AW255529 ML562 peppermint glandular trichome Mentha... 319 3e-93
 emb|AW221896|AW221896 EST298707 tomato fruit red ripe, TAMU Lyco... 215 2e-78
 emb|AW678275|AW678275 WS1_14_A02.b1_A002 Water-stressed 1 (WS1) ... 157 1e-77
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 45 emb|AI730573|AI730573 BNLGH17295 Six-day Cotton fiber Gossypium ... 272 3e-72
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 50 emb|AW695662|AW695662 NF097C11ST1F1085 Developing stem Medicago ... 166 4e-45
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 emb|AW598595|AW598595 sj93f10.y1 Gm-c1023 Glycine max cDNA clone... 118 5e-26
 55 emb|AW684174|AW684174 NF013F01NR1F1000 Nodulated root Medicago t... 112 3e-24
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 60 emb|AE001381|AE001381 Plasmodium falciparum chromosome 2, sectio... 57 2e-07
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	emb AW685637 AW685637 NF032F04NR1F1000 Nodulated root Medicago t...	35	0.66
	emb AW930970 AW930970 EST356813 tomato fruit mature green, TAMU ...	35	0.91
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	emb AW035833 AW035833 EST281987 tomato callus, TAMU Lycopersicon...	35	0.91
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	emb X06689 PCLIGH8 Phanerochaete chrysosporium gene for ligninas...	29	2.5
	gb M27401 PHALIGH8 Phanerochaete chrysosporium ligninase isozyme...	29	2.5
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50	Database: plantfungal		
	661,018 sequences; 426,114,510 total letters		
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55	Score E		
	Sequences producing significant alignments: (bits) Value		
	gb BE053277 BE053277 GA_Ea0035A14f Gossypium arboreum 7-10 dpa ...		
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60	emb AW678776 AW678776 WS1_1_A04.b2_A002 Water-stressed 1 (WS1) S...		
	224 1e-77		
	emb AW678614 AW678614 WS1_1_A04.b1_A002 Water-stressed 1 (WS1) S...		
	224 1e-77		

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	emb AW757260 AW757260 sl32a03.y1 Gm-c1027 Glycine max cDNA clone...	194	1e-74
	emb AW684123 AW684123 NF012F07NR1F1000 Nodulated root Medicago t...	179	7e-70
	emb AW933688 AW933688 EST359531 tomato fruit mature green, TAMU ...	261	1e-68
5	emb AW035607 AW035607 EST281345 tomato callus, TAMU Lycopersicon...	255	8e-67
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	emb AW680760 AW680760 WS1_7_B05.b1_A002 Water-stressed 1 (WS1) S...	168	1e-65
	emb AW564408 AW564408 LG1_292_D08.b1_A002 Light Grown 1 (LG1) So...	251	1e-65
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10	emb AW926737 AW926737 HVSMEg0008A08 Hordeum vulgare pre-anthesis...	210	6e-64
	emb AW443003 AW443003 EST307933 tomato mixed elicitor, BTI Lycop...	160	8e-64
	emb AW928933 AW928933 EST337817 tomato flower buds 8 mm to pre-a...	244	1e-63
	emb AW684792 AW684792 NF021B07NR1F1000 Nodulated root Medicago t...	221	1e-63
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	emb AW508088 AW508088 si50f10.y1 Gm-r1030 Glycine max cDNA clone...	156	4e-60
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	emb AW094255 AW094255 EST287435 tomato mixed elicitor, BTI Lycop...	195	1e-48
25	emb AV424875 AV424875 AV424875 Lotus japonicus young plants (two...	159	3e-48
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30	emb AW203607 AW203607 sf36b08.y1 Gm-c1028 Glycine max cDNA clone...	174	2e-42
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	emb AW755419 AW755419 sl03g08.y1 Gm-c1036 Glycine max cDNA clone...	104	3e-40
	emb AW329571 AW329571 N200823e rootphos(-) Medicago truncatula c...	97	1e-37
35	emb AW774738 AW774738 EST333889 KV3 Medicago truncatula cDNA clo...	157	1e-37
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	emb AW781444 AW781444 sl78f03.y1 Gm-c1037 Glycine max cDNA clone...	154	2e-36
	emb AW037635 AW037635 EST279093 tomato mixed elicitor, BTI Lycop...	148	1e-34
	emb AI823132 AI823132 L30-1015T3 Ice plant Lambda Uni-Zap XR exp...	142	6e-33
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	emb AI896179 AI896179 EST265622 tomato callus, TAMU Lycopersicon...	135	1e-30
	emb AW756882 AW756882 sk82d02.y1 Gm-c1016 Glycine max cDNA clone...	131	2e-29
	emb AW756279 AW756279 sl18d04.y1 Gm-c1036 Glycine max cDNA clone...	130	2e-29
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	emb AW736643 AW736643 EST333135 KV3 Medicago truncatula cDNA clo...	104	2e-21
50	emb AA231652 AA231652 BCD98.F cDNA from barley Hordeum vulgare c...	99	1e-19
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	emb AW568172 AW568172 si57d03.y1 Gm-r1030 Glycine max cDNA clone...	84	2e-15
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55	emb AI728294 AI728294 BNLGHi10384 Six-day Cotton fiber Gossypium...	76	6e-13
	emb AI822771 AI822771 L30-604T3 Ice plant Lambda Uni-Zap XR expr...	76	9e-13
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	emb AW760716 AW760716 sl36b09.y1 Gm-c1027 Glycine max cDNA clone...	45	2e-07

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	emb AW706467 AW706467 sj58g06.y1 Gm-c1033 Glycine max cDNA clone...	54	4e-06
	emb AW704696 AW704696 sk39d04.y1 Gm-c1028 Glycine max cDNA clone...	45	1e-05
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[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac007017|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac007017|/ncgi)
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45 (713 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

55	emb AF212183 AF212183 Nicotiana tabacum harpin inducing protein ...	221	3e-62
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	emb AW099273 AW099273 sd37e04.y1 Gm-c1016 Glycine max cDNA clone...	89	5e-37
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	emb AI896215 AI896215 EST265658 tomato callus, TAMU Lycopersicon...	126	1e-34
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	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par...	280	1e-91
	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein.	268	1e-91
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	278	3e-91
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(1953 letters)

Database: plantfungal

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Sequences producing significant alignments:

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gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 297 e-104

15

dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 285 e-103

emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 287 e-103

gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 304 e-102

emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 289 e-102

emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 292 e-102

20

emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 291 e-101

emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 303 e-101

emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 299 e-101

gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 294 e-101

emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 301 e-101

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emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 302 e-101

dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 287 e-100

emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 295 e-100

dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 288 e-100

emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 303 e-100

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gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 290 2e-99

emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 270 3e-93

emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 264 3e-93

gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 286 2e-92

emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 199 6e-92

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gb|BE057261|BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ... 310 3e-83

emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 277 1e-80

emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 127 7e-80

emb|Y12530|BOARLKGEN B.oleraceae gene encoding serine/threonine ... 129 3e-76

emb|AW760240|AW760240 sl59g07.y1 Gm-c1027 Glycine max cDNA clone... 284 2e-75

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emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 126 3e-75

emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 126 4e-75

emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 126 2e-74

emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 119 3e-74

emb|X79432|BOSRK3 B.oleracea SRK3 gene. 118 8e-74

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emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 117 1e-73

emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 116 2e-73

emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 121 8e-73

emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 275 8e-73

emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 116 1e-72

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dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 124 1e-71

emb|AW831390|AW831390 sm22a06.y1 Gm-c1028 Glycine max cDNA clone... 211 3e-71

emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 109 3e-68

emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 206 9e-67

emb|AW309544|AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone... 254 1e-66

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emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 179 3e-66

gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 225 2e-65

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emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 176 4e-63

emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 176 1e-62

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emb|AW203661|AW203661 sf36g06.y1 Gm-c1028 Glycine max cDNA clone... 202 4e-61

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	emb AW220676 AW220676 EST297145 tomato fruit mature green, TAMU ...	231	1e-59
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	emb AW220677 AW220677 EST297146 tomato fruit mature green, TAMU ...	227	2e-58
	emb AI901283 AI901283 sc31d08.y1 Gm-cl014 Glycine max cDNA clone...	180	3e-57
5	emb AA738544 AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg...	124	8e-57
	emb AW736407 AW736407 EST332421 KV3 Medicago truncatula cDNA clo...	194	2e-56
	emb AW667985 AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ...	91	4e-56
	emb AA738545 AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg...	127	1e-54
	emb Y16999 TCA16999 Theobroma cacao microsatellite DNA, clone mT...	125	1e-53
10	emb Z18884 BOSRKRPC B.oleracea encoding S-receptor kinase relate...	129	2e-53
	emb AW031816 AW031816 EST275270 tomato callus, TAMU Lycopersicon...	141	2e-53
	emb AI896953 AI896953 EST266396 tomato callus, TAMU Lycopersicon...	184	3e-53
	emb AI967314 AI967314 Ljimpest00-017 Ljirnp Lambda HybriZap two...	143	6e-53
	emb AW033458 AW033458 EST277029 tomato callus, TAMU Lycopersicon...	184	8e-53
15	emb AI899009 AI899009 EST268452 tomato ovary, TAMU Lycopersicon ...	161	4e-52
	emb AI771857 AI771857 EST252957 tomato ovary, TAMU Lycopersicon ...	157	5e-51
	emb AI488101 AI488101 EST246423 tomato ovary, TAMU Lycopersicon ...	157	5e-51
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	emb AI898581 AI898581 EST268024 tomato ovary, TAMU Lycopersicon ...	161	1e-50
20	emb AW684339 AW684339 NF015G04NR1F1000 Nodulated root Medicago t...	105	2e-50
	emb AI822907 AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr...	112	5e-50
	emb AI899156 AI899156 EST268599 tomato ovary, TAMU Lycopersicon ...	161	6e-50
	emb AI822355 AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre...	112	1e-49
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25	emb AI729170 AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium...	128	2e-48
	emb Y14600 SBRLK1 Sorghum bicolor mRNA for protein serine/threon...	78	2e-48
	emb Z18861 BOSRKRPC B.oleracea encoding S-receptor kinase relate...	119	3e-48
	emb AW034624 AW034624 EST278308 tomato callus, TAMU Lycopersicon...	166	1e-47
	emb AI486331 AI486331 EST244652 tomato ovary, TAMU Lycopersicon ...	161	1e-47
30	emb AW279355 AW279355 sf65g10.y1 Gm-cl013 Glycine max cDNA clone...	115	2e-47
	emb AW054349 AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR expi...	112	2e-47
	emb AW687233 AW687233 NF007D09RT1F1077 Developing root Medicago ...	86	3e-47
	emb Z18883 BOSRKRPB B.oleracea encoding S-receptor kinase relate...	176	3e-46
	emb AW706972 AW706972 sk20a03.y1 Gm-cl028 Glycine max cDNA clone...	157	8e-46
35	emb AI822347 AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre...	107	1e-45
	emb AI895623 AI895623 EST265066 tomato callus, TAMU Lycopersicon...	185	1e-45
	emb AB030083 AB030083 Populus nigra PnLPK mRNA for lectin-like p...	86	1e-45
	gb BE058691 BE058691 sn19e05.y1 Gm-cl016 Glycine max cDNA clone ...	99	2e-45
	emb AW278186 AW278186 sf40g07.y1 Gm-cl009 Glycine max cDNA clone...	95	4e-45
40	emb AF142596 AF142596 Nicotiana tabacum LRR receptor-like protei...	72	8e-45
	gb U51330 TAU51330 Triticum aestivum leaf rust resistance kinase...	80	5e-44
	emb Z18862 BOSRKRPD B.oleracea encoding S-receptor kinase protein.	89	1e-43
	emb AW621923 AW621923 EST312721 tomato root during/after fruit s...	78	1e-43
	emb AI484701 AI484701 EST242962 tomato ovary, TAMU Lycopersicon ...	89	2e-43
45	gb U28007 LEU28007 Lycopersicon esculentum Pto kinase interactor...	129	5e-43
	emb AW982539 AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi...	82	5e-43
	emb AW034993 AW034993 EST279222 tomato callus, TAMU Lycopersicon...	164	6e-43
	emb AW687052 AW687052 NF005E02RT1F1017 Developing root Medicago ...	175	9e-43
	emb AW597214 AW597214 si71g06.y1 Gm-cl031 Glycine max cDNA clone...	127	2e-42
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thaliana] /blast_score 0 /ec_number ec_3.2.1.26 /family hydrolase
55 /chip nova /gb_link
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[post/entrez/query?db=n&form=6&dopt=g&uid=gb|x74514|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x74514|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?x74514>
(1947 letters)

60

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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5	Score	E	
	Sequences producing significant alignments:	(bits)	Value
	emb AF000521 AF000521 <i>Fragaria x ananassa</i> cell wall invertase pr...	413	0.0
	emb Z35163 VFCWINV2 <i>V.faba</i> VFCWINV2 mRNA for cell wall invertase...	418	0.0
10	gb M58362 DARBFRUC <i>D.carota</i> cell wall beta-fructosidase mRNA, co...	239	0.0
	emb X81792 CRCIN1 <i>C.rubrum</i> CIN1 mRNA for extracellular invertase.	181	0.0
	emb X81834 NTMRNABDF <i>N.tabacum</i> mRNA for beta-fructosidase.	205	0.0
	emb AF030420 AF030420 <i>Triticum aestivum</i> cell wall invertase (TVR...	240	0.0
	emb Y11176 CIFRUCTOS <i>C.intybus</i> mRNA for fructosidase.	144	0.0
15	emb Z21486 STBETFRUA <i>S.tuberosum</i> mRNA for invertase gene encodin...	196	e-180
	emb AJ272305 LPE272305 <i>Lycopersicon pennellii</i> mRNA for beta-fruc...	190	e-170
	emb X85327 PSRNABFRU <i>P.sativum</i> mRNA for beta-fructofuranosidase.	398	e-169
	emb AF063246 AF063246 <i>Pisum sativum</i> cell wall invertase (bfructl...	398	e-169
	emb AJ272304 LES272304 <i>Lycopersicon esculentum</i> mRNA for beta-fru...	190	e-169
20	emb Z22645 STBETFRCA <i>S.tuberosum</i> invertase gene encoding beta-fr...	204	e-166
	emb AF000520 AF000520 <i>Fragaria x ananassa</i> cell wall invertase (I...	210	e-164
	emb AB004558 AB004558 <i>Lycopersicon esculentum</i> mRNA for acid inve...	200	e-164
	emb X69321 DCBFRUCT <i>D.carota</i> (Queen Anne's Lace) Inv*Dc1 gene.	178	e-145
	emb X78424 DCINC1 <i>D.carota</i> (Queen Anne's Lace) Inv*Dc2 gene, 343...	161	e-136
25	emb Z35162 VFCWINV1 <i>V.faba</i> VFCWINV1 mRNA for cell wall invertase I.	207	e-132
	emb AF030421 AF030421 <i>Triticum aestivum</i> cell wall invertase (TVR...	138	e-130
	emb AJ133765 STU133765 <i>Solanum tuberosum</i> invGE and invGF genes.	148	e-128
	gb U87849 CAU87849 <i>Capsicum annuum</i> acid beta-fructosidase mRNA, ...	200	e-126
	emb AJ006067 ACE6067 <i>Allium cepa</i> mRNA for invertase.	210	e-126
30	emb A94218 A94218 Sequence 1 from Patent EP0952222.	176	e-122
	emb AF002656 AF002656 <i>Asparagus officinalis</i> acid invertase mRNA,...	198	e-120
	gb U81520 CIU81520 <i>Cichorium intybus</i> sucrose:sucrose 1-fructosyl...	173	e-120
	emb X75351 DCRNABF <i>D.carota</i> (Nantaise) mRNA for soluble acid bet...	202	e-120
	emb X75353 DCRNAABF <i>D.carota</i> (Nantaise) mRNA for soluble acid b...	203	e-120
35	emb AJ272307 LPE272307 <i>Lycopersicon pennellii</i> lin 5 gene for bet...	145	e-119
	emb X75352 DCRNAABF <i>D.carota</i> (Nantaise) mRNA for soluble acid be...	203	e-119
	emb X78423 DCINUC1 <i>D.carota</i> (Queen Anne's Lace) Inv*Dc3 gene, 44...	160	e-118
	emb A94222 A94222 Sequence 5 from Patent EP0952222.	173	e-117
	emb Y09662 CSSS1FT <i>C.scolymus</i> mRNA for sucrose sucrose 1-fructos...	170	e-117
40	emb A86530 A86530 Sequence 1 from Patent WO9839460.	170	e-117
	emb AJ272306 LES272306 <i>Lycopersicon esculentum</i> lin 5 gene for be...	145	e-116
	emb AJ250634 TOF250634 <i>Taraxacum officinale</i> mRNA for sucrose:suc...	169	e-116
	emb Z49831 VFVCINVMR <i>V.faba</i> VFVCINV mRNA for invertase (beta-fru...	199	e-115
	gb U92438 PVU92438 <i>Phaseolus vulgaris</i> soluble acid invertase mRN...	198	e-114
45	emb AW686881 AW686881 NF003E07RT1F1000 Developing root <i>Medicago</i> ...	413	e-114
	dbj D10265 VIRINVA <i>Vigna radiata</i> mRNA for invertase, complete cds.	194	e-114
	emb AJ009757 HTU9757 <i>Helianthus tuberosus</i> sst-1 gene.	171	e-113
	emb A52468 A52468 Sequence 1 from Patent WO9621023.	171	e-113
	emb X70368 STPAIN1A <i>S.tuberosum</i> PAIN-1 mRNA for beta-fructofuran...	200	e-108
50	emb X67163 DCSBFRU <i>D.carota</i> mRNA for soluble beta-fructosidase.	140	e-107
	gb L29099 POTBFRUASE <i>Solanum tuberosum</i> beta-fructosidase mRNA, c...	198	e-107
	dbj E07108 E07108 cDNA encoding acid invertase.	198	e-106
	dbj D11350 TOMBFSO <i>Tomato</i> mRNA for beta-fructosidase, complete cds.	198	e-106
	emb Z12026 LPBFRUCM <i>L.pimpinellifolium</i> beta-fructosidase mRNA fo...	198	e-106
55	emb Z12025 LEBFRUCM <i>L.esculentum</i> beta-fructosidase mRNA for vacu...	198	e-106
	gb M81081 TOMACIN <i>Tomato</i> acid invertase (TTV1) mRNA, complete cds.	198	e-106
	gb S70040 S70040 acid invertase [<i>Lycopersicon esculentum</i> =tomatoe...	198	e-106
	dbj E16293 E16293 cDNA encoding invertase.	198	e-106
	dbj E08976 E08976 cDNA encoding tomato invertase.	198	e-106
60	emb AF017082 AF017082 <i>Ipomoea batatas</i> beta-fructofuranosidase (S...	141	e-103
	emb Y11124 CIPINVERT <i>C.intybus</i> mRNA for putative invertase.	138	e-102

emb|X97642|TGINV5GEN T.gesneriana mRNA for invertase 5. 180 6e-97
 emb|X95651|TGINV11GN T.gesneriana mRNA for invertase. 186 7e-96
 emb|X97643|TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94
 emb|Y18706|DCA18706 Daucus carota Inv*Dc5 gene. 130 2e-93
 5 emb|Y18707|DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge... 161 2e-93
 emb|AF062735|AF062735 Saccharum officinarum soluble acid inverta... 129 1e-91
 emb|AF062734|AF062734 Saccharum robustum soluble acid invertase ... 129 1e-91
 emb|AF091549|AF091549 Hamamelis virginiana clone 7 beta-fructofu... 331 9e-90
 emb|AJ000481|CSFF1FRUC Cynara scolymus mRNA for fructan fructan ... 162 3e-89
 10 emb|AF091550|AF091550 Hamamelis virginiana clone C beta-fructofu... 330 3e-89
 emb|A94220|A94220 Sequence 3 from Patent EP0952222. 161 1e-88
 emb|AF091548|AF091548 Hamamelis virginiana clone 3 beta-fructofu... 327 1e-88
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 emb|Z12028|LPBFRUCG L.pimpinellifolium gene encoding vacuolar in... 157 6e-88
 15 emb|Z12027|LEBFRUCG L.esculentum gene for vacuolar invertase. 157 6e-88
 emb|AJ009756|HTU9756 Helianthus tuberosus fit-1 gene. 161 2e-87
 emb|A52470|A52470 Sequence 3 from Patent WO9621023. 161 2e-87
 emb|X81795|BVBIN35 B.vulgaris BIN35 mRNA for extracellular inver... 265 5e-86
 gb|BE055183|BE055183 GA_Ea0035H23f Gossypium arboreum 7-10 dpa ... 203 4e-83
 20 emb|X91392|LELIN8 L.esculentum mRNA for invertase (LIN8). 133 2e-82
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 emb|X81793|CRCIN2 C.rubrum CIN2 mRNA for intracellular invertase. 135 2e-80
 emb|X91389|LELIN5 L.esculentum mRNA for invertase (LIN5). 129 1e-78
 emb|X91391|LELIN7 L.esculentum mRNA for invertase (LIN7). 133 5e-78
 25 emb|Y07838|ACY07838 A.cepa mRNA for fructan:fructan 6G-fructosyl... 156 2e-77
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 30 emb|A48282|A48282 Sequence 3 from Patent WO9601904. 152 4e-75
 emb|AW685050|AW685050 NF024F09NR1F1000 Nodulated root Medicago t... 248 5e-75
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 35 emb|A48284|A48284 Sequence 5 from Patent WO9601904. 130 1e-69
 emb|AW666614|AW666614 GA_Ea0005C10 Gossypium arboreum 7-10 dpa ... 207 3e-69
 emb|AW730389|AW730389 GA_Ea0023K22 Gossypium arboreum 7-10 dpa ... 141 2e-68
 emb|A48280|A48280 Sequence 1 from Patent WO9601904. 82 2e-68
 emb|X83233|HVSF6FT Hordeum vulgare mRNA for sucrose:fructan 6-fr... 82 2e-68
 40 emb|AF069309|AF069309 Triticum aestivum vacuolar invertase (WIVR... 127 5e-67
 emb|AW350139|AW350139 GM210007B20F11R Gm-r1021 Glycine max cDNA ... 112 4e-66
 emb|AW618261|AW618261 EST314311 L. pennellii trichome, Cornell U... 248 1e-64
 emb|AW738685|AW738685 EST340112 tomato flower buds, anthesis, Co... 189 3e-64
 emb|X91390|LELIN6 L.esculentum mRNA for invertase (LIN6). 133 5e-64
 45 emb|AI522941|AI522941 sa92d01.y1 Gm-c1004 Glycine max cDNA clone... 201 1e-63
 emb|AW441409|AW441409 EST310805 tomato fruit red ripe, TAMU Lyco... 114 4e-62
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 (1947 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments:

(bits) Value

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emb|X81834|NTMRNABDF N.tabacum mRNA for beta-fructosidase. 205 0.0
5 emb|AF030420|AF030420 Triticum aestivum cell wall invertase (IVR... 240 0.0
emb|Y11176|CIFRUCTOS C.intybus mRNA for fructosidase. 144 0.0
emb|Z21486|STBETFRUA S.tuberosum mRNA for invertase gene encodin... 196 e-180
emb|AJ272305|LPE272305 Lycopersicon pennellii mRNA for beta-fruc... 190 e-170
emb|X85327|PSRNABFRU P.sativum mRNA for beta-fructofuranosidase. 398 e-169
10 emb|AF063246|AF063246 Pisum sativum cell wall invertase (bfruct1... 398 e-169
emb|AJ272304|LES272304 Lycopersicon esculentum mRNA for beta-fru... 190 e-169
emb|Z22645|STBETFRCA S.tuberosum invertase gene encoding beta-fr... 204 e-166
emb|AF000520|AF000520 Fragaria x ananassa cell wall invertase (I... 210 e-164
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15 emb|X69321|DCBFRUCT D.carota (Queen Anne's Lace) Inv*Dc1 gene. 178 e-145
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emb|A94218|A94218 Sequence 1 from Patent EP0952222. 176 e-122
emb|AF002656|AF002656 Asparagus officinalis acid invertase mRNA,... 198 e-120
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25 emb|X75351|DCRNABF D.carota (Nantaise) mRNA for soluble acid bet... 202 e-120
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emb|X75352|DCRNAABF D.carota (Nantaise) mRNA for soluble acid be... 203 e-119
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30 emb|A94222|A94222 Sequence 5 from Patent EP0952222. 173 e-117
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emb|A86530|A86530 Sequence 1 from Patent WO9839460. 170 e-117
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emb|AJ250634|TOF250634 Taraxacum officinale mRNA for sucrose:suc... 169 e-116
35 emb|Z49831|VFVCINV MR V.faba VFVCINV mRNA for invertase (beta-fru... 199 e-115
gb|U92438|PVU92438 Phaseolus vulgaris soluble acid invertase mRN... 198 e-114
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dbj|D10265|VIRINVA Vigna radiata mRNA for invertase, complete cds. 194 e-114
emb|AJ009757|HTU9757 Helianthus tuberosus sst-1 gene. 171 e-113
40 emb|A52468|A52468 Sequence 1 from Patent WO9621023. 171 e-113
emb|X70368|STPAIN1A S.tuberosum PAIN-1 mRNA for beta-fructofuran... 200 e-108
emb|X67163|DCSBFRU D.carota mRNA for soluble beta-fructosidase. 140 e-107
gb|L29099|POTBFRUASE Solanum tuberosum beta-fructosidase mRNA, c... 198 e-107
dbj|E07108|E07108 cDNA encoding acid invertase. 198 e-106
45 dbj|D11350|TOMBFS D Tomato mRNA for beta-fructosidase, complete cds. 198 e-106
emb|Z12026|LPBFRUCM L.pimpinellifolium beta-fructosidase mRNA fo... 198 e-106
emb|Z12025|LEBFRUCM L.esculentum beta-fructosidase mRNA for vacu... 198 e-106
gb|M81081|TOMACIN Tomato acid invertase (TIV1) mRNA, complete cds. 198 e-106
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50 dbj|E16293|E16293 cDNA encoding invertase. 198 e-106
dbj|E08976|E08976 cDNA encoding tomato invertase. 198 e-106
emb|AF017082|AF017082 Ipomoea batatas beta-fructofuranosidase (S... 141 e-103
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emb|X97642|TGINV5GEN T.gesneriana mRNA for invertase 5. 180 6e-97
55 emb|X95651|TGINV11GN T.gesneriana mRNA for invertase. 186 7e-96
emb|X97643|TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94
emb|Y18706|DCA18706 Daucus carota Inv*Dc5 gene. 130 2e-93
emb|Y18707|DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge... 161 2e-93
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60 emb|AF062734|AF062734 Saccharum robustum soluble acid invertase ... 129 1e-91
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- emb|AJ000481|CSFF1FRUC Cynara scolymus mRNA for fructan fructan ... 162 3e-89
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5 emb|AF091548|AF091548 Hamamelis virginiana clone 3 beta-fructofu... 327 1e-88
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emb|Z12027|LEBFRUCG L.esculentum gene for vacuolar invertase. 157 6e-88
emb|AJ009756|HTU9756 Helianthus tuberosus fft-1 gene. 161 2e-87
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10 emb|X81795|BVBIN35 B.vulgaris BIN35 mRNA for extracellular inver... 265 5e-86
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emb|AF091547|AF091547 Hamamelis virginiana clone 1 beta-fructofu... 295 3e-81
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15 emb|X91389|LELIN5 L.esculentum mRNA for invertase (LIN5). 129 1e-78
emb|X91391|LELIN7 L.esculentum mRNA for invertase (LIN7). 133 5e-78
emb|Y07838|ACY07838 A.cepa mRNA for fructan:fructan 6G-fructosyl... 156 2e-77
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emb|AF014925|AF014925 Citrus unshiu acid invertase (CUAI1) gene,... 138 4e-76
20 emb|AJ006066|ACE6066 Allium cepa mRNA for sucrose sucrose 1-fruc... 132 2e-75
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emb|A48282|A48282 Sequence 3 from Patent WO9601904. 152 4e-75
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emb|Z83339|PSZ83339 P.sativum mRNA for cell wall invertase II. 280 2e-74
25 emb|AF091546|AF091546 Hamamelis virginiana clone 6 beta-fructofu... 193 3e-74
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emb|AW730389|AW730389 GA_Ea0023K22 Gossypium arboreum 7-10 dpa ... 141 2e-68
30 emb|A48280|A48280 Sequence 1 from Patent WO9601904. 82 2e-68
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45 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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50 Score E
Sequences producing significant alignments: (bits) Value

- emb|Z69369|SPAC3F10 S.pombe chromosome I cosmid c3F10. 314 e-119
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gb|U33010|SPU33010 Schizosaccharomyces pombe cosmids 359, 1198 a... 291 e-112
emb|AL356012|SPBC359 Schizosaccharomyces pombe cosmid c359. 291 e-112
emb|AW278374|AW278374 sf43c10.y1 Gm-c1009 Glycine max cDNA clone... 383 e-105
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60 emb|AI781883|AI781883 EST262762 tomato susceptible, Cornell Lyco... 370 e-101
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- emb|X97560|SC32KBF *S.cerevisiae* 32kb DNA fragment of chromosome ... 159 1e-94
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5 emb|AW686402|AW686402 NF037F01NR1F1000 Nodulated root *Medicago t...* 244 7e-78
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25 emb|AW037624|AW037624 EST279082 tomato mixed elicitor, BTI Lycop... 242 1e-62
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40 emb|AW459613|AW459613 sh89d10.y1 *Gm-c1016* Glycine max cDNA clone... 219 1e-55
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emb|AW761593|AW761593 sl69g02.y1 *Gm-c1027* Glycine max cDNA clone... 205 2e-51
45 emb|Z99262|SPAC9E9 *S.pombe* chromosome I cosmid c9E9. 129 2e-51
emb|Y09354|SPABC1 *S.pombe* ABC1 gene. 129 2e-51
emb|AL136538|SPAC30 *S.pombe* chromosome I cosmid c30. 144 1e-48
emb|AI974480|AI974480 T110430e KV0 *Medicago truncatula* cDNA clon... 196 1e-48
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50 emb|AW736468|AW736468 EST332482 KV3 *Medicago truncatula* cDNA clo... 191 3e-47
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55 emb|AI777095|AI777095 EST258060 tomato resistant, Cornell Lycop... 177 6e-43
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60 emb|AW155943|AW155943 ga22b09.y1 Moss EST library PPU Physcomitr... 167 7e-40
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- emb|AW759534|AW759534 sl44f02.y1 Gm-c1027 Glycine max cDNA clone... 166 9e-40
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 10 emb|AW350529|AW350529 GM210009A10F6R Gm-r1021 Glycine max cDNA 3... 157 7e-37
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(2055 letters)

Database: plantfungal

40 661,018 sequences; 426,114,510 total letters

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45 Score E
 Sequences producing significant alignments: (bits) Value

- emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 356 e-115
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 50 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 312 9e-99
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 60 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 266 1e-90
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- dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 260 1e-89
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5 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 258 3e-87
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40 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 166 5e-53
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60 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 118 8e-47
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5 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 161 2e-45
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emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 65 7e-44
10 emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 178 1e-43
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(1533 letters)

Database: plantfungal
35 661,018 sequences; 426,114,510 total letters

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Score E
40 Sequences producing significant alignments: (bits) Value

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gb|U82975|CSU82975 Citrus sinensis pectinesterase (PECS-2.1) gen... 421 e-116
45 emb|AF152172|AF152172 Solanum tuberosum cultivar Desiree pectin ... 208 e-111
emb|AF229849|AF229849 Vigna radiata pectin methylesterase isoform... 208 e-107
gb|U49330|SLU49330 Solanum lycopersicum pectin methylesterase (P... 205 e-106
emb|Z71752|NPPME2MR N.plumbaginifolia mRNA for pectin methyleste... 177 e-104
emb|Z71753|NPPME3MR N.plumbaginifolia mRNA for pectin methyleste... 177 e-103
50 emb|X94443|VRPECMEST V.radiata mRNA for pectinmethylesterase. 175 e-100
gb|U82973|CSU82973 Citrus sinensis pectinesterase (PECS-1.1) gen... 218 8e-97
emb|AF056493|AF056493 Pisum sativum pectin methylesterase mRNA, ... 163 3e-95
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55 emb|A17011|A17011 tomato fruit pectin esterase with pPel DNA seq... 190 5e-94
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60 gb|S66607|S66607 Lycopersicon esculentum pectinmethylesterase-li... 190 8e-93
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10 emb|AB029461|AB029461 *Salix gilgiana* SgPME1 mRNA for pectin meth... 144 1e-82
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(825 letters)

30 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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 35 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 118 4e-57
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(825 letters)

Database: plantfungal
 25 661,018 sequences; 426,114,510 total letters

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emb|X57187|PVCHITIN P.vulgaris mRNA for chitinase. 238 e-123
 gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 248 e-112
 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p... 201 e-107
 35 gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 247 1e-97
 dbj|D45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 197 8e-96
 dbj|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 136 6e-95
 dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 136 4e-94
 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 227 5e-91
 40 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 143 5e-91
 emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 164 1e-90
 gb|U52848|DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 137 3e-90
 gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 142 4e-90
 emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 158 2e-89
 45 gb|U52847|DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... 133 4e-89
 emb|X61488|BNCHITIN B.napus mRNA for chitinase. 181 5e-85
 emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 166 2e-84
 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... 164 2e-84
 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 185 9e-83
 50 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 127 8e-80
 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 127 8e-80
 emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 126 2e-78
 gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 167 4e-78
 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem Medicago ... 131 5e-78
 55 emb|AW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 126 1e-77
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 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 126 2e-77
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 dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 136 2e-76
 60 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 156 7e-75
 emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 215 1e-74

- gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 160 1e-74
emb|AI776153|AI776153 EST257241 tomato resistant, Cornell Lycopersicon... 164 1e-74
emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 139 1e-74
emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 126 2e-74
5 gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 104 3e-74
emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 156 4e-72
emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 238 6e-71
emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 126 2e-70
gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 132 2e-68
10 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 126 3e-68
gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 114 2e-67
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emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 122 5e-66
emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 215 5e-65
15 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 79 2e-64
gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 208 6e-63
emb|AW680953|AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S... 224 7e-63
emb|AI729668|AI729668 BNLGHi13889 Six-day Cotton fiber Gossypium... 121 1e-61
emb|AI055037|AI055037 coau0002N18 Cotton Boll Abcission Zone cD... 111 3e-60
20 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 101 3e-60
gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 100 4e-59
emb|AW924422|AW924422 WS1_69_C06.b1_A002 Water-stressed 1 (WS1) ... 171 4e-59
emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 108 2e-58
emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 224 6e-58
25 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 224 6e-58
gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 108 2e-57
gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 208 2e-57
emb|AI488583|AI488583 EST246922 tomato ovary, TAMU Lycopersicon ... 126 3e-57
emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 118 4e-57
30 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 221 4e-57
emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 111 1e-56
emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 111 1e-56
emb|AI897391|AI897391 EST266834 tomato ovary, TAMU Lycopersicon ... 126 1e-56
emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 110 7e-56
35 emb|AW924229|AW924229 WS1_51_H04.b1_A002 Water-stressed 1 (WS1) ... 215 3e-55
emb|AW676775|AW676775 DG1_14_C09.g1_A002 Dark Grown 1 (DG1) Sorg... 215 3e-55
emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 105 4e-55
emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 109 6e-55
emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 214 7e-55
40 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54
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emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 110 6e-54
gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 110 7e-54
45 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 105 1e-53
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emb|AF043247|AF043247 Solanum tuberosum class I chitinase (ChtC1... 105 1e-53
gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 104 2e-53
gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 110 6e-53
50 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 112 9e-53
emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 112 9e-53
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emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 114 1e-51
55 gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 83 1e-51
emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 108 2e-51
emb|AF043248|AF043248 Solanum tuberosum-class I chitinase (ChtC2... 100 3e-51
gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 112 4e-51
gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 112 4e-51
60 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 102 7e-51
gb|U02608|STU02608 Solanum tuberosum chitinase (chtB4) mRNA, par... 107 1e-50

emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 107 2e-50
 emb|AF000964|AF000964 Poa pratensis chitinase (Chi1) gene, compl... 100 2e-50
 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 103 4e-50
 emb|X63899|PSCHITIN P.sativum mRNA for chitinase. 94 1e-49
 5 emb|AB015655|AB015655 Cucurbita sp. mRNA for chitinase, complete... 100 7e-49
 gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 84 1e-48
 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 111 3e-48
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 108 6e-48
 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 108 6e-48
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 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 15 /gb_link /ncgi
 (1788 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters
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25 gb L34344 RTAANTSYNB Ruta graveolens anthranilate synthase alpha...	772	0.0
gb L34343 RTAANTSYNA Ruta graveolens anthranilate synthase alpha...	467	0.0
emb AF079168 AF079168 Nicotiana tabacum feedback-insensitive ant...	365	0.0
emb AW931942 AW931942 EST357785 tomato fruit mature green, TAMU ...	356	3e-97
30 emb AW218352 AW218352 EST303535 tomato radicle, 5 d post-imbibit...	210	1e-73
emb AL031966 SPCC1442 S.pombe chromosome III cosmid c1442.	209	6e-69
emb AW651095 AW651095 EST329549 tomato germinating seedlings, TA...	222	2e-64
dbj D89256 D89256 Schizosaccharomyces pombe mRNA, partial cds, c...	205	5e-64
emb AW982499 AW982499 HVSMEg0003G22f Hordeum vulgare pre-anthesi...	215	2e-58
35 emb AW460005 AW460005 si07d11.y1 Gm-cl029 Glycine max cDNA clone...	116	1e-57
gb U18839 SCE9747 Saccharomyces cerevisiae chromosome V cosmids ...	123	4e-48
emb X68327 SCTRP2 S.cerevisiae TRP2 gene for anthranilate syntha...	123	4e-48
emb AW719463 AW719463 LjNEST5b1r Lotus japonicus nodule library,...	184	1e-45
emb AI736775 AI736775 sb33d01.y1 Gm-cl012 Glycine max cDNA clone...	104	2e-40
40 gb K01388 YSCTRP2 Yeast (S.cerevisiae) TRP2 gene coding for anth...	122	4e-38
emb AL032684 SPBP8B7 S.pombe chromosome II p1 p8B7.	95	6e-25
emb AW509018 AW509018 si39b01.y1 Gm-r1030 Glycine max cDNA clone...	113	5e-24
gb T14852 T14852-crs299 lambdaZAPST Ricinus communis cDNA clone ...	107	2e-22
emb AW223881 AW223881 EST300692 tomato fruit red ripe, TAMU Lyco...	103	4e-21
45 emb AF119554 AF119554 Plasmodium falciparum para-aminobenzoic ac...	67	6e-10
emb AL111470 CNS019CM Botrytis cinerea strain T4 cDNA library un...	45	2e-05
emb AI329873 AI329873 b9g02ne.r1 Neurospora crassa evening cDNA ...	48	3e-04
emb AW224247 AW224247 EST300974 tomato fruit red ripe, TAMU Lyco...	46	7e-04
emb AF149719 AF149719 Aspergillus fumigatus para aminobenzoic ac...	42	0.012
50 emb AQ448372 AQ448372 mgxb0020C12f CUGI Rice Blast BAC Library P...	39	0.15
emb AQ324360 AQ324360 mgxb0018K01r CUGI Rice Blast BAC Library P...	39	0.15
emb AQ160089 AQ160089 mgxb0003G09r CUGI Rice Blast BAC Library P...	39	0.15
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emb AW599000 AW599000 ga99h03.y1 Moss EST library PPN Physcomitr...	37	0.38
55 emb AW678847 AW678847 WS1_1_A04.g1_A002 Water-stressed 1 (WS1) S...	35	0.88
emb AW680390 AW680390 WS1_52_D12.g1_A002 Water-stressed 1 (WS1) ...	35	0.89
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emb AW747146 AW747146 WS1_66_E07.b1_A002 Water-stressed 1 (WS1) ...	35	0.89
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5	emb AW746170 AW746170 WS1_39_B05.g1_A002 Water-stressed 1 (WS1) ...	35	0.90
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	emb AW309961 AW309961 s27b12.x1 Gm-c1028 Glycine max cDNA clone...	35	1.4
	emb AW678582 AW678582 WS1_16_E09.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
15	emb AW317198 AW317198 s38f03.x1 Gm-c1028 Glycine max cDNA clone...	35	1.4
	emb AW678305 AW678305 WS1_14_G05.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
	emb AW680905 AW680905 WS1_8_A08.b1_A002 Water-stressed 1 (WS1) S...	35	1.4
	emb AW679666 AW679666 WS1_30_B11.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
	emb AL031746 PFMAL1P3 Plasmodium falciparum MAL1P3, complete seq...	35	1.9
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	emb AW696796 AW696796 NF109A07ST1F1052 Developing stem Medicago ...	35	1.9
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25	gb M98871 SOYCHS7A Glycine max chalcone synthase (chs7) gene, co...	35	2.6
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	emb AW310362 AW310362 s35a09.x1 Gm-c1028 Glycine max cDNA clone...	35	2.6
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30	gb BE023927 BE023927 sm94c05.y1 Gm-c1015 Glycine max cDNA clone ...	35	2.6
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	emb AW309356 AW309356 sfl6d02.x1 Gm-c1028 Glycine max cDNA clone...	35	2.6
35	emb AL355932 NCB5022 Neurospora crassa DNA linkage group II BAC ...	34	3.5
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	emb AW725836 AW725836 GA_Ea0019N24 Gossypium arboreum 7-10 dpa ...	33	9.2
60	emb AQ324451 AQ324451 mgxb0018L23r CUGI Rice Blast BAC Library P...	33	9.2
	gb M73492 LEIHSP90 Leishmania donovani heat shock protein 90 mRN...	33	9.2

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 emb|AI166186|AI166186 a032p32u Hybrid aspen plasmid library Popu... 33 9.2
 gb|BE053953|BE053953 GA_Ea0031D23f Gossypium arboreum 7-10 dpa ... 33 9.2

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 (1342 letters)

Database: plantfungal
 15 661,018 sequences; 426,114,510 total letters

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25	emb AW729492 AW729492 GA_Ea0025C18 Gossypium arboreum 7-10 dpa ...	291	8e-78
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	emb AW755778 AW755778 sl09c05.y1 Gm-c1036 Glycine max cDNA clone...	248	1e-64
	emb AW737762 AW737762 EST339189 tomato flower buds, anthesis, Co...	169	1e-60
30	emb AW621695 AW621695 EST312493 tomato root during/after fruit s...	206	3e-52
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	emb AW034075 AW034075 EST277570 tomato callus, TAMU Lycopersicon...	150	2e-35
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	emb AI773775 AI773775 EST254875 tomato resistant, Cornell Lycopersicon...	63	5e-09
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	emb AI487017 AI487017 EST245339 tomato ovary, TAMU Lycopersicon ...	36	1e-04
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30	emb Z11613 VRACCSYNM V.radiata mRNA for ACC synthase.	41	0.016
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(1752 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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emb|A92833|A92833 Sequence 7 from Patent WO9804586. 261 e-116

emb|A92828|A92828 Sequence 2 from Patent WO9804586. 261 e-116

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emb|AW216578|AW216578 EST295292 tomato callus, TAMU Lycopersicon... 165 6e-78

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emb|AI054629|AI054629 coau0001J02 Cotton Boll Abscission Zone cD... 133 2e-44

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emb|AI731933|AI731933 BNLGH11440 Six-day Cotton fiber Gossypium... 136 3e-40

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 5 emb|AW567653|AW567653 si77b05.y1 Gm-cl031 Glycine max cDNA clone... 55 2e-06
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(1125 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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	emb Y11485 TAESERPIN T.aestivum mRNA for serpin WZS2.	116	2e-62
15	emb Z49890 TAWZCISPIN T.aestivum WZCI mRNA for serpin.	109	3e-60
	emb X95277 HVSEH H.vulgare mRNA for serpin.	98	6e-58
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	emb Z15116 HVPAXXG H.vulgare pazx gene encoding protein zx.	80	6e-32
	emb AF118560 AF118560 Avena fatua barley protein Z homolog mRNA,...	73	7e-32
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25	emb AI730301 AI730301 BNLGHi6607 Six-day Cotton fiber Gossypium ...	77	8e-31
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30	emb AW219573 AW219573 EST302055 tomato root during/after fruit s...	83	4e-26
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 emb|AL113815|CNS01B5R Botrytis cinerea strain T4 cDNA library un... 34 2.1
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 15 gb|L25681|HYBRG18S Hydнора africana Thunb. 18S ribosomal RNA (18... 33 4.0
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 20 emb|AI494738|AI494738 sb14f02.y1 Gm-cl004 Glycine max cDNA clone... 33 5.5
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 30 emb|AL356172|NCB23L21 Neurospora crassa DNA linkage group II BAC... 32 7.5
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 emb|X64519|NTCHN50G N.tabacum chitinase gene 50 for class I chit... 32 7.5
 emb|AF123299|AF123299 Chrysosphaera parvula small subunit riboso... 32 7.5
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Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters

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emb X77110 NTCHIVR N.tabacum chi-V mRNA for chitinase class V.	312	e-137
55 emb AF088885 AF088885 Nicotiana tabacum receptor-like kinase CHR...	189	3e-84
emb X77111 NTCHIVD N.tabacum chi-V gene.	204	1e-69
emb A72844 A72844 Sequence 7 from Patent WO9505467.	204	7e-69
emb AW690230 AW690230 NF030F05ST1F1000 Developing stem Medicago ...	139	4e-66
emb AF108893 AF108893 AF108893 Capsicum annuum root 1st-branched...	201	7e-51
60 emb AW032116 AW032116 EST275570 tomato callus, TAMU Lycopersicon...	186	2e-46
emb AW560415 AW560415 EST315463 DSIR Medicago truncatula cDNA cl...	169	3e-41

- emb|AW351251|AW351251 GM210011A20A4R Gm-r1021 Glycine max cDNA 3... 145 6e-34
- emb|AV423067|AV423067 AV423067 Lotus japonicus young plants (two... 129 2e-32
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- emb|AI495953|AI495953 sb18c04.y1 Gm-c1004 Glycine max cDNA clone... 111 1e-23
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- emb|AF188932|AF188932 Hypocrea rufa strain Hy9 42 kDa endochitin... 68 1e-20
- emb|AF188921|AF188921 Trichoderma atroviride strain DAOM 165782 ... 70 3e-20
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- emb|AF188918|AF188918 Hypocrea koningii 42 kDa endochitinase gen... 71 3e-20
- emb|AF188930|AF188930 Trichoderma asperellum strain CBS 361.97, ... 68 6e-20
- emb|AF188926|AF188926 Trichoderma asperellum strain GJS 90-14 42... 68 6e-20
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- emb|AF188929|AF188929 Trichoderma asperellum strain CBS 433.97, ... 68 9e-20
- emb|AF188933|AF188933 Trichoderma asperellum strain BBA 68646R 4... 68 9e-20
- 20 gb|S78423|S78423 chit42=endochitinase [Trichoderma harzianum, mR... 67 9e-20
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- emb|AF188928|AF188928 Trichoderma viride strain BBA 66069R 42 kD... 68 4e-19
- emb|AF188925|AF188925 Trichoderma viride strain Tr6 42 kDa endoc... 68 4e-19
- emb|AF188919|AF188919 Trichoderma viride strain ATCC 18652, syno... 66 2e-18
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- emb|AJ243014|MFL243014 Metarhizium flavoviride mRNA for chitinas... 62 8e-17
- emb|AF027498|AF027498 Metarhizium anisopliae chitinase CHIT42 (C... 60 9e-16
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- emb|AI967677|AI967677 Ljirmp08-687-g4 Ljirnp Lambda HybriZap ... 72 5e-14
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- emb|AI899627|AI899627 EST269070 tomato susceptible, Cornell Lyco... 75 1e-12
- dbj|D87894|D87894 Rhizopus oligosporus DNA for chitinase, comple... 59 2e-10
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- emb|AF009354|AF009354 Leishmania donovani chitinase (Chi-1) gene... 57 4e-09
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- emb|AI212420|AI212420 x5f11a1.r1 Aspergillus nidulans 24hr asexu... 43 6e-08
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- gb|U60806|CIU60806 Coccidioides immitis complement-fixation chit... 44 5e-06
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- 55 emb|Z71415|THENDOCHS T.hamatum endochitinase gene. 50 3e-05
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- emb|X01095|KLKILL1L Yeast DNA killer plasmid pGKL1. 39 1e-04
- 60 emb|X00762|KLKILL05 Kluyveromyces lactis (killer strain) plasmid... 39 1e-04
- emb|X07127|KLK1P Kluyveromyces lactis killer plasmid k1 DNA. 39 1e-04

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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(864 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments: (bits) Value

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45 emb|X87374|PSZINCFIN P.sativum putative zinc finger protein. 64 3e-11
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emb|AW032112|AW032112 EST275566 tomato callus, TAMU Lycopersicon... 45 5e-10
55 emb|AB006598|AB006598 Petunia x hybrida mRNA for ZPT2-11, comple... 64 7e-10
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AW774727 AW774727 EST333878 KV3 Medicago truncatula cDNA clo...	169	6e-41
	emb AV423915 AV423915 AV423915 Lotus japonicus young plants (two...	163	3e-39
20	emb AW559836 AW559836 EST314884 DSIR Medicago truncatula cDNA cl...	131	6e-37
	emb AW349142 AW349142 GM210003B22H5R Gm-r1021 Glycine max cDNA 3...	107	3e-23
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	emb AI855891 AI855891 sc30h08.y1 Gm-c1014 Glycine max cDNA clone...	100	4e-21
25	emb AW560073 AW560073 EST315121 DSIR Medicago truncatula cDNA cl...	77	5e-21
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	emb AW870069 AW870069 NXNV_123_G03_F Nsf Xylem Normal wood Verti...	68	3e-17
	emb AW587665 AW587665 ST63B10 Pine TriplEx shoot tip library Pin...	87	4e-17
	emb AW011208 AW011208 ST18A05 Pine TriplEx shoot tip library Pin...	89	1e-16
30	emb AW438038 AW438038 ST83G07 Pine TriplEx shoot tip library Pin...	84	5e-15
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	emb AW980840 AW980840 EST391993 GVN Medicago truncatula cDNA clo...	35	0.019
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(762 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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	emb AW395529 AW395529 sg72c09.y1 Gm-c1007 Glycine max cDNA clone...	88	7e-24
	emb AW507599 AW507599 si53h08.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24
	emb AW318205 AW318205 sg62d04.y1 Gm-c1007 Glycine max cDNA clone...	88	7e-24
20	emb AW568476 AW568476 si59c06.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24
	emb AW567816 AW567816 si66b10.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24
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	emb AW678335 AW678335 WS1_14_F02.g1_A002 Water-stressed 1 (WS1) ...	75	7e-13
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	gb M19388 COTSPG G.hirsutum (cotton) storage protein (late embry...	57	2e-07

	gb U47096 DCU47096 Daucus carota LEA protein mRNA, somatic embry...	57	2e-07
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5	gb L47932 L47932 BNAF1873 Mustard flower buds Brassica rapa cDNA...	56	4e-07
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	emb X92955 BOPC15 B.oleracea mRNA for pollen coat protein.	51	1e-05
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(885 letters)

60 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	emb AW441466 AW441466	EST310862	tomato fruit red ripe, TAMU Lyco... 311 4e-84
	emb AW775237 AW775237	EST331959	GVN Medicago truncatula cDNA clo... 278 4e-74
	emb AW564397 AW564397	LG1_292_F08.b1_A002	Light Grown 1 (LG1) So... 275 2e-73
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	emb AI897460 AI897460	EST266903	tomato ovary, TAMU Lycopersicon ... 158 7e-67
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20	emb AW011189 AW011189	ST17G07	Pine TriplEx shoot tip library Pin... 172 4e-48
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55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AL353821 NC68B2 Neurospora crassa DNA linkage group V Cosmid...	34	7.3
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(1140 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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	emb AW707234 AW707234	sk22d10.y1	Gm-c1028	Glycine max cDNA clone...	50 3e-07
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50	emb AI442516 AI442516 sa32e08.y1 Gm-c1004 Glycine max cDNA clone...	48 7e-06

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60 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	emb AI896298 AI896298 EST265741 tomato callus, TAMU Lycopersicon...	69	5e-22
	emb AI352900 AI352900 MB73-10F PZ204.BNlib Brassica napus cDNA c...	83	3e-15
10	emb AI960998 AI960998 sc93g09.y1 Gm-cl019 Glycine max cDNA clone...	58	2e-14
	emb AW618619 AW618619 EST320605 L. pennellii trichome, Cornell U...	67	4e-10
	emb AW618077 AW618077 EST314127 L. pennellii trichome, Cornell U...	67	5e-10
	emb AW684309 AW684309 NF015D01NR1F1000 Nodulated root Medicago t...	60	4e-08
	emb AW477120 AW477120 ga42b04.y1 Moss EST library PPU Physcomitr...	57	2e-07
15	emb AW459393 AW459393 sh23f12.y1 Gm-cl016 Glycine max cDNA clone...	44	1e-06
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	gb M82834 TRBAEMAJ Trypanosoma cruzi DNA, repeat region.	44	0.005
	emb AL031746 PFMAL1P3 Plasmodium falciparum MAL1P3, complete seq...	39	0.11
	gb J03998 PFAGAR Plasmodium falciparum glutamic acid-rich protei...	39	0.11
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40	gb BE052627 BE052627 GA_Ea0032J13f Gossypium arboreum 7-10 dpa ...	34	2.6
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	emb AC004157 AC004157 Plasmodium falciparum chromosome 12 clone ...	34	3.6
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50	emb X53731 SCSPA2G S. cerevisiae SPA2 gene.	34	4.8
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55	emb AI437671 AI437671 sa38b01.y1 Gm-cl004 Glycine max cDNA clone...	34	4.8
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60	emb Z37997 SC9877 S.cerevisiae chromosome IX cosmid 9877.	33	5.0
	emb X52898 TCGAP T. cruzi gap gene for glyceraldehyde-3-phosphat...	33	5.0

- emb|AF052832|AF052832 Trypanosoma cruzi CL Brener cosmid 1b21 ch... 33 5.0
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 5 gb|L06323|THEGLUMEMP Theileria parva glutamine rich membrane pro... 33 6.5
 emb|W66263|W66263 TgESTzy71f09.r1 TgME49 Tachyzoite cDNA Toxopla... 33 6.5
 emb|AQ948528|AQ948528 Sheared DNA-37G19.TR Sheared DNA Trypanoso... 33 6.9
 emb|AL035476|PFMAL4P3 Plasmodium falciparum chromosome 4 strain ... 33 6.9
 emb|AI080842|AI080842 TENU3699 T. cruzi epimastigote normalized ... 33 6.9
 10 gb|U75347|ENU75347 Emericella nidulans fatty acid synthase, alph... 33 6.9
 emb|AQ659013|AQ659013 Sheared DNA-13G3.TR Sheared DNA Trypanosom... 33 6.9
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 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 32 9.4
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 25 emb|AF102653|AF102653 Podranea ricasoliana ribulose 1,5-bisphosp... 32 9.4
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 35 (2196 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Score E

Sequences producing significant alignments: (bits) Value

- 45 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 375 e-120
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 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 339 e-105
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 330 e-105
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 333 e-104
 50 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 332 e-104
 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 328 e-103
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 329 e-100
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 321 1e-99
 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 316 2e-98
 55 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 323 2e-98
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 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 195 4e-97
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 60 emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 285 3e-94
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- gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 221 1e-93
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 40 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 176 7e-56
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10 emb|AI930642|AI930642 sb37f05.y1 Gm-c1013 Glycine max cDNA clone... 182 1e-44
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15 emb|Z18861|BOSRK RPA B.oleracea encoding S-receptor kinase relate... 114 7e-44
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30 http://www.ncgr.org/cgi-bin/ff?ac002392
(2631 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

35 Searching.....done

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45 gb U59317 LPU59317 Lycopersicon pimpinellifolium serine/threonin...	108	7e-54
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50 emb AW200786 AW200786 se93e06.y1 Gm-c1027 Glycine max cDNA clone...	206	5e-52
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emb AF108892 AF108892 AF108892 Capsicum annuum root 1st-branched...	194	3e-48
emb AI967314 AI967314 Ljirnp00-017 Ljirnp Lambda HybriZap two...	129	5e-48
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60 gb U02271 LEU02271 Lycopersicon pimpinellifolium Rio Grande-PtoR...	103	1e-47
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dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 112 2e-46
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5 emb|AF053127|AF053127 Mahus domestica leucine-rich receptor-like... 130 4e-46
dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 110 4e-46
emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 111 5e-46
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10 emb|AI736063|AI736063 sb22d04.y1 Gm-c1007 Glycine max cDNA clone... 147 6e-46
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dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 94 2e-45
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15 emb|AI895365|AI895365 EST264808 tomato callus, TAMU Lycopersicon... 184 2e-45
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30 emb|AI730776|AI730776 BNLGHi7867 Six-day Cotton fiber Gossypium ... 151 2e-42
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45 emb|AW615998|AW615998 EST325448 tomato flower buds 0-3 mm, Corne... 117 3e-40
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50 emb|AI771280|AI771280 EST252296 tomato ovary, TAMU Lycopersicon ... 165 2e-39
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5	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	107	3e-38
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	emb A16119 A16119 Intracellular chitinase mRNA (SEQ ID NO: 2).	493	e-158
	emb X15494 STCHITIN Potato endochitinase gene (EC 3.2.1.14).	541	e-153
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 emb|AF135144|AF135144 *Arabis lemmonii* country USA class I chitin... 451 e-126
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 40 emb|AF043248|AF043248 *Solanum tuberosum* class I chitinase (ChtC2... 431 e-122
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 45 emb|AF135138|AF135138 *Arabis glabra* country USA class I chitinas... 431 e-120
 emb|AF135133|AF135133 *Arabis blepharophylla* country USA class I ... 423 e-118
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 55 emb|AF141373|AF141373 *Petroselinum crispum* chitinase precursor (... 237 e-104
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 emb|AW030745|AW030745 EST274000 tomato callus, TAMU *Lycopersicon*... 360 e-104
 emb|AF141374|AF141374 *Petroselinum crispum* chitinase precursor (... 237 e-104
 emb|AW033034|AW033034 EST276593 tomato callus, TAMU *Lycopersicon*... 367 e-103
 60 emb|AW216454|AW216454 EST295084 tomato callus, TAMU *Lycopersicon*... 373 e-102
 emb|AW267781|AW267781 EST305909 DSIR *Medicago truncatula* cDNA cl... 316 e-102

emb|AW033757|AW033757 EST277328 tomato callus, TAMU Lycopersicon... 285 e-101
 emb|AW037673|AW037673 EST279276 tomato mixed elicitor, BTI Lycop... 281 e-100
 emb|AW216787|AW216787 EST295501 tomato callus, TAMU Lycopersicon... 364 e-100
 emb|AI771248|AI771248 EST252264 tomato ovary, TAMU Lycopersicon ... 363 1e-99
 5 emb|AW031102|AW031102 EST274409 tomato callus, TAMU Lycopersicon... 275 1e-98
 emb|X15349|HVENDCHT Barley (H.vulgare) mRNA for endochitinase. 359 2e-98
 emb|AW622028|AW622028 EST312826 tomato root during/after fruit s... 269 9e-97
 emb|Z15139|LECHI17 L.esculentum mRNA for chitinase. 242 2e-96
 emb|AW032161|AW032161 EST275615 tomato callus, TAMU Lycopersicon... 334 2e-96
 10 emb|AW560177|AW560177 EST315225 DSIR Medicago truncatula cDNA cl... 295 1e-95

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emb|caal6619.1| (al021637) vacuolar sorting receptor-like protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 15 /gb_link /ncgi
 (1881 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

20

Searching.....done

	Score	E.	(bits)	Value
25	Sequences producing significant alignments:			
	gb U79958 PSU79958 Pisum sativum BP-80 vacuolar sorting receptor...	810	0.0	
	emb AB006809 AB006809 Cucurbita sp. mRNA for PV72, complete cds. .	780	0.0	
	emb AW267745 AW267745 EST305873 DSIR Medicago truncatula cDNA cl...	453	e-126	
	emb AW931583 AW931583 EST357426 tomato fruit mature green, TAMU ...	308	e-112	
30	emb AW309187 AW309187 sg05d06.y1 Gm-cl019 Glycine max cDNA clone...	405	e-112	
	gb BE054150 BE054150 GA__Ea0034H17f Gossypium arboreum 7-10 dpa ...	398	e-110	
	emb AW622833 AW622833 EST306903 tomato flower buds 3-8 mm, Corne...	387	e-106	
	emb AW689392 AW689392 NF018F12ST1F1000 Developing stem Medicago ...	371	e-102	
	emb AW737948 AW737948 EST339375 tomato flower buds, anthesis, Co...	342	3e-94	
35	emb AW774434 AW774434 EST333585 KV3 Medicago truncatula cDNA clo...	263	2e-90	
	emb AW932529 AW932529 EST358372 tomato fruit mature green, TAMU ...	326	3e-88	
	emb AW615949 AW615949 EST325315 tomato flower buds 0-3 mm, Corne...	216	1e-87	
	emb AI728635 AI728635 BNLGHi11276 Six-day Cotton fiber Gossypium...	281	8e-84	
	emb AI782787 AI782787 EST263666 tomato susceptible, Cornell Lyco...	307	2e-82	
40	emb AI443067 AI443067 sa47a01.y1 Gm-cl1004 Glycine max cDNA clone...	305	6e-82	
	emb AW747297 AW747297 WS1_67_G06.b1_A002 Water-stressed 1 (WS1) ...	292	8e-78	
	emb AI727826 AI727826 BNLGHi9195 Six-day Cotton fiber Gossypium ...	280	1e-77	
	emb AI484571 AI484571 EST242801 tomato ovary, TAMU Lycopersicon ...	284	1e-75	
	emb AW685785 AW685785 NF030C07NR1F1000 Nodulated root Medicago t...	166	1e-71	
45	emb AV406766 AV406766 AV406766 Lotus japonicus young plants (two...	260	2e-68	
	emb AW509740 AW509740 ga63h11.y1 Moss EST library PPU Physcomitr...	232	1e-65	
	emb AV428420 AV428420 AV428420 Lotus japonicus young plants (two...	249	4e-65	
	emb AW695542 AW695542 NF096C05ST1F1037 Developing stem Medicago ...	124	1e-58	
	emb AW289687 AW289687 NXNV004E04F Nsf Xylem Normal wood Vertical...	226	4e-58	
50	emb AW064744 AW064744 ST35C06 Pine TriplEx shoot tip library Pin...	198	2e-56	
	emb AW309191 AW309191 sg05d10.y1 Gm-cl019 Glycine max cDNA clone...	171	3e-52	
	emb AW096632 AW096632 EST289812 tomato mixed elicitor, BTI Lycop...	165	7e-52	
	emb AW568619 AW568619 si60a11.y1 Gm-r1030 Glycine max cDNA clone...	205	1e-51	
	emb AF209910 AF209910 Prunus dulcis vacuolar sorting receptor pr...	160	5e-51	
55	emb AW623959 AW623959 EST321904 tomato flower buds 3-8 mm, Corne...	75	1e-50	
	emb AW397829 AW397829 sg68h03.y1 Gm-cl1007 Glycine max cDNA clone...	201	2e-50	
	emb AW256542 AW256542 EST304679 KV2 Medicago truncatula cDNA clo...	151	2e-50	
	emb AI967865 AI967865 Ljimp14-100-f3 Ljimp Lambda HybriZap ...	197	3e-49	
	emb AW680054 AW680054 WS1_3_A01.g1_A002 Water-stressed 1 (WS1) S...	150	6e-47	
60	emb AA660289 AA660289 00158 MtRHE Medicago truncatula cDNA 5', m...	107	9e-44	
	emb AW056624 AW056624 ST53G07 Pine TriplEx shoot tip library Pin...	178	1e-43	

	emb AW690002 AW690002 NF026G04ST1F1000 Developing stem Medicago ...	109	2e-43
	emb AW290400 AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical...	177	3e-43
	emb AI162330 AI162330 A016P01U Hybrid aspen plasmid library Popu...	131	2e-39
	emb AI161766 AI161766 A006P54U Hybrid aspen plasmid library Popu...	93	3e-38
5	emb AW737369 AW737369 EST338892 tomato flower buds, anthesis, Co...	149	5e-35
	gb BE125908 BE125908 DG1_59_E01.b1_A002 Dark Grown 1 (DG1) Sorgh...	149	5e-35
	emb AW201441 AW201441 sf03b09.y1 Gm-cl027 Glycine max cDNA clone...	113	1e-34
	emb AW398931 AW398931 EST309431 L. pennellii trichome, Cornell U...	95	2e-34
	gb BE049814 BE049814 NXNV_144_F04_F Nsf Xylem Normal wood Vertic...	143	6e-33
10	emb AW126100 AW126100 N100297e rootphos(-) Medicago truncatula c...	100	5e-30
	emb AW508719 AW508719 si35f03.y1 Gm-r1030 Glycine max cDNA clone...	125	1e-27
	gb L38113 L38113 BNAF0628E Mustard flower buds Brassica rapa cDN...	117	4e-26
	emb AW317388 AW317388 sg48g10.y1 Gm-cl025 Glycine max cDNA clone...	80	1e-25
	emb AW706755 AW706755 sk02f10.y1 Gm-cl023 Glycine max cDNA clone...	118	2e-25
15	emb AA660955 AA660955 00852 MtRHE Medicago truncatula cDNA 5' si...	74	7e-25
	emb AW616461 AW616461 EST322872 L. hirsutum trichome, Cornell Un...	69	2e-24
	emb AW348825 AW348825 GM210003B11E6R Gm-r1021 Glycine max cDNA 3...	68	8e-24
	emb AW932524 AW932524 EST358367 tomato fruit mature green, TAMU ...	80	1e-23
	emb AW774190 AW774190 EST333273 KV3 Medicago truncatula cDNA clo...	101	2e-20
20	emb AW125944 AW125944 N100139e rootphos(-) Medicago truncatula c...	66	6e-20
	emb AW093844 AW093844 EST287024 tomato mixed elicitor, BTI Lycop...	96	7e-19
	emb AW906386 AW906386 EST342508 potato stolon, Cornell Universit...	67	2e-16
	gb BE060808 BE060808 HVSMEg0013H06f Hordeum vulgare pre-anthesis...	87	4e-16
	emb AW620693 AW620693 sj08d10.y1 Gm-cl032 Glycine max cDNA clone...	76	1e-15
25	emb AW256398 AW256398 EST304465 KV2 Medicago truncatula cDNA clo...	74	6e-14
	emb AW037563 AW037563 EST278890 tomato mixed elicitor, BTI Lycop...	79	8e-14
	emb AW691052 AW691052 NF037B05ST1F1000 Developing stem Medicago ...	72	4e-13
	emb AW686287 AW686287 NF040A08NR1F1000 Nodulated root Medicago t...	77	4e-13
	emb AW685952 AW685952 NF036G09NR1F1000 Nodulated root Medicago t...	46	2e-11
30	emb AW760128 AW760128 sl58d09.y1 Gm-cl027 Glycine max cDNA clone...	58	1e-10
	emb AW119909 AW119909 sd54d08.y1 Gm-cl016 Glycine max cDNA clone...	66	8e-10
	emb AI794754 AI794754 sb68f11.y1 Gm-cl019 Glycine max cDNA clone...	64	4e-09
	emb AW774852 AW774852 EST334003 KV3 Medicago truncatula cDNA clo...	64	4e-09
	emb AW127457 AW127457 M110648 DSIL Medicago truncatula cDNA clon...	58	3e-07
35	emb AW443352 AW443352 EST308282 tomato mixed elicitor, BTI Lycop...	56	1e-06
	emb AW747372 AW747372 WS1_67_G06.g1_A002 Water-stressed 1 (WS1) ...	55	2e-06
	emb AI939286 AI939286 sc69h02.y1 Gm-cl016 Glycine max cDNA clone...	46	0.001
	emb AF198615 AF198615 Neospora caninum microneme protein Nc-P38 ...	43	0.009
	emb AI822258 AI822258 L0-701T3 Ice plant Lambda Uni-Zap XR expre...	36	0.019
40	gb BE035779 BE035779 MO16H05 MO Mesembryanthemum crystallinum cD...	36	0.025
	emb AI822869 AI822869 L30-712T3 Ice plant Lambda Uni-Zap XR expr...	36	0.025
	emb AI822754 AI822754 L0-1287T3 Ice plant Lambda Uni-Zap XR expr...	36	0.025
	emb AI756736 AI756736 EtESTea24h07.y1 Eimeria S5-2 Sporozoite st...	34	0.035
	gb M36941 BLYHORDCA Hordeum vulgare C-hordein gene, complete cds.	33	0.079
45	emb AU036628 AU036628 Schizosaccharomyces pombe genomic clone ha...	40	0.083
	emb AA948752 AA948752 L0-271M13R Ice plant Lambda Uni-Zap XR exp...	35	0.086
	emb AW760788 AW760788 sl35a03.y1 Gm-cl027 Glycine max cDNA clone...	39	0.11
	emb AW830924 AW830924 sm19c06.y1 Gm-cl027 Glycine max cDNA clone...	39	0.11
	emb AQ008266 AQ008266 CpG0480B CpIOWAgDNA1 Cryptosporidium parvu...	39	0.16
50	emb AW696326 AW696326 NF106G11ST1F1087 Developing stem Medicago ...	38	0.21
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	emb AV408651 AV408651 AV408651 Lotus japonicus young plants (two...	38	0.21
	emb AQ651638 AQ651638 Sheared DNA-7G23.TF Sheared DNA Trypanosom...	37	0.40
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55	gb BE036036 BE036036 MO18H02 MO Mesembryanthemum crystallinum cD...	36	0.76
	gb C95899 C95899 C95899 Marchantia polymorpha immature sex organ...	36	1.0
	emb AA966307 AA966307 v8c01a1.r1 Aspergillus nidulans 24hr asexu...	36	1.0
	emb AI759219 AI759219 EtESTea26c02.y1 Eimeria S5-2 Sporozoite st...	28	1.3
	gb U11583 YSCH9196 Saccharomyces cerevisiae chromosome VIII cosm...	35	1.4
60	emb AQ639257 AQ639257 927P1-10E12.TV 927P1 Trypanosoma brucei ge...	35	1.4
	emb AQ943504 AQ943504 Sheared DNA-43F22.TF Sheared DNA Trypanoso...	35	1.4

emb|AW623282|AW623282 EST321227 tomato flower buds 3-8 mm, Corne... 35 1.4
dbj|D85226|D85226 Brassica campestris DNA for S glycoprotein, pa... 28 1.6
emb|AF001525|AF001525 Musa acuminata ripening-associated protein... 35 2.0

5 Query= X84728.6_s_at 12349_s_at /id_source genbank /description
gb|aaa17993.1|(m91192) phenylalanine ammonia-lyase [trifolium
subterraneum] /blast_score 0 /ec_number /family /chip nova /gb_link
/ncgi
(1962 letters)

10 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

15

Score E
Sequences producing significant alignments: (bits) Value

20 gb|L11747|POPPALGA Populus tricarpha X Populus deltoides (hybri... 354 0.0
emb|X99997|BFPAL B.finlaysoniana mRNA for phenylalanine ammonia-... 352 0.0
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gb|U43338|CLU43338 Citrus limon phenylalanine ammonia-lyase (pal... 350 0.0
gb|L36822|SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas... 350 0.0
emb|AF036948|AF036948 Prunus avium phenylalanine ammonia-lyase (... 349 0.0
25 emb|AJ250836|CAR250836 Cicer arietinum mRNA for phenylalanine am... 349 0.0
emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 349 0.0
emb|X81158|PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 349 0.0
emb|X81159|PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 348 0.0
30 dbj|D83075|D83075 Lithospermum erythrorhizon mRNA for phenylalan... 348 0.0
emb|AF237955|AF237955 Rubus idaeus phenylalanine ammonia-lyase 2... 348 0.0
emb|AJ002221|DLJ002221 Digitalis lanata mRNA for phenylalanine a... 347 0.0
gb|M29232|IPBPAL Sweet potato phenylalanine ammonia-lyase mRNA (... 345 0.0
dbj|D26596|CMEPAL Camellia sinensis mRNA for phenylalanine ammon... 344 0.0
dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase,... 344 0.0
35 emb|X78269|NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine ... 343 0.0
dbj|D83076|D83076 Lithospermum erythrorhizon mRNA for phenylalan... 343 0.0
dbj|D78640|IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni... 342 0.0
emb|Y12461|HAPHAMLY Helianthus annuus mRNA for phenylalanine amm... 341 0.0
emb|AB042520|AB042520 Catharanthus roseus mRNA for phenylalanine... 339 0.0
40 emb|AF237954|AF237954 Rubus idaeus phenylalanine ammonia-lyase 1... 330 0.0
dbj|D10001|PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase... 349 0.0
emb|X63103|STPAL1 S.tuberosum PAL-1 gene for phenylalanine ammon... 353 0.0
emb|AJ238754|CCL238754 Citrus clementina X Citrus reticulata mRN... 350 0.0
emb|AJ238753|CCL238753 Citrus clementina X Citrus reticulata mRN... 353 0.0
45 dbj|D10003|PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas... 349 0.0
dbj|E04042|E04042 cDNA sequence coding for pea phenylalanine amm... 349 0.0
emb|AF165998|AF165998 Vigna unguiculata phenylalanine ammonia-ly... 355 0.0
gb|U16130|PAU16130 Persea americana phenylalanine ammonia lyase ... 331 0.0
dbj|D30656|POPPALA Populus kitakamiensis gene for phenylalanine ... 356 0.0
50 gb|M84466|TOBTPA1A Tobacco phenylalanine ammonialyase (tpal) gen... 352 0.0
emb|AB008200|AB008200 Nicotiana tabacum palB gene for phenylalan... 352 0.0
dbj|D85850|D85850 Daucus carota gDcPAL1 gene for phenylalanine a... 347 0.0
emb|X52953|DMPAL1 Glycine max PAL1 gene for phenylalanine ammoni... 355 0.0
emb|X99705|TAPALGEN1 T.aestivum PAL gene. 342 0.0
55 gb|M91192|TFRPAL1X Trifolium subterraneum phenylalanine ammonia-... 345 0.0
gb|M90692|TOMPAL5A Lycopersicon esculentum phenylalanine ammonia... 347 0.0
emb|AB008199|AB008199 Nicotiana tabacum palA gene for phenylalan... 344 0.0
emb|Y07654|PCPAL1 P.crispum pal1 gene. 350 0.0
emb|X16772|PCPAL1EX2 P.crispum PAL-1 gene for phenylalanine ammo... 350 0.0
60 dbj|D43803|POPPALG4B Populus kitakamiensis gene for phenylalanin... 336 0.0
gb|M83314|TOMPHEAMLY Lycopersicon esculentum phenylalanine ammon... 353 0.0

- emb|X76130|CMPAL C.melo (cantaloupe) pal mRNA. 318 0.0
 dbj|D30657|POPPALB Populus kitakamiensis gene for phenylalanine ... 333 0.0
 dbj|D43802|POPPALG2BA Populus kitakamiensis gene for phenylalani... 336 0.0
 emb|AF081215|AF081215 Capsicum chinense phenylalanine ammonia-ly... 346 0.0
 5 dbj|D10002|PEAPAL1 P.sativum gene for phenylalanine ammonia-lyas... 349 0.0
 emb|Z49147|HVPAL7RM H.vulgare partial PAL mRNA for phenylalanine... 342 0.0
 emb|X63104|STPAL2 S.tuberosum PAL-2 gene for phenylalanine ammon... 353 0.0
 gb|U39792|PTU39792 Pinus taeda phenylalanine ammonia-lyase (lpPA... 311 0.0
 gb|MI1939|PHVPAL Phaseolus vulgaris L. phenylalanine ammonia-lya... 354 0.0
 10 dbj|E04043|E04043 cDNA sequence coding for kidney bean phenylala... 354 0.0
 emb|AB015871|AB015871 Vitis vinifera gene for phenylalanine ammo... 350 0.0
 emb|Z49145|HVPAL2MR H.vulgare partial PAL mRNA for phenylalanine... 341 0.0
 emb|Z49146|HVPAL3MR H.vulgare partial PAL mRNA for phenylalanine... 311 0.0
 emb|X75967|VVPAL V.vinifera PAL mRNA for phenylalanine ammonia l... 350 0.0
 15 gb|S46988|S46988 phenylalanine ammonia-lyase [soybeans, mRNA, 14... 344 0.0
 emb|AF206634|AF206634 Prunus persica cultivar Loring phenylalani... 336 0.0
 emb|AF167487|AF167487 Eucalyptus globulus phenylalanine ammonia ... 334 e-178
 emb|X99725|TAPALGEN2 T.aestivum PAL gene, coding region. 300 e-137
 emb|AW218834|AW218834 EST301314 tomato root during/after fruit s... 347 e-134
 20 emb|AW031612|AW031612 EST275066 tomato callus, TAMU Lycopersicon... 327 e-132
 emb|AJ289609|BPE289609 Betula pendula partial pal gene for pheny... 205 e-128
 emb|AJ278116|BPE278116 Betula pendula partial pal1 gene for phen... 205 e-128
 emb|AW219303|AW219303 EST301785 tomato root during/after fruit s... 339 e-126
 emb|AW726548|AW726548 GA_Ea0022A01 Gossypium arboreum 7-10 dpa ... 323 e-124
 25 emb|AI166817|AI166817 xylem.est.611 Poplar xylem Lambda ZAPII li... 251 e-117
 gb|BE035366|BE035366 MM06H04 MM Mesembryanthemum crystallinum cD... 235 e-115
 emb|AW776946|AW776946 EST336011 DSIL Medicago truncatula cDNA cl... 280 e-114
 gb|BE020072|BE020072 sm38f08.y1 Gm-c1028 Glycine max cDNA clone ... 233 e-112
 emb|AF019965|AF019965 Pinus monticola phenylalanine ammonia lyas... 205 e-110
 30 emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanin... 247 e-105
 emb|AW216505|AW216505 EST295219 tomato callus, TAMU Lycopersicon... 209 e-104
 emb|AI166477|AI166477 xylem.est.305 Poplar xylem Lambda ZAPII li... 291 e-100
 emb|AV428905|AV428905 AV428905 Lotus japonicus young plants (two... 243 1e-98
 emb|AW220322|AW220322 EST302805 tomato root during/after fruit s... 255 2e-98
 35 emb|AW734312|AW734312 sk81e07.y1 Gm-c1016 Glycine max cDNA clone... 324 6e-98
 emb|AW034774|AW034774 EST278810 tomato callus, TAMU Lycopersicon... 325 3e-93
 emb|AW329762|AW329762 N201031e rootphos(-) Medicago truncatula c... 337 1e-91
 emb|AI777483|AI777483 EST258362 tomato susceptible, Cornell Lyco... 294 3e-90
 emb|AW621418|AW621418 EST312216 tomato root during/after fruit s... 330 2e-89
 40 emb|AW443181|AW443181 EST308111 tomato mixed elicitor, BTI Lycop... 329 6e-89
 emb|AW781748|AW781748 sl90e11.y1 Gm-c1037 Glycine max cDNA clone... 326 3e-88
 emb|X68126|MSPALMR Malus sp. PAL mRNA for phenylalanine ammonia-... 324 1e-87
 emb|AW760268|AW760268 sl48b08.y1 Gm-c1027 Glycine max cDNA clone... 323 3e-87
 emb|AW278641|AW278641 sf63c08.y1 Gm-c1013 Glycine max cDNA clone... 316 4e-85
 45 emb|AF218454|AF218454 Coffea arabica clone 430.4 phenylalanine a... 243 6e-85
 emb|AI899698|AI899698 EST269141 tomato susceptible, Cornell Lyco... 314 2e-84
 emb|AW455294|AW455294 EST311832 tomato root during/after fruit s... 313 3e-84
 emb|AW685111|AW685111 NF026A05NR1F1000 Nodulated root Medicago t... 236 6e-84
 emb|AW667320|AW667320 GA_Ea0008P06 Gossypium arboreum 7-10 dpa ... 189 2e-83
 50 gb|BE021354|BE021354 sm57e05.y1 Gm-c1028 Glycine max cDNA clone ... 308 9e-83
 emb|AI772657|AI772657 EST253757 tomato resistant, Cornell Lycope... 299 2e-80
 emb|AI894514|AI894514 EST263957 tomato callus, TAMU Lycopersicon... 294 1e-78
 gb|L11883|WHTWAL14A Triticum aestivum phenylalanine ammonia-lyas... 87 4e-16
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- 55 Query= AL022347.131_at 12360_at /id_source genbank /description
 emb|caa18468.1| (al022347) serine/threonine kinase-like protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
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 60 http://www.ncgr.org/cgi-bin/ff?al022347
 (1554 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5 Searching.....done

Score. E

Sequences producing significant alignments:

(bits) Value

- 10 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 251 1e-65
 gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 231 8e-60
 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 231 1e-59
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 230 2e-59
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 227 1e-58
- 15 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 226 4e-58
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 225 7e-58
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 225 7e-58
 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 224 1e-57
 gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 186 1e-57
- 20 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 222 6e-57
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 221 8e-57
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 221 2e-56
 gb|BE057261|BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ... 220 3e-56
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 219 6e-56
- 25 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 218 8e-56
 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 216 3e-55
 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 215 5e-55
 emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 213 3e-54
 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 211 1e-53
- 30 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 116 6e-53
 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 207 2e-52
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 117 1e-51
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- 45 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 112 3e-47
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- 60 emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 171 9e-42
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55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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- emb|AW310634|AW310634 sg22e01.x1 Gm-c1024 Glycine max cDNA clone... 82 1e-14
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 5 emb|AW923051|AW923051 DG1_48_G08.g1_A002 Dark Grown 1 (DG1) Sorg... 74 2e-12
 emb|AW695860|AW695860 NF099D07ST1F1061 Developing stem Medicago ... 74 3e-12
 emb|AW704472|AW704472 sk53e05.y1 Gm-c1019 Glycine max cDNA clone... 74 3e-12
 emb|AA901983|AA901983 NCM5F6T7 Mycelial Neurospora crassa cDNA c... 72 9e-12
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 10 emb|AI756356|AI756356 EtESTea42h07.y1 Eimeria S5-2 Sporozoite st... 67 3e-10
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 15 emb|AW694277|AW694277 NF074D01ST1F1012 Developing stem Medicago ... 58 1e-07
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 20 emb|AI043540|AI043540 L30-547T3 Ice plant Lambda Uni-Zap XR expr... 48 2e-04
 emb|AW221661|AW221661 EST298472 tomato fruit red ripe, TAMU Lyco... 48 2e-04
 emb|AW285659|AW285659 LG1_319_G05.g1_A002 Light Grown 1 (LG1) So... 46 5e-04
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 25 emb|AV424693|AV424693 AV424693 Lotus japonicus young plants (two... 46 7e-04
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 55 emb|AW429110|AW429110 EST306566 tomato flower buds 0-3 mm, Corne... 135 5e-32
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 gb|U49330|SLU49330 Solanum lycopersicum pectin methylesterase (P... 135 5e-32
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- emb|X94443|VRPECMEST V.radiata mRNA for pectinmethylesterase. 133 2e-31
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 5 emb|AI494978|AI494978 sa93d09.y1 Gm-cl004 Glycine max cDNA clone... 132 3e-31
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 emb|AW623150|AW623150 EST321095 tomato flower buds 3-8 mm, Corne... 131 6e-31
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 10 emb|X97762|STBPE1 S.tuberosum mRNA BPE1 for pectin methylesterase. 131 7e-31
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 20 emb|AW784073|AW784073 NXNV_117_D06_F Nsf Xylem Normal wood Verti... 126 2e-29
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 25 emb|A17010|A17010 tomato fruit pectin esterase seq ID no1. 121 1e-27
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 30 emb|AW221911|AW221911 EST298722 tomato fruit red ripe, TAMU Lyco... 121 1e-27
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 emb|Z71751|NPPME1MR N.plumbaginifolia mRNA for pectin methyleste... 118 8e-27
 40 emb|AW932254|AW932254 EST358097 tomato fruit mature green, TAMU ... 118 8e-27
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 emb|AI897776|AI897776 EST267219 tomato ovary, TAMU Lycopersicon ... 117 2e-26
 45 gb|U50985|SLU50985 Solanum lycopersicum pectin methylesterase PM... 116 3e-26
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 55 emb|AW687047|AW687047 NF005D06RT1F1057 Developing root Medicago ... 113 2e-25
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 10 emb|Y07899|CPSPE1 C.papaya mRNA for pectinesterase. 97 3e-20
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 20 emb|AA556385|AA556385 240 Loblolly pine C Pinus taeda cDNA clone... 71 1e-12
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 30 http://www.ncgr.org/cgi-bin/ff?al079344
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 Database: plantfungal
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 45 emb|AW704801|AW704801 sk55f12.y1 Gm-c1019 Glycine max cDNA clone... 148 3e-43
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 60 emb|AW596708|AW596708 sj15g06.y1 Gm-c1032 Glycine max cDNA clone... 46 5e-04
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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	gb S35175 S35175 linamarase=beta-glucosidase [Manihot esculenta=...	92	2e-19
	emb AF072736 AF072736 Pinus contorta beta-glucosidase mRNA, comp...	92	2e-19
30	emb AW568866 AW568866 si73c03.y1 Gm-c1031 Glycine max cDNA clone...	91	4e-19
	gb U50201 PSU50201 Prunus serotina prunasin hydrolase precursor ...	90	5e-19
	emb AW560545 AW560545 EST315593 DSIR Medicago truncatula cDNA cl...	90	7e-19
	emb AI900802 AI900802 sb93e10.y1 Gm-c1017 Glycine max cDNA clone...	89	2e-18
	gb BE058816 BE058816 sn21c08.y1 Gm-c1016 Glycine max cDNA clone ...	89	2e-18
35	emb AW597982 AW597982 sj40c05.y1 Gm-c1008 Glycine max cDNA clone...	89	2e-18
	emb AW395210 AW395210 sh45c06.y1 Gm-c1017 Glycine max cDNA clone...	89	2e-18
	emb AW570004 AW570004 si85e02.y1 Gm-c1031 Glycine max cDNA clone...	89	2e-18
	emb AW733524 AW733524 sk74g01.y1 Gm-c1016 Glycine max cDNA clone...	89	2e-18
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40	emb AW423387 AW423387 sh65b01.y1 Gm-c1015 Glycine max cDNA clone...	89	2e-18
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	emb AB003089 AB003089 Polygonum tinctorium mRNA for beta-glucosi...	86	9e-18
50	emb AW279169 AW279169 sf67c06.y1 Gm-c1013 Glycine max cDNA clone...	85	2e-17
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 5 emb|AJ005950|AJ005950 AJ005950 chickpea mRNA CAP-4 Cicer arietin... 79 1e-15
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 emb|AW677220|AW677220 DG1_6_D11.g1_A002 Dark Grown 1 (DG1) Sorgh... 77 7e-15
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 15 emb|AW923628|AW923628 DG1_56_E12.g1_A002 Dark Grown 1 (DG1) Sorg... 77 7e-15
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 20 emb|AB003109|AB003109 Humicola grisea var. thermoidea bgl4 gene ... 76 1e-14
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 35 emb|AF149311|AF149311 Rauvolfia serpentina raucaffricine-O-beta-... 75 3e-14
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 40 emb|AF163097|AF163097 Dalbergia cochinchinensis dalcocinin 8'-O... 62 2e-13
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 emb|X56733|TRBG104 T.repens mRNA for cyanogenic beta-glucosidase... 52 2e-11
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 55 emb|X59881|SAMYRMB1 S.alba thioglucoside glucohydrolase (myrosin... 63 7e-11
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 (1374 letters)

5

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

10

Score E

Sequences producing significant alignments:

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 emb|AI772760|AI772760 EST253860 tomato resistant, Cornell Lycope... 108 7e-33
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 20 emb|AW686482|AW686482 NF041H08NR1F1000 Nodulated root Medicago t... 112 8e-28
 emb|AW704059|AW704059 sk27d01.y1 Gm-c1028 Glycine max cDNA clone... 119 2e-27
 emb|AW350257|AW350257 GM210007B20B11R Gm-r1021 Glycine max cDNA ... 122 5e-27
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 25 emb|AI776363|AI776363 EST257463 tomato resistant, Cornell Lycope... 114 1e-24
 emb|AI731720|AI731720 BNLGHi10579 Six-day Cotton fiber Gossypium... 112 5e-24
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 40 emb|AW565825|AW565825 LG1_352_B09.g1_A002 Light Grown 1 (LG1) So... 57 8e-14
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 45 emb|AW398760|AW398760 EST309260 L. pennellii trichome, Cornell U... 54 2e-12
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 50 emb|AI728748|AI728748 BNLGHi11497 Six-day Cotton fiber Gossypium... 57 4e-12
 emb|AW697758|AW697758 Str1-D8 Sugar Beet germination cDNA librar... 46 5e-11
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 55 emb|AW734790|AW734790 sk88g11.y1 Gm-c1035 Glycine max cDNA clone... 42 5e-09
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 emb|AW775488|AW775488 EST334553 DSIL Medicago truncatula cDNA cl... 58 2e-07
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 60 emb|AW282482|AW282482 LG1_313_B10.g1_A002 Light Grown 1 (LG1) So... 57 3e-07
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emb|AW731593|AW731593 GA_Ea0030P10 Gossypium arboreum 7-10 dpa ... 37 1e-06
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5 emb|AI736841|AI736841 sb34c09.y1 Gm-c1012 Glycine max cDNA clone... 50 5e-05
emb|AW154916|AW154916 EST290281 tomato root deficiency, Cornell ... 40 6e-05
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emb|AI487433|AI487433 EST245755 tomato ovary, TAMU Lycopersicon ... 44 1e-04
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10 emb|AW564044|AW564044 LG1_281_A09.b1_A002 Light Grown 1 (LG1) So... 47 4e-04
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15 emb|AI486814|AI486814 EST245136 tomato ovary, TAMU Lycopersicon ... 46 5e-04
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20 emb|AI728904|AI728904 BNLGHi11968 Six-day Cotton fiber Gossypium... 41 0.002
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25 emb|AI485669|AI485669 EST243990 tomato ovary, TAMU Lycopersicon ... 44 0.003
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30 emb|AV411141|AV411141 AV411141 Lotus japonicus young plants (two... 41 0.023
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35 emb|AW099588|AW099588 sd43h11.y1 Gm-c1016 Glycine max cDNA clone... 40 0.031
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50 emb|AW688707|AW688707 NF010F12ST1F1000 Developing stem Medicago ... 37 0.29
emb|AI483679|AI483679 EST249550 tomato ovary, TAMU Lycopersicon ... 37 0.39
emb|AB029365|AB029365 Cephalotaxus harringtonia mitochondrial ge... 29 0.83

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60 (1512 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments:

(bits) Value

- emb|AF223643|AF223643 Pisum sativum xyloglucan fucosyltransferas... 311 e-147
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- emb|AW693268|AW693268 NF064A03ST1F1000 Developing stem Medicago ... 109 5e-32
- emb|AW508697|AW508697 si35c12.y1 Gm-r1030 Glycine max cDNA clone... 77 6e-31
- emb|AW689377|AW689377 NF018E07ST1F1000 Developing stem Medicago ... 78 2e-30
- 15 gb|BE058474|BE058474 sn16f08.y1 Gm-c1016 Glycine max cDNA clone ... 102 6e-21
- emb|AW704030|AW704030 sk27a04.y1 Gm-c1028 Glycine max cDNA clone... 64 5e-20
- emb|AU089974|AU089974 AU089974 Hordeum vulgare subsp. vulgare Up... 45 1e-19
- emb|AW720399|AW720399 LjNEST22c8r Lotus japonicus nodule library... 83 1e-18
- emb|AU089968|AU089968 AU089968 Hordeum vulgare subsp. vulgare Up... 45 5e-17
- 20 emb|AV417193|AV417193 AV417193 Lotus japonicus young plants (two... 88 2e-16
- emb|AQ855554|AQ855554 CpG1646A CpIOWAgDNA1 Cryptosporidium parvu... 35 1.1
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- emb|AW934637|AW934637 EST353529 tomato flower buds 0-3 mm, Corne... 35 2.1
- emb|AF050740|AF050740 Plasmodium falciparum variant-specific sur... 35 2.1
- 25 emb|AI329848|AI329848 b8h09ne.r1 Neurospora crassa evening cDNA ... 35 2.1
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- emb|AW933190|AW933190 EST359033 tomato fruit mature green, TAMU ... 35 2.1
- emb|AL109832|SPAC630 S.pombe chromosome I cosmid c630. 34 2.9
- emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 34 4.0
- 30 emb|A85491|A85491 Sequence 150 from Patent EP0866129. 34 4.0
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- emb|AL356172|NCB23L21 Neurospora crassa DNA linkage group II BAC... 33 5.5
- 35 emb|AW617216|AW617216 EST323627 L. hirsutum trichome, Cornell Un... 33 5.5
- emb|AL160493|LMFLCHR26 Leishmania major Friedlin assembled chrom... 33 7.6
- emb|AF056622|AF056622 Vitis vinifera putative Cu/Zn superoxide d... 33 7.6
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(1488 letters)

45

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments:

(bits) Value

- emb|AW203670|AW203670 sf36h04.y1 Gm-c1028 Glycine max cDNA clone... 334 1e-90
- 55 emb|AW268012|AW268012 EST306234 DSIR Medicago truncatula cDNA cl... 246 2e-83
- emb|AW041000|AW041000 EST283864 tomato mixed elicitor, BTI Lycop... 307 1e-82
- emb|AW472433|AW472433 si25b07.y1 Gm-c1029 Glycine max cDNA clone... 306 3e-82
- emb|AW560118|AW560118 EST315166 DSIR Medicago truncatula cDNA cl... 166 3e-64
- emb|AW394771|AW394771 sh35b02.y1 Gm-c1017 Glycine max cDNA clone... 213 3e-54
- 60 emb|AW622568|AW622568 EST313368 tomato root during/after fruit s... 181 5e-51
- emb|AW737712|AW737712 EST339139 tomato flower buds, anthesis, Co... 162 1e-45

	emb AW694002 AW694002 NF071F03ST1F1029 Developing stem Medicago ...	135	2e-45
	gb BE124930 BE124930 EST393965 GVN Medicago truncatula cDNA clon...	183	2e-45
	emb Z98974 SPAC19A8 S.pombe chromosome I cosmid c19A8.	114	1e-38
5	emb AL111746 CNS019KA Botrytis cinerea strain T4 cDNA library un...	123	2e-38
	emb AL111744 CNS019K8 Botrytis cinerea strain T4 cDNA library un...	123	3e-37
	emb AW922483 AW922483 DG1_19_A10.g1_A002 Dark Grown 1 (DG1) Sorg...	155	8e-37
	emb Z49211 SC9711X S.cerevisiae chromosome XIII cosmid 9711.	113	3e-36
	gb U34636 SCU34636 Saccharomyces cerevisiae cytochrome P450 gene...	113	3e-36
	emb AW928489 AW928489 EST337277 tomato flower buds 8 mm to pre-a...	149	5e-35
10	emb AL033396 CAC35A5 C.albicans cosmid Ca35A5.	117	2e-34
	emb AW310494 AW310494 sf36h04.x1 Gm-c1028 Glycine max cDNA clone...	124	2e-30
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	emb AW496913 AW496913 ga50a07.y1 Moss EST library PPU Physcomitr...	98	2e-19
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	emb AV425399 AV425399 AV425399 Lotus japonicus young plants (two...	66	9e-10
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40	emb AW728587 AW728587 GA_Ea0017C12 Gossypium arboreum 7-10 dpa ...	37	2e-05
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	emb AW254794 AW254794 ML1076 peppermint glandular trichome Menth...	38	6e-05
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	emb AW254868 AW254868 ML1290 peppermint glandular trichome Menth...	37	7e-05
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55	emb AI855736 AI855736 sc23f01.y1 Gm-c1013 Glycine max cDNA clone...	49	1e-04
	emb AI900822 AI900822 sb93h05.y1 Gm-c1017 Glycine max cDNA clone...	49	1e-04
	emb AW234028 AW234028 sf33c07.y1 Gm-c1028 Glycine max cDNA clone...	49	1e-04
	emb AW706535 AW706535 sj57g05.y1 Gm-c1033 Glycine max cDNA clone...	49	1e-04
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60	emb AW255346 AW255346 ML357 peppermint glandular trichome Mentha...	37	1e-04
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40 (417 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Score E

Sequences producing significant alignments: (bits) Value

50	emb AW760536 AW760536 sl51e12.y1 Gm-c1027 Glycine max cDNA clone...	82	2e-15
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	emb AI775217 AI775217 EST256317 tomato resistant, Cornell Lycop...	59	7e-13
55	emb AW458973 AW458973 sh17e01.y1 Gm-c1016 Glycine max cDNA clone...	61	3e-12
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	emb AW102493 AW102493 sd88h04.y1 Gm-c1009 Glycine max cDNA clone...	61	4e-12
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emb|AI563167|AI563167 EST00291 watermelon lambda zap library Cit... 38 0.046

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35 (1161 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	emb AI055338 AI055338 coau0003L11 Cotton Boll Abscission Zone cD...	56	2e-07
	emb AW693058 AW693058 NF059E03ST1F1021 Developing stem Medicago ...	49	9e-05
50	emb AW686062 AW686062 NF033A11NR1F1000 Nodulated root Medicago t...	49	9e-05
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	emb AW761333 AW761333 sl66b07.y1 Gm-c1027 Glycine max cDNA clone...	32	6.9
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	gb M80656 EIMPEM Eimeria maxima 230 kDa protein (pEM230) mRNA, 3...	32	7.3
	emb AI026260 AI026260 L0-455T3 Ice plant Lambda Uni-Zap XR expre...	32	7.3
	emb AQ640247 AQ640247 927P1-18B12.TV 927P1 Trypanosoma brucei ge...	32	7.3
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50	emb AW038822 AW038822 EST280778 tomato mixed elicitor, BTI Lycop...	282	3e-75
	emb AI488594 AI488594 EST246933 tomato ovary, TAMU Lycopersicon ...	280	2e-74
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	emb AW201152 AW201152 se98d11.y1 Gm-c1027 Glycine max cDNA clone...	137	1e-49
	emb AW011518 AW011518 ST21G07 Pine TripleX shoot tip library Pin...	178	5e-44
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60	emb AW459302 AW459302 sh23c04.y1 Gm-c1016 Glycine max cDNA clone...	166	3e-40
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30	emb AF106079 AF106079 Chlamydomonas reinhardtii dynein heavy cha...	34	1.8
	gb M80437 YSCSEQ Saccharomyces cerevisiae gene, complete cds.	34	2.5
	gb J05603 YSCCTR Saccharocycles cerevisiae choline transport prot...	34	2.5
	emb Z72599 SCYGL077C S.cerevisiae chromosome VII reading frame O...	34	2.5
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5 emb|AW696053|AW696053 NF102A09ST1F1068 Developing stem Medicago ... 32 8.9
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emb|X55347|LPHSF24 Tomato mRNA for heat stress transcription fac... 32 8.9
10 emb|X54488|CRAH2 Chlamydomonas reinhardtii CAH2 gene for carbon... 32 8.9
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emb|AF020814|AF020814 Pisum sativum glucose-6-phosphate/phosphat... 32 8.9
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(1869 letters)

30 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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40 emb|AW596038|AW596038 si97b04.y1 Gm-c1032 Glycine max cDNA clone... 98 4e-28
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45 emb|AW651335|AW651335 EST329789 tomato germinating seedlings, TA... 82 8e-15
gb|BE052602|BE052602 GA_Ea0032J02f Gossypium arboreum 7-10 dpa ... 50 2e-13
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emb|AW226419|AW226419 ST82B05 Pine TriplEx shoot tip library Pin... 62 2e-08
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60 emb|AB002141|AB002141 Pyrus pyrifolia mRNA for S5-RNase, complet... 35 1.3
dbj|D88282|D88282 Pyrus serotina mRNA for S5-RNase, complete cds. 35 1.3

- emb|AB025421|AB025421 *Pyrus pyrifolia* gene for S3-RNase, complet... 35 1.3
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 5 emb|AW677734|AW677734 WS1_10_E07.g1_A002 Water-stressed 1 (WS1) ... 35 1.8
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 emb|AL355928|NCB1D4 *Neurospora crassa* DNA linkage group II BAC c... 34 2.4
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 10 gb|M23080|BLYHORA *Hordeum vulgare* alpha-hordothionin (Hth-1) gen... 26 3.3
 emb|AQ989014|AQ989014 35C1D04NE.R1 *C. parvum* Lambda Zap Express ... 34 3.3
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 15 emb|AL035064|SPAC1687 *S.pombe* chromosome I cosmid c1687. 34 3.3
 emb|AJ223010|SCP223010 *Schizosaccharomyces pombe* pmt2 gene. 34 3.3
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 emb|AW683291|AW683291 NF010B07LF1F1060 Developing leaf Medicago ... 34 3.3
 emb|X63357|HVNREHTH *H.vulgare* Hth-1 gene (promoter region). 26 3.3
 20 emb|AW710511|AW710511 e4c05ne.fl *Neurospora crassa* evening cDNA ... 34 4.4
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 emb|AA901701|AA901701 NCP2A2T7 Perithecial *Neurospora crassa* cDN... 33 4.6
 emb|AF128526|AF128526 *Theileria lestoquardi* sporozoite antigen S... 33 4.6
 25 gb|M76671|TOMEXTENB *L.esculentum* extensin (class II) gene, compl... 33 4.6
 emb|AL049181|PFMAL13P4 *Plasmodium falciparum* chromosome 13 strai... 33 4.6
 emb|AB036809|AB036809 *Saccharomyces cerevisiae* DNA, plasmid pTLU... 33 4.6
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 gb|L12467|YSCGCN1A *Saccharomyces cerevisiae* translational activa... 33 6.1
 30 emb|AW725958|AW725958 GA_Ea0020E02 *Gossypium arboreum* 7-10 dpa ... 33 6.1
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 emb|Z72717|SCYGL195W *S.cerevisiae* chromosome VII reading frame O... 33 6.1
 emb|X55694|LEEXTEN14 Tomato extensin mRNA (clone w10-1 L). 33 6.3
 emb|X55693|LEEXTEN13 Tomato mRNA for a glycine-rich protein (clo... 33 6.3
 35 emb|AV427911|AV427911 AV427911 *Lotus japonicus* young plants (two... 33 6.3
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 emb|AW690872|AW690872 NF039H07ST1F1000 Developing stem Medicago ... 33 6.3
 emb|AW688252|AW688252 NF005C01ST1F1000 Developing stem Medicago ... 33 6.3
 gb|L38908|TOBEXTE *Nicotiana tabacum* extensin gene, complete cds. 33 6.3
 40 dbj|D13951|TOBEXTS Tobacco gene for extensin, complete cds. 33 6.3
 dbj|E05393|E05393 DNA sequence encoding *Nicotiana tabacum* extensin. 33 6.3
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 emb|AW704352|AW704352 sk18c03.y1 Gm-c1028 Glycine max cDNA clone... 33 8.3
 emb|AF085735|AF085735 *Trypanosoma triglae* kinetoplast minicircle... 33 8.3
 45 emb|AW457944|AW457944 sh97h02.y1 Gm-c1016 Glycine max cDNA clone... 33 8.3
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 emb|AF046120|AF046120 *Candida glabrata* ATP-binding cassette tran... 32 8.6
 50 emb|AW725268|AW725268 GA_Ea0015L23 *Gossypium arboreum* 7-10 dpa ... 32 8.6
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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emb AI488047 AI488047 EST246369 tomato ovary, TAMU Lycopersicon ...	78	3e-24
emb AW671633 AW671633 LG1_349_D04.b1_A002 Light Grown 1 (LG1) So...	111	4e-24
emb AI495965 AI495965 sb18d07.y1 Gm-c1004 Glycine max cDNA clone...	102	3e-21
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emb AT001714 AT001714 AT001714 Flower bud cDNA Brassica rapa sub...	52	3e-09
emb AW621058 AW621058 sj95d05.y1 Gm-c1023 Glycine max cDNA clone...	52	3e-08
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25 emb AW040524 AW040524 EST283484 tomato mixed elicitor, BTI Lycop...	35	0.12
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35 emb AI055583 AI055583 coau0004G11 Cotton Boll Abscission Zone cD...	33	2.0
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15 Database: plantfungal
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 (393 letters)

Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

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5 gb|U25841|YSCP9677 Saccharomyces cerevisiae chromosome XVI cosmi... 32 2.6
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emb|Y10156|BNMYAP12 B.napus for myrosinase-associated protein, c... 31 3.5
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(777 letters)

Database: plantfungal
25 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
30 Sequences producing significant alignments: (bits) Value

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emb|AW348772|AW348772 GM210003A22G1R Gm-r1021 Glycine max cDNA 3... 222 3e-
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emb|AW133238|AW133238 se16b04.y1 Gm-c1013 Glycine max cDNA clone... 200 8e-51
emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 190 9e-48
emb|AW930095|AW930095 EST340552 tomato fruit mature green, TAMU ... 190 9e-48
40 emb|AW399412|AW399412 EST309912 L. pennellii trichome, Cornell U... 189 2e-47
emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 189 2e-47
emb|AI896756|AI896756 EST266199 tomato callus, TAMU Lycopersicon... 188 4e-47
emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 188 4e-47
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15 (777 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments: (bits) Value

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	emb AW185963 AW185963 se61h02.y1 Gm-c1019 Glycine max cDNA clone...	52	6e-06
	emb AW153055 AW153055 se34d02.y1 Gm-c1015 Glycine max cDNA clone...	45	7e-04
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	emb AW398499 AW398499 EST308999 L. pennellii trichome, Cornell U...	33	2.6
	emb AW349705 AW349705 GM210005B21C6R Gm-r1021 Glycine max cDNA 3...	33	2.6
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	emb AW102268 AW102268 sd85e07.y1 Gm-c1009 Glycine max cDNA clone...	33	3.5
	emb AI441442 AI441442 sa86a02.y1 Gm-c1004 Glycine max cDNA clone...	33	3.5
	emb X78037 MIOB250 O.berteriana mitochondrial DNA for orf250.	33	3.5
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30	emb AW719534 AW719534 LjNEST5c5rW Lotus japonicus nodule library...	32	4.8
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S...	32	4.8
	emb AF119172 AF119172 Cyanophora paradoxa alpha-tubulin (atub) g...	32	4.8
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	gb U56098 AOU56098 Aspergillus oryzae putative DNA binding prote...	32	4.8
35	emb AI507866 AI507866 sa88b06.y1 Gm-c1004 Glycine max cDNA clone...	32	4.8
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	emb AI043302 AI043302 TENU0942 T. cruzi epimastigote normalized ...	32	6.6
	emb AI043452 AI043452 TENU1011 T. cruzi epimastigote normalized ...	32	6.6
50	emb AW773882 AW773882 EST332868 KV3 Medicago truncatula cDNA clo...	32	6.6
	emb AW219946 AW219946 EST302429 tomato root during/after fruit s...	32	6.6
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	emb AW442607 AW442607 EST307537 tomato mixed elicitor, BTI Lycop...	31	9.1
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	emb AI780125 AI780125 EST261004 tomato susceptible, Cornell Lyco...	31	9.1
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10	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac006587 /ncgi http://www.ncgr.org/cgi-bin/ff?ac006587 (504 letters)		
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25	emb AC005139 AC005139 Plasmodium falciparum chromosome 12, *** S...	36	0.22
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	emb AL034559 PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq...	35	0.30
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	emb AL049184 PFMAL13P3 Plasmodium falciparum chromosome 13 strai...	35	0.56
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	gb L27838 PFARHPR Plasmodium yoelii rhoptry protein, complete cds.	29	1.1
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55	gb U84395 PFU84395 Plasmodium falciparum sarcalumenin/eps15 homo...	33	1.5
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30	emb AL008970 PFMAL3P4 Plasmodium falciparum MAL3P4, complete seq...	31 2.9
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50	emb AA557046 AA557046 888 Loblolly pine N Pinus taeda cDNA clone...	32 3.8
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Database: plantfungal
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(844 letters)

Database: plantfungal

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	emb AI165879 AI165879 B002P45U Hybrid aspen plasmid library Popu...	84	2e-15
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	emb AA787149 AA787149 m8a03a1.fl Aspergillus nidulans 24hr asexu...	46	5e-04
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 (2553 letters)

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E
 Sequences producing significant alignments: (bits) Value

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emb|Y00268|BOSLSG Brassica oleracea mRNA for S-locus specific gl... 408 e-174
emb|X03170|BOSLSGR Brassica oleracea mRNA 3' end for S-locus-spe... 408 e-174
dbj|D84468|BNASLG8A Brassica campestris mRNA for S-glycoprotein ... 478 e-173
30 emb|AB009681|AB009681 Raphanus sativus SLG(S5) gene for S glycop... 406 e-173
gb|S70937|S70937 self-incompatibility gene [Brassica campestris,... 283 e-173
dbj|D85218|D85218 Brassica campestris DNA for S glycoprotein, pa... 286 e-173
dbj|D85213|D85213 Brassica campestris DNA for S glycoprotein, pa... 283 e-173
emb|AB009683|AB009683 Raphanus sativus SLG(S8) gene for S glycop... 284 e-173
35 dbj|D85227|D85227 Brassica campestris DNA for S glycoprotein, pa... 293 e-172
dbj|D85211|D85211 Brassica oleracea DNA for S glycoprotein, part... 281 e-172
emb|X16123|BOS292 B. oleracea mRNA for S-locus specific glycopro... 397 e-172
gb|M36301|BNASLSGRA B.campestris S-locus-specific glycoprotein m... 402 e-172
dbj|D85225|D85225 Brassica campestris DNA for S glycoprotein, pa... 281 e-172
40 dbj|D85216|D85216 Brassica campestris DNA for S glycoprotein, pa... 409 e-171
dbj|D85204|D85204 Brassica oleracea DNA for S glycoprotein, part... 283 e-171
dbj|D85201|D85201 Brassica oleracea DNA for S glycoprotein, part... 490 e-171
emb|AB009684|AB009684 Raphanus sativus SLG(S7) gene for S glycop... 397 e-171
emb|X79432|BOSRK3 B.oleracea SRK3 gene. 396 e-171
45 dbj|D85208|D85208 Brassica oleracea DNA for S glycoprotein, part... 282 e-171
emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 286 e-170
dbj|D84469|BNASLG12B Brassica campestris mRNA for S-glycoprotein... 287 e-170
emb|AB013717|AB013717S1 Brassica rapa gene for SRK46Bra, exon 1. 269 e-170
dbj|D85209|D85209 Brassica oleracea DNA for S glycoprotein, part... 286 e-170
50 dbj|D85205|D85205 Brassica oleracea DNA for S glycoprotein, part... 395 e-170
dbj|D85221|D85221 Brassica campestris DNA for S glycoprotein, pa... 348 e-170
emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 288 e-169
emb|AB032471|AB032471 Brassica oleracea SLG pseudogene for S-loc... 398 e-169
gb|L08608|BNASLOCGLY Brassica napus S-locus glycoprotein mRNA, c... 477 e-168
55 emb|Z21608|BNESLOGPA B.napus mRNA for endogenous S-locus glycopr... 477 e-168
gb|L10736|BNASLGGA Brassica napus S-locus related glycoprotein (... 477 e-168
dbj|D85222|D85222 Brassica campestris DNA for S glycoprotein, pa... 243 e-166
dbj|D85229|D85229 Brassica oleracea DNA for S glycoprotein, part... 401 e-166
emb|AB009679|AB009679 Raphanus sativus SLG(S3) gene for S glycop... 285 e-166
60 dbj|D85212|D85212 Brassica oleracea DNA for S glycoprotein, part... 244 e-164
dbj|D85214|D85214 Brassica campestris DNA for S glycoprotein, pa... 395 e-163

	emb AB009677 AB009677 Raphanus sativus SLG(S1) gene for S glycop...	266	e-163
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	emb AB008190 AB008190 Brassica rapa gene for SLG29, complete cds.	290	e-163
	emb Y18261 BOY18261 Brassica oleracea SLGB gene, partial.	286	e-163
5	emb Z19548 BNSLGPII B.napus mRNA for S-locus glycoprotein type II.	286	e-163
	emb Z11724 BNWSLGLP B. napus mRNA for S-locus glycoprotein.	278	e-160
	emb AJ245480 BNA245480 Brassica napus slg gene for S-locus glyco...	380	e-160
	emb AB024415 AB024415 Brassica oleracea SLG2-b mRNA, complete cds.	282	e-160
	dbj D85226 D85226 Brassica campestris DNA for S glycoprotein, pa...	221	e-160
10	dbj D85223 D85223 Brassica campestris DNA for S glycoprotein, pa...	224	e-160
	emb AB032472 AB032472 Brassica oleracea SLG60 pseudogene for S60...	160	e-159
	emb Z18921 BOSRKL B.oleracea gene for S-receptor kinase-like pro...	198	e-158
	emb AB012105 AB012105 Brassica rapa mRNA for SLG45; complete cds.	221	e-158
	dbj D88193 D88193 Brassica rapa DNA for S-receptor kinase, compl...	160	e-158
15	emb X51637 BOSLSGA B.oleracea SLSG mRNA for self-incompatibility...	263	e-155
	dbj D88192 D88192 Brassica rapa DNA for S-locus glycoprotein, co...	148	e-153
	dbj D30050 BOLSRKB Turnip mRNA for S-glycoprotein SLG9, complete...	148	e-153
	emb AF161333 AF161333 Raphanus raphanistrum subsp. raphanistrum ...	310	e-150
	emb AF162908 AF162908 Hirschfeldia incana S-locus related (SLR) ...	261	e-150
20	emb Y12321 BOY12321 Brassica oleracea SLG-Sc and SLA-Sc genes an...	285	e-149
	emb AB009872 AB009872 Orychophragmus violaceus gene for SLR1, pa...	413	e-149
	emb X57673 BOSLR2RNA B.oleraceae RNA for S-locus-related glycopr...	167	e-149
	emb AB009873 AB009873 Cheiranthus cheiri gene for SLR1, partial ...	163	e-147
	emb X58440 BCNS1 B.campestris NS1 mRNA for NS1 glycoprotein.	273	e-145
25	emb X52089 BOSLRG Brassica gene for S locus related glycoprotein.	272	e-143

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http://www.ncgr.org/cgi-bin/ff?ac003974
(2673 letters)

35 Database: plantfungal
661,018 sequences; 426,114,510 total letters

40 Searching.....done

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45	emb AF053998 AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ...	148	4e-74
	emb A67434 A67434 Sequence 7 from Patent WO9743429.	148	4e-74
	emb AF053993 AF053993 Lycopersicon esculentum disease resistance...	148	4e-74
	emb A67429 A67429 Sequence 2 from Patent WO9743429.	148	4e-74
	emb A67428 A67428 Sequence 1 from Patent WO9743429.	148	4e-74
50	emb AF053995 AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ...	150	4e-74
	emb AF053997 AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) ...	146	1e-72
	emb A67432 A67432 Sequence 5 from Patent WO9743429.	146	1e-72
	gb U42445 U42445 Lycopersicon pimpinellifolium leucine rich repe...	150	3e-71
	emb A57133 A57133 Sequence 4 from Patent WO9531564.	150	3e-71
	gb U42444 U42444 Lycopersicon pimpinellifolium leucine rich repe...	150	8e-71
55	emb A57130 A57130 Sequence 1 from Patent WO9531564.	150	8e-71
	emb AB029327 AB029327 Nicotiana tabacum mRNA for elicitor-induci...	97	4e-65
	emb AF053994 AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) ...	149	6e-37
	emb AF119040 AF119040 Lycopersicon esculentum haplotype Northern...	143	3e-36
	emb AF053996 AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr...	144	3e-35
60	emb AF119041 AF119041 Lycopersicon esculentum haplotype Southern...	139	2e-33
	emb AJ002235 LHJ002235 Lycopersicon hirsutum Cf-4 resistance gen...	139	3e-33

- emb|AJ002236|LPJ002236 *Lycopersicon pimpinellifolium* Cf-9 resist... 140 4e-33
emb|AJ002237|LEJ002237 *Lycopersicon esculentum* haplotype of the ... 138 1e-32
emb|Y12640|LECF4A *L. esculentum* Cf-4A gene. 137 1e-32
emb|A58270|A58270 Sequence 1 from Patent WO9635790. 138 2e-31
5 gb|U15936|LPU15936 *Lycopersicon pimpinellifolium* Cf-9 precursor ... 138 2e-31
emb|AI778581|AI778581 EST259460 tomato susceptible, Cornell Lyco... 92 1e-29
emb|AW458587|AW458587 sh11a09.y1 Gm-cl016 Glycine max cDNA clone... 131 3e-29
emb|AW306725|AW306725 sf47e12.y1 Gm-cl009 Glycine max cDNA clone... 129 1e-28
emb|AF215729|AF215729 Glycine max RFLP clone A 45-10 sequence; a... 123 5e-27
10 emb|X81370|TAAWJL236 *T. aestivum* (subclone pAWJL236) AWJL236 gene. 115 8e-27
emb|AF140552|AF140552 *Lycopersicon esculentum* plant disease resi... 121 2e-26
emb|AI895949|AI895949 EST265392 tomato callus, TAMU *Lycopersicon*... 70 5e-25
emb|AW624314|AW624314 EST322175 tomato flower buds 3-8 mm, Corne... 113 5e-24
emb|X81369|TAAWJL218 *T. aestivum* (subclone pAWJL218) AWJL218 gene. 104 1e-23
15 emb|X81367|TAAWJL172 *T. aestivum* (subclone pAWJL172) AWJL172 gene. 99 7e-23
emb|X81368|TAAWJL175 *T. aestivum* (subclone pAWJL175) AWJL175 gene. 101 2e-22
emb|AW705275|AW705275 sk59a10.y1 Gm-cl019 Glycine max cDNA clone... 108 2e-22
emb|AF166121|AF166121 *Hordeum vulgare* Cf2/Cf5 disease resistance... 94 3e-22
emb|AI779817|AI779817 EST260696 tomato susceptible, Cornell Lyco... 100 1e-21
20 emb|AW888094|AW888094 NXNV_108_E11_F Nsf Xylem Normal wood Verti... 105 2e-21
emb|AQ917191|AQ917191 T233043b *Medicago truncatula* BAC library M... 93 1e-20
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25 emb|AW064561|AW064561 ST33A08 Pine TriPEX shoot tip library Pin... 98 3e-19
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emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 82 1e-18
30 emb|AW032163|AW032163 EST275617 tomato callus, TAMU *Lycopersicon*... 64 1e-18
emb|AW979663|AW979663 EST341269 tomato root deficiency, Cornell ... 61 1e-18
emb|AW650508|AW650508 EST328962 tomato germinating seedlings, TA... 91 1e-18
emb|AI488023|AI488023 EST246345 tomato ovary, TAMU *Lycopersicon* ... 91 1e-18
emb|AI896676|AI896676 EST266119 tomato callus, TAMU *Lycopersicon*... 91 1e-18
35 emb|AW307311|AW307311 sf55d03.y1 Gm-cl009 Glycine max cDNA clone... 66 2e-18
emb|AV415568|AV415568 AV415568 *Lotus japonicus* young plants (two... 85 2e-18
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emb|AI727073|AI727073 BNLGHi7256 Six-day Cotton fiber *Gossypium* ... 95 2e-18
emb|AW306675|AW306675 se53h08.y1 Gm-cl017 Glycine max cDNA clone... 95 3e-18
40 emb|X79130|TSLRRR *Triticum* sp. (pAWJL3) leucine rich repeat regi... 84 4e-18
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emb|AW775087|AW775087 EST334238 KV3 *Medicago truncatula* cDNA clo... 94 6e-18
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emb|AW267958|AW267958 EST306300 DSIR *Medicago truncatula* cDNA cl... 80 7e-18
45 emb|AI895893|AI895893 EST265336 tomato callus, TAMU *Lycopersicon*... 61 9e-18
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50 emb|AW929854|AW929854 EST354124 tomato flower buds 8 mm to pre-a... 91 4e-17
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emb|AW033367|AW033367 EST276938 tomato callus, TAMU *Lycopersicon*... 89 1e-16
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55 emb|AI896313|AI896313 EST265756 tomato callus, TAMU *Lycopersicon*... 60 1e-16
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emb|AI488443|AI488443 EST246782 tomato ovary, TAMU *Lycopersicon* ... 88 3e-16
emb|AW033129|AW033129 EST276688 tomato callus, TAMU *Lycopersicon*... 78 3e-16
60 emb|AW127035|AW127035 ga20c02.y1 Moss EST library PPU *Physcomitr*... 88 4e-16
emb|AI895669|AI895669 EST265112 tomato callus, TAMU *Lycopersicon*... 88 4e-16

emb|AW618685|AW618685 EST320671 *L. pennellii* trichome, Cornell U... 88 4e-16
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5 emb|AW694942|AW694942 NF081G02ST1F1018 Developing stem Medicago ... 78 6e-16
emb|AV415057|AV415057 AV415057 *Lotus japonicus* young plants (two... 87 7e-16
emb|AW399097|AW399097 EST309597 *L. pennellii* trichome, Cornell U... 63 8e-16
emb|AW761367|AW761367 sl66e07.y1 Gm-c1027 Glycine max cDNA clone... 86 1e-15
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10 emb|AV428126|AV428126 AV428126 *Lotus japonicus* young plants (two... 85 2e-15
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emb|AW455303|AW455303 EST311841 tomato root during/after fruit s... 85 3e-15
15 emb|AW869870|AW869870 NXNV_122_E02_F Nsf Xylem Normal wood Verti... 85 3e-15
emb|AW398651|AW398651 EST309151 *L. pennellii* trichome, Cornell U... 84 4e-15
emb|AW398661|AW398661 EST309161 *L. pennellii* trichome, Cornell U... 84 4e-15
emb|AF049920|AF049920 *Petunia x hybrida* PGPS/D4 (PGPS/D4) mRNA, ... 84 4e-15
emb|AW624634|AW624634 EST322579 tomato flower buds 3-8 mm, Corne... 59 4e-15
20 emb|AW618879|AW618879 EST320865 *L. pennellii* trichome, Cornell U... 62 4e-15
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25 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
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(1488 letters)

Database: plantfungal
30 661,018 sequences; 426,114,510 total letters

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	emb X82273 BOACCS <i>B. oleracea</i> mRNA for ACC synthase.	986 0.0
	emb X72676 BJMACC <i>B. juncea</i> mRNA for 1-Aminocyclopropane-1-carbo...	875 0.0
	emb AF057563 AF057563 <i>Nicotiana glutinosa</i> 1-aminocyclopropane-1-...	765 0.0
40	emb AJ005002 NTAJ5002 <i>Nicotiana tabacum</i> mRNA for 1-aminocyclopro...	761 0.0
	emb AB034992 AB034992 <i>Malus domestica</i> MdACS-5A mRNA for 1-aminoc...	754 0.0
	emb AB034993 AB034993 <i>Malus domestica</i> MdACS-5B mRNA for 1-aminoc...	755 0.0
	gb U72389 LEU72389 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1...	756 0.0
	gb U72390 LEU72390 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1...	753 0.0
45	emb AB033503 AB033503 <i>Populus euramericana</i> peacs-2 mRNA for 1-am...	741 0.0
	gb U68216 CPU68216 <i>Carica papaya</i> ACC synthase mRNA, complete cds.	461 0.0
	emb AF061605 AF061605 <i>Nicotiana glutinosa</i> ACC synthase mRNA, com...	742 0.0
	emb AB013100 AB013100 <i>Lycopersicon esculentum</i> LE-ACS6 mRNA for 1...	741 0.0
	emb AJ012551 CSI012551 <i>Citrus sinensis</i> mRNA for ACC synthase.	449 0.0
50	emb AB013346 AB013346 <i>Lycopersicon esculentum</i> mRNA for 1-aminocy...	739 0.0
	emb AB033502 AB033502 <i>Populus euphratica</i> peacs-1 mRNA for 1-amin...	620 0.0
	gb U88971 PHU88971 <i>Pelargonium hortorum</i> 1-aminocyclopropane-1-ca...	455 0.0
	emb Z11613 VRACCSYNM <i>V. radiata</i> mRNA for ACC synthase.	456 0.0
	emb X98492 NTACCS <i>Nicotiana tabacum</i> mRNA for ACC-synthase (clone...	455 0.0
55	emb X67100 GMCACCS1 <i>G. max</i> mRNA for ACC synthase.	454 0.0
	emb Z18952 DCAMCRBSY <i>D. caryophyllus</i> mRNA for 1-aminocyclopropane...	716 0.0
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	emb AJ011095 CSI011095 <i>Citrus sinensis</i> mRNA for ACC synthase (ac...	452 0.0
	emb Z18953 PHAMCRBSY <i>P. hybrida</i> mRNA for 1-aminocyclopropane 1-ca...	450 0.0
60	emb AB006804 AB006804 <i>Cucumis sativus</i> CS-ACS2 mRNA for ACC synth...	451 0.0
	emb AF080258 AF080258 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	711 0.0

	emb AF016459 AF016459 Pisum sativum 1-aminocyclopropane-1-carbox...	445	0.0
	emb AF109927 AF109927 Musa acuminata 1-aminocyclopropane-1-carbo...	707	0.0
	dbj D30805 CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy...	705	0.0
	emb AB021906 AB021906 Musa acuminata MA-ACS1 mRNA for ACC syntha...	703	0.0
5	emb AB006803 AB006803 Cucumis sativus CS-ACS1 mRNA for ACC synth...	703	0.0
	emb AF129508 AF129508 Musa acuminata 1-aminocyclopropane-1-carbo...	702	0.0
	emb X65982 NTXACCSYN N.tabacum mRNA for 1-aminocyclopropane-1-ca...	438	0.0
	emb AB031026 AB031026 Prunus mume PM-ACS1 mRNA for ACC synthase,...	434	0.0
	emb AB015625 AB015625 Pyrus pyrifolia pPPACS3 mRNA for 1-aminocy...	418	0.0
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	dbj E03724 E03724 cDNA encoding detriment induced type 1-aminocy...	695	0.0
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	emb Y11357 CP1A1CS C.papaya mRNA for 1-aminocyclopropane-1-carbo...	430	0.0
	emb X62536 LEACC L.esculentum mRNA for ACC synthase.	327	0.0
15	emb AF057562 AF057562 Nicotiana glutinosa 1-aminocyclopropane-1-...	437	0.0
	emb X59145 LEACC2MR Lycopersicon esculentum LE-ASCC2 mRNA (ptACC...	326	0.0
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	emb Y15739 MAACSYNTH Musa acuminata mRNA for 1-aminocyclopropane...	687	0.0
	gb M34289 TOMACS Tomato 1-aminocyclopropane-1-carboxylate syntha...	327	0.0
20	gb M63490 TOMACCS Tomato 1-aminocyclopropane-1-carboxylate synth...	682	0.0
	emb X59146 LEACC4MR Lycopersicon esculentum LE-ACC4 mRNA (ptACC4...	681	0.0
	gb U17229 PHU17229 Pelargonium hortorum clone pGAC-1 1-aminocycl...	438	0.0
	gb U17231 PHU17231 Pelargonium hortorum clone pGAC-2 1-aminocycl...	423	0.0
	emb AF038945 AF038945 Rumex palustris 1-aminocyclopropane-1-carb...	407	0.0
25	gb L20634 POTACCSYN Solanum tuberosum 1-aminocyclopropane-1-carb...	403	0.0
	emb AJ276295 CSI276295 Citrus sinensis partial mRNA for ACC synt...	446	0.0
	emb AF239987 AF239987 Prunus persica ACC synthase ACS1 mRNA, par...	662	0.0
	emb AF178076 AF178076 Carica papaya 1-aminocyclopropane-1-carbox...	395	0.0
	emb X82265 CAACC1 C.anuum mRNA for 1-aminocyclopropane-1-carboxyl...	639	0.0
30	gb U70842 STU70842 Solanum tuberosum 1-aminocyclopropane-1-carbo...	637	0.0
	emb AF144746 AF144746 Solanum melongena 1-aminocyclopropane-1-ca...	636	0.0
	emb AJ012577 CPA012577 Carica papaya mRNA for 1-aminocyclopropan...	387	e-180
	gb U73815 MDU73815 Malus domestica ACC synthase (MdACS-2) mRNA, ...	623	e-178
	dbj D37937 D37937 Cucumis melo mRNA for 1-aminocyclopropane-1-ca...	380	e-177
35	emb Z11562 VRACCSYN V.radiata mRNA for 1-aminocyclopropane-1-car...	375	e-176
	emb AF177769 AF177769 Carica papaya 1-aminocyclopropane-1-carbox...	369	e-175
	emb AF083814 AF083814 Antirrhinum majus ACC synthase 1 (ACS1) mR...	605	e-172
	emb AF178077 AF178077 Carica papaya 1-aminocyclopropane-1-carbox...	316	e-172
	emb AF239989 AF239989 Prunus persica ACC synthase ACS25 mRNA, pa...	597	e-170
40	gb U22523 MIU22523 Mangifera indica 1-aminocyclopropane-carboxyl...	359	e-169
	emb X66605 DCACCS D.caryophyllus mRNA for 1-aminocyclopropane-1-...	396	e-168
	gb L31347 MAUACCSYN Malus domestica 1-aminocyclopropane-1-carbox...	378	e-168
	emb AB015624 AB015624 Pyrus pyrifolia mRNA for 1-aminocyclopropa...	377	e-168
	emb AF049137 AF049137 Dianthus caryophyllus 1-aminocyclopropane-...	338	e-167
45	emb AF170705 AF170705 Mangifera indica 1-aminocyclopropane-1-car...	290	e-167
	gb U03294 MSU03294 Malus sylvestris 1-aminocyclopropane-1-carbox...	372	e-166
	emb Z77854 PSPACS1 Phalaenopsis species mRNA for 1-aminocyclopro...	513	e-166
	emb AJ277160 CPA277160 Carica papaya partial paccs1A gene for 1-...	266	e-165
	gb U73816 MDU73816 Malus domestica ACC synthase (MdACS-3) mRNA, ...	505	e-164
50	emb AB007449 AB007449 Actinidia deliciosa mRNA for 1-aminocyclop...	355	e-164
	emb AB007639 AB007639 Pyrus pyrifolia mRNA for 1-aminocyclopropa...	502	e-164
	dbj D01033 CUCACCA Cucurbita maxima mRNA for 1-aminocyclopropane...	366	e-164
	emb X87112 PCPCACS1G P.communis mRNA for 1-aminocyclopropane-1-c...	363	e-163
	gb U17972 LEU17972 Lycopersicon esculentum 1-aminocyclopropane-1...	362	e-163
55	emb AB015495 AB015495 Passiflora edulis PE-ACS2 mRNA for ACC syn...	368	e-162
	emb AB006805 AB006805 Cucumis sativus CS-ACS3 mRNA for ACC synth...	360	e-160
	emb AB000679 AB000679 Vigna radiata mRNA for 1-aminocyclopropane...	365	e-158
	gb U34987 VRU34987 Vigna radiata 1-aminocyclopropane-1-carboxyli...	325	e-157
	gb M66619 DINCARACC D.caryophyllus 1-aminocyclopropane-1-carboxy...	496	e-156
60	gb U34986 VRU34986 Vigna radiata 1-aminocyclopropane-1-carboxyli...	362	e-156
	gb U64031 DCU64031 Dendrobium crumenatum ACC synthase gene, comp...	259	e-154

emb|AF016458|AF016458 Pisum sativum 1-aminocyclopropane-1-carbox... 355 e-154
emb|Z27233|STACCAS1 S.tuberosum (STAC1) gene for amino cycloprop... 237 e-152
emb|Z27234|STACCAS2 S.tuberosum STACS2 gene for 1-Aminocycloprop... 232 e-152
5 emb|AF043122|AF043122 Lycopersicon esculentum ACC synthase (LE-A... 236 e-150
gb|U37774|CMU37774 Cucurbita maxima 1-aminocyclopropane-1-carbox... 234 e-150
gb|L34171|TOMACS3A Lycopersicon esculentum 1-aminocyclopropane-1... 235 e-149
gb|U18055|LEU18055 Lycopersicon esculentum 1-aminocyclopropane-1... 235 e-149
emb|AF151961|AF151961 Vigna radiata 1-aminocyclopropane-1-carbox... 232 e-146
10 emb|Z12135|VRACCSYN4 V.radiata gene for ACC synthase (pMAC-4). 376 e-145
gb|L07883|DORAMICARB Moth orchid 1-aminocyclopropane-1-carboxyla... 243 e-144
emb|AF074927|AF074927 Sinapis arvensis 1-aminocyclopropane-1-car... 330 e-142
emb|AF083815|AF083815 Antirrhinum majus ACC synthase 2 (ACS2) mR... 482 e-141
emb|AB021907|AB021907 Musa acuminata MA-ACS2 mRNA for ACC syntha... 310 e-140
emb|AB021908|AB021908 Musa acuminata MA-ACS3 mRNA for ACC syntha... 298 e-138
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20 http://www.ncgr.org/cgi-bin/ff?ac000107
(1950 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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30	Sequences producing significant alignments:		
	gb U79958 PSU79958 Pisum sativum BP-80 vacuolar sorting receptor...	630	0.0
	emb AB006809 AB006809 Cucurbita sp. mRNA for PV72, complete cds.	606	0.0
	emb AW267745 AW267745 EST305873 DSIR Medicago truncatula cDNA cl...	350	e-124
	emb AW931583 AW931583 EST357426 tomato fruit mature green, TAMU ...	165	e-112
35	emb AW309187 AW309187 sg05d06.y1 Gm-c1019 Glycine max cDNA clone...	326	e-108
	emb AW622833 AW622833 EST306903 tomato flower buds 3-8 mm, Corne...	387	e-106
	emb AW774434 AW774434 EST333585 KV3 Medicago truncatula cDNA clo...	294	e-100
	emb AW689392 AW689392 NF018F12ST1F1000 Developing stem Medicago ...	338	e-100
	gb BE054150 BE054150 GA_Ea0034H17f Gossypium arboreum 7-10 dpa ...	195	2e-99
40	emb AI782787 AI782787 EST263666 tomato susceptible, Cornell Lyco...	332	6e-90
	emb AW737948 AW737948 EST339375 tomato flower buds, anthesis, Co...	225	1e-89
	emb AW615949 AW615949 EST325315 tomato flower buds 0-3 mm, Corne...	217	3e-86
	emb AW932529 AW932529 EST358372 tomato fruit mature green, TAMU ...	303	1e-83
	emb AW685785 AW685785 NF030C07NR1F1000 Nodulated root Medicago t...	157	2e-81
45	emb AW747297 AW747297 WS1_67_G06.b1_A002 Water-stressed 1 (WS1) ...	286	4e-76
	emb AI443067 AI443067 sa47a01.y1 Gm-c1004 Glycine max cDNA clone...	265	6e-76
	emb AI728635 AI728635 BNLGHi11276 Six-day Cotton fiber Gossypium...	135	1e-75
	emb AI484571 AI484571 EST242801 tomato ovary, TAMU Lycopersicon ...	278	1e-73
	emb AI727826 AI727826 BNLGHi9195 Six-day Cotton fiber Gossypium ...	135	9e-71
50	emb AW695542 AW695542 NF096C05ST1F1037 Developing stem Medicago ...	153	2e-65
	emb AV406766 AV406766 AV406766 Lotus japonicus young plants (two...	170	5e-65
	emb AW509740 AW509740 ga63h11.y1 Moss EST library PPU Physcomitr...	226	6e-63
	emb AW256542 AW256542 EST304679 KV2 Medicago truncatula cDNA clo...	181	8e-60
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55	emb AW289687 AW289687 NXNV004E04F Nsf Xylem Normal-wood Vertical...	182	7e-55
	emb AW690002 AW690002 NF026G04ST1F1000 Developing stem Medicago ...	143	4e-54
	emb AA660289 AA660289 00158 MrHE Medicago truncatula cDNA 5', m...	138	2e-53
	emb AW064744 AW064744 ST35C06 Pine TripleEx shoot tip library Pin...	141	6e-53
	emb AV428420 AV428420 AV428420 Lotus japonicus young plants (two...	134	1e-51
60	emb AW623959 AW623959 EST321904 tomato flower buds 3-8 mm, Corne...	74	1e-49
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	emb AI967865 AI967865 Ljirmpst14-100-f3 Ljirmp Lambda HybriZap ...	180	5e-47
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	emb AW398931 AW398931 EST309431 L. pennellii trichome, Cornell U...	132	2e-45
	emb AW737369 AW737369 EST338892 tomato flower buds, anthesis, Co...	182	6e-45
5	emb AW096632 AW096632 EST289812 tomato mixed elicitor, BTI Lycop...	81	7e-45
	emb AF209910 AF209910 Prunus dulcis vacuolar sorting receptor pr...	76	8e-44
	emb AW056624 AW056624 ST53G07 Pine TripleEx shoot tip library Pin...	178	1e-43
	emb AW680054 AW680054 WS1_3_A01.g1_A002.Water-stressed 1 (WS1) S...	77	1e-41
10	emb AW290400 AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical...	170	4e-41
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	emb AI161766 AI161766 A006P54U Hybrid aspen plasmid library Popu...	76	3e-39
	emb AI162330 AI162330 A016P01U Hybrid aspen plasmid library Popu...	130	2e-37
	gb BE049814 BE049814 NXNV_144_F04_F Nsf Xylem Normal wood Vertic...	156	4e-37
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15	gb L38113 L38113 BNAF0628E Mustard flower buds Brassica rapa cDN...	153	4e-36
	emb AW616461 AW616461 EST322872 L. hirsutum trichome, Cornell Un...	102	4e-33
	emb AA660955 AA660955 00852 MtRHE Medicago truncatula cDNA 5' si...	72	4e-31
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	emb AW906386 AW906386 EST342508 potato stolon, Cornell Universit...	78	2e-27
	emb AW126100 AW126100 N100297e rootphos(-) Medicago truncatula c...	73	9e-27
	emb AW620693 AW620693 sj08d10.y1 Gm-c1032 Glycine max cDNA clone...	77	1e-26
	emb AW317388 AW317388 sg48g10.y1 Gm-c1025 Glycine max cDNA clone...	72	2e-26
	emb AW706755 AW706755 sk02f10.y1 Gm-c1023 Glycine max cDNA clone...	117	3e-25
25	emb AW125944 AW125944 N100139e rootphos(-) Medicago truncatula c...	71	1e-23
	emb AW932524 AW932524 EST358367 tomato fruit mature green, TAMU ...	69	1e-22
	emb AW348825 AW348825 GM210003B11E6R Gm-r1021 Glycine max cDNA 3...	66	2e-22
	emb AW093844 AW093844 EST287024 tomato mixed elicitor, BTI Lycop...	98	3e-19
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	emb AW774852 AW774852 EST334003 KV3 Medicago truncatula cDNA clo...	83	9e-15
	emb AI794754 AI794754 sb68f11.y1 Gm-c1019 Glycine max cDNA clone...	82	1e-14
	gb BE060808 BE060808 HVSMEg0013H06f Hordeum vulgare pre-anthesis...	78	6e-14
35	emb AW760128 AW760128 sl58d09.y1 Gm-c1027 Glycine max cDNA clone...	66	8e-14
	emb AW037563 AW037563 EST278890 tomato mixed elicitor, BTI Lycop...	77	6e-13
	emb AW256398 AW256398 EST304465 KV2 Medicago truncatula cDNA clo...	72	7e-13
	emb AW686287 AW686287 NF040A08NR1F1000 Nodulated root Medicago t...	67	6e-10
	emb AW443352 AW443352 EST308282 tomato mixed elicitor, BTI Lycop...	65	2e-09
40	emb AW747372 AW747372 WS1_67_G06.g1_A002 Water-stressed 1 (WS1) ...	64	4e-09
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	emb AF083502 AF083502 Plasmodium vivax ookinete surface protein ...	37	0.42
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	emb AC008054 AC008054 Leishmania major chromosome 35 clone L8453...	36	0.55
50	emb AF114171 AF114171 Sorghum bicolor BAC clone 25.M18, complete...	35	1.5
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 emb|AI822187|AI822187 L0-664T3 Ice plant Lambda Uni-Zap XR expre... 31 3.3
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 15 Database: plantfungal
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 Sequences producing significant alignments: (bits) Value

 25 emb|X97606|MSRNAAAA *M.sativa* mRNA translated from abscisic activ... 306 e-115
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 emb|AW760494|AW760494 sl51a09.y1 *Gm-c1027* Glycine max cDNA clone... 178 1e-69
 emb|AW831516|AW831516 sm27a02.y1 *Gm-c1028* Glycine max cDNA clone... 261 4e-69
 40 emb|AJ223291|SRAJ3291 *Sesbania rostrata* mRNA for putative chalco... 115 2e-64
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 45 gb|U13925|MSU13925 *Medicago sativa* Apollo clone CHR7 chalcone re... 117 6e-61
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 50 gb|U13924|MSU13924 *Medicago sativa* Apollo clone CHR12 chalcone r... 114 8e-60
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 emb|AW694657|AW694657 NF078G04ST1F1035 Developing stem *Medicago* ... 164 3e-59
 55 emb|X59465|PSXYL1RE *P.stipitis* XYL1-gene for NAD(P)H-dependent X... 125 2e-58
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- dbj|D83718|GYCPKR Glycyrrhiza echinata mRNA for polyketide reduc... 111 6e-57
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 emb|AF219625|AF219625 Aspergillus niger D-xylose reductase (xylA... 86 6e-49
 15 emb|AF108435|AF108435 Papaver somniferum NADPH-dependent codeino... 85 1e-48
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 20 emb|AL021815|SPBC8E4 S.pombe chromosome I cosmid c8E4. 84 3e-47
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 emb|AW266162|AW266162 L30-2855T3 Ice plant Lambda Uni-Zap XR exp... 185 7e-47
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 25 emb|AL110661|CNS018Q6 Botrytis cinerea strain T4 cDNA library un... 108 2e-45
 emb|AB014493|AB014493 Gibberella zeae gene for reductase, partia... 91 5e-45
 emb|X94335|SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 57 2e-44
 emb|X90518|SCXVORFS S.cerevisiae DNA of 51 Kb from chromosome XV... 57 2e-44
 emb|Z75028|SCYOR120W S.cerevisiae chromosome XV reading frame OR... 57 2e-44
 30 emb|X13228|SCGCY Yeast GCY gene (homologous to vertebrate eye le... 57 2e-44
 emb|X96740|SCGCY1 S.cerevisiae GCY1 gene. 57 2e-44
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 35 gb|BE036644|BE036644 MP03B08 MP Mesembryanthemum crystallinum cD... 80 9e-43
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 emb|AW704367|AW704367 sk30b12.y1 Gm-c1028 Glycine max cDNA clone... 109 2e-38
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 55 emb|AW728632|AW728632 GA_Ea0017G17 Gossypium arboreum 7-10 dpa ... 80 3e-36
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 emb|AI939278|AI939278 sc69f11.y1 Gm-c1016 Glycine max cDNA clone... 150 1e-35
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 60 emb|AW756704|AW756704 sl26b12.y1 Gm-c1027 Glycine max cDNA clone... 79 2e-35
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10 http://www3.ncbi.nlm.nih.gov/htbin-
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http://www.ncgr.org/cgi-bin/ff?ac004392
(1233 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

20

emb|AF020814|AF020814 Pisum sativum glucose-6-phosphate/phosphat... 626 e-179

emb|AF020816|AF020816 Solanum tuberosum glucose-6-phosphate/phos... 359 e-167

emb|AW761153|AW761153 sl63h08.y1 Gm-c1027 Glycine max cDNA clone... 403 e-111

25 emb|AI973973|AI973973 sd14e11.y1 Gm-c1020 Glycine max cDNA clone... 387 e-106

emb|AW832261|AW832261 sm21g08.y1 Gm-c1027 Glycine max cDNA clone... 372 e-102

emb|AW507609|AW507609 si42a06.y1 Gm-r1030 Glycine max cDNA clone... 365 e-100

emb|AI974103|AI974103 sd16e09.y1 Gm-c1020 Glycine max cDNA clone... 202 9e-91

emb|AV421952|AV421952 AV421952 Lotus japonicus young plants (two... 304 1e-81

30 emb|AW509448|AW509448 si37c07.y1 Gm-r1030 Glycine max cDNA clone... 297 4e-81

emb|AW985263|AW985263 NXNV_135_B02_F Nsf Xylem Normal wood Verti... 209 5e-73

emb|AI352923|AI352923 MB73-9C PZ204.BNlib Brassica napus cDNA cl... 226 1e-70

gb|U13630|BOU13630 Brassica oleracea var. botrytis chloroplast p... 189 2e-69

emb|X75088|NTRNPHTR Nicotiana tabacum mRNA for phosphate translo... 185 8e-69

35 emb|X13754|SOPHTRAN Spinach mRNA for chloroplast phosphate trans... 186 8e-69

emb|X67045|STTPTMR S.tuberosum mRNA TPT for triose phosphate tra... 183 1e-67

emb|AW234628|AW234628 sf17d12.y1 Gm-c1028 Glycine max cDNA clone... 254 1e-66

gb|BE060177|BE060177 HVSMEg0011C12f Hordeum vulgare pre-anthesis... 249 3e-65

emb|AV413897|AV413897 AV413897 Lotus japonicus young plants (two... 229 3e-59

40 emb|AI894606|AI894606 EST264049 tomato callus, TAMU Lycopersicon... 228 6e-59

emb|AW926251|AW926251 HVSMEg0006L14 Hordeum vulgare pre-anthesis... 226 2e-58

emb|AW472436|AW472436 si25b11.y1 Gm-c1029 Glycine max cDNA clone... 221 2e-57

emb|AF173679|AF173679 Beta vulgaris phosphate translocator (pt) m... 135 2e-53

emb|AW560889|AW560889 EST315937 DSIR Medicago truncatula cDNA cl... 205 2e-53

emb|AI939281|AI939281 sc69g06.y1 Gm-c1016 Glycine max cDNA clone... 204 1e-51

45 emb|AW688995|AW688995 NF014B11ST1F1000 Developing stem Medicago ... 150 2e-50

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emb|X54639|PSCIRP36 P. sativum mRNA for chloroplast import recep... 193 2e-48

emb|X68077|PSPTCPA P. sativum mRNA for phosphate translocator. 193 2e-48

emb|AW760040|AW760040 sl57c08.y1 Gm-c1027 Glycine max cDNA clone... 193 3e-48

50 emb|AW691966|AW691966 NF051A06ST1F1000 Developing stem Medicago ... 166 3e-47

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emb|AW217547|AW217547 EST296261 tomato flower buds 3-8 mm, Corne... 188 8e-47

emb|X92656|LETPT L.esculentum mRNA for triose phosphate transloc... 188 8e-47

emb|Z26633|CHFPCT F.pringlei fpcpt mRNA for triose phosphate/ph... 188 1e-46

55 emb|AW758970|AW758970 sl33a11.y1 Gm-c1027 Glycine max cDNA clone... 187 2e-46

emb|Z26632|CHFTCT F.trinervia ftcpt mRNA for triose phosphate/p... 184 1e-45

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60 emb|AI773418|AI773418 EST254518 tomato resistant, Cornell Lycopersicon... 182 3e-45

emb|AI812950|AI812950 22G7 Pine Lambda Zap Xylem library Pinus t... 176 3e-43

emb|AI774019|AI774019 EST255119 tomato resistant, Cornell Lycopersicon... 175 6e-43

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	emb AW933284 AW933284 EST359127 tomato fruit mature green, TAMU ...	175	8e-43
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5	emb AW626582 AW626582 NXNV067A01 Nsf Xylem Normal wood Vertical ...	107	2e-42
	emb AW671381 AW671381 LG1_335_G10.b1_A002 Light Grown 1 (LG1) So...	173	3e-42
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	emb AW559735 AW559735 EST314727 DSIR Medicago truncatula cDNA cl...	167	3e-42
	gb BE034606 BE034606 MK02F02 MK Mesembryanthemum crystallinum cD...	170	2e-41
10	emb AW690541 AW690541 NF035G02ST1F1000 Developing stem Medicago ...	166	5e-41
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15	emb AW776623 AW776623 EST335688 DSIL Medicago truncatula cDNA cl...	162	4e-39
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	emb AW038916 AW038916 EST280872 tomato mixed elicitor, BTI Lycop...	158	1e-37
20	emb AW930290 AW930290 EST340747 tomato fruit mature green, TAMU ...	157	2e-37
	emb AV415709 AV415709 AV415709 Lotus japonicus young plants (two...	153	2e-36
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	emb AI736196 AI736196 sb24f10.y1 Gm-c1008 Glycine max cDNA clone...	151	8e-36
	emb AV426398 AV426398 AV426398 Lotus japonicus young plants (two...	149	6e-35
25	emb AV422882 AV422882 AV422882 Lotus japonicus young plants (two...	147	2e-34
	emb AF173660 AF173660 Beta vulgaris clone GPTII09UNI glucose-6-p...	146	4e-34
	emb AI822397 AI822397 L0-856T3 Ice plant Lambda Uni-Zap XR expre...	125	7e-34
	emb AW040008 AW040008 EST282499 tomato mixed elicitor, BTI Lycop...	144	1e-33
	emb AW039997 AW039997 EST282488 tomato mixed elicitor, BTI Lycop...	144	1e-33
30	gb BE059998 BE059998 sn39f10.y1 Gm-c1027 Glycine max cDNA clone ...	143	3e-33
	emb AW671168 AW671168 LG1_330_E06.b1_A002 Light Grown 1 (LG1) So...	142	5e-33
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35	emb AW781979 AW781979 sl99a06.y1 Gm-c1027 Glycine max cDNA clone...	138	8e-32
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40	emb AW924990 AW924990 WS1_74_A05.b1_A002 Water-stressed 1 (WS1) ...	134	1e-30
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45	emb AW738715 AW738715 EST340142 tomato flower buds, anthesis, Co...	132	7e-30
	emb AW040512 AW040512 EST283472 tomato mixed elicitor, BTI Lycop...	131	1e-29
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	emb AW287673 AW287673 LG1_271_A05.b1_A002 Light Grown 1 (LG1) So...	129	5e-29
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	emb AW596590 AW596590 sj14c04.y1 Gm-c1032 Glycine max cDNA clone...	128	9e-29
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(834 letters)

5

Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments: (bits) Value

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	gb U97521 VVU97521 Vitis vinifera class IV endochitinase (VvChi4...	173	3e-77
	gb U97522 VVU97522 Vitis vinifera class IV endochitinase (VvChi4...	174	2e-76
	emb X57187 PVCHITIN P.vulgaris mRNA for chitinase.	149	2e-74
	emb AF112966 AF112966 Triticum aestivum chitinase IV precursor (...)	157	5e-70
20	dbj D45181 D45181 Chenopodium amaranticolor mRNA for chitinase, ...	100	5e-67
	gb U52845 DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP...	114	7e-67
	gb U52846 DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP...	111	9e-66
	gb BE034166 BE034166 MG05H02 MG Mesembryanthemum crystallinum cD...	129	1e-65
	gb U52847 DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP...	110	8e-65
25	gb U52848 DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3...	111	2e-64
	gb BE034975 BE034975 ML07H10 ML Mesembryanthemum crystallinum cD...	125	2e-64
	gb BE034428 BE034428 MH04G02 MH Mesembryanthemum crystallinum cD...	123	2e-63
	gb BE034976 BE034976 ML07H11 ML Mesembryanthemum crystallinum cD...	120	6e-63
	dbj D45183 D45183 Chenopodium amaranticolor mRNA for chitinase, ...	96	1e-62
30	dbj D45184 D45184 Chenopodium amaranticolor mRNA for chitinase, ...	100	3e-62
	dbj D45182 D45182 Chenopodium amaranticolor mRNA for chitinase, ...	100	4e-60
	emb X75945 BVCH4RNA B.vulgaris Ch4 mRNA for chitinase.	92	6e-60
	emb A23392 A23392 B.vulgaris mRNA for chitinase 4 (B15).	92	6e-60
	emb X88803 VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p...	118	3e-59
35	emb AI897733 AI897733 EST267176 tomato ovary, TAMU Lycopersicon ...	110	1e-58
	gb BE034406 BE034406 MH04D10 MH Mesembryanthemum crystallinum cD...	105	2e-58
	gb L25826 BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds.	158	3e-58
	gb BE034497 BE034497 MH05H03 MH Mesembryanthemum crystallinum cD...	89	8e-58
	gb L42467 PIACHI Picea glauca chitinase (chi) mRNA, complete cds.	93	2e-57
40	emb AF090336 AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA...	166	2e-57
	emb AI897843 AI897843 EST267286 tomato ovary, TAMU Lycopersicon ...	103	1e-56
	emb AF112963 AF112963 Triticum aestivum chitinase II precursor (...)	149	9e-56
	gb BE035287 BE035287 MM04H04 MM Mesembryanthemum crystallinum cD...	162	4e-54
	emb AW680953 AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S...	178	3e-52
45	gb BE033502 BE033502 ME03F10-ME Mesembryanthemum crystallinum cD...	87	4e-50
	gb M94105 ALCCHITIN Allium sativum chitinase mRNA, 3' end.	100	6e-49
	emb AI898279 AI898279 EST267722 tomato ovary, TAMU Lycopersicon ...	83	1e-48
	gb U83592 MSU83592 Medicago sativa class I chitinase mRNA, compl...	109	1e-48
	gb U83591 MSU83591 Medicago sativa class I chitinase mRNA, compl...	109	1e-48
50	emb AW030814 AW030814 EST274069 tomato callus, TAMU Lycopersicon...	83	3e-48
	emb AW035013 AW035013 EST279284 tomato callus, TAMU Lycopersicon...	83	3e-48
	emb AW029733 AW029733 EST272988 tomato callus, TAMU Lycopersicon...	83	3e-48
	gb BE034481 BE034481 MH05F02 MH Mesembryanthemum crystallinum cD...	162	5e-48
	emb AW924422 AW924422 WS1_69_C06.b1_A002 Water-stressed 1 (WS1) ...	140	7e-48
55	emb AI485982 AI485982 EST244303 tomato ovary, TAMU Lycopersicon ...	83	1e-47
	emb AF061805 AF061805 Elaeagnus umbellata acidic chitinase mRNA,...	99	1e-47
	emb AW648023 AW648023 EST326477 tomato germinating seedlings, TA...	83	3e-47
	gb L37876 PEACHI2I Pisum sativum chitinase class I (chi2) gene, ...	109	3e-47
	gb BE034447 BE034447 MH05A08 MH Mesembryanthemum crystallinum cD...	87	5e-47
60	emb X15494 STCHITIN Potato endochitinase gene (EC 3.2.1.14).	95	6e-47
	emb X07130 STCHIT Solanum tuberosum mRNA for endochitinase (EC 3...	95	6e-47

- gb|M13968|PHVCHM *P.vulgaris* chitinase mRNA, complete cds. 106 1e-46
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 gb|S43926|S43926 CH5B=chitinase [*Phaseolus vulgaris*=beans, cv Sa... 106 5e-46
 emb|X88800|VURNACHI1 *V.unguiculata* mRNA for chitinase clase 1 (p... 105 1e-45
 5 emb|AJ012821|CAR012821 *Cicer arietinum* mRNA for class I chitinase. 108 6e-45
 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem *Medicago* ... 78 8e-45
 emb|Y10373|MTCHITIN1 *M.truncatula* mRNA for chitinase. 109 8e-45
 emb|AW033122|AW033122 EST276681 tomato callus, TAMU *Lycopersicon*... 83 2e-44
 gb|M94106|ALCCHINTIA *Allium sativum* chitinase mRNA, 3' end. 102 3e-44
 10 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 170 3e-44
 emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 178 4e-44
 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 178 4e-44
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 95 5e-44
 gb|M15173|TOBECH Tobacco (*N.tabacum*) endochitinase mRNA, partial... 95 5e-44
 15 emb|AF061806|AF061806 *Elaeagnus umbellata* basic chitinase mRNA, ... 105 1e-43
 emb|Z54234|VVCHIT1MR *V.vinifera* mRNA for chitinase. 98 1e-43
 gb|S44869|S44869 basic chitinase [*Nicotiana tabacum*=tobacco, cv ... 95 2e-43
 emb|X16939|NTECHITR *Nicotiana tabacum* mRNA for endochitinase (EC... 95 2e-43
 emb|X76041|TACHIG *T.aestivum* (Chinese spring) chi gene for endoc... 93 4e-43
 20 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 97 6e-43
 emb|Z46948|SNCHJET15 *S.nigra* mRNA for chitinase, pathogenesis-re... 104 2e-42
 gb|U02605|STU02605 *Solanum tuberosum* chitinase (chtB1) mRNA, par... 95 3e-42
 gb|U02606|STU02606 *Solanum tuberosum* chitinase (chtB2) mRNA, par... 95 4e-42
 emb|Z46950|SNCHJET19 *S.nigra* mRNA chitinase class II, pathogenes... 104 6e-42
 25 gb|U78888|GHU78888 *Gossypium hirsutum* class I endochitinase mRNA... 102 1e-41
 gb|BE034450|BE034450 MH05B01 MH *Mesembryanthemum crystallinum* cD... 81 3e-41
 emb|Z15140|LECHI9 *L.esculentum* mRNA for chitinase. 95 3e-41
 gb|U02607|STU02607 *Solanum tuberosum* chitinase (chtB3) mRNA, par... 95 6e-41
 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 95 6e-41
 30 emb|AF034566|AF034566 *Gossypium hirsutum* class I chitinase mRNA,... 100 6e-41
 gb|BE033398|BE033398 ME01A01 ME *Mesembryanthemum crystallinum* cD... 165 7e-41
 gb|M25337|POPCHIB *Populus* sp. chitinase (win8) mRNA, complete cds. 89 8e-41
 gb|BE034267|BE034267 MH02D06 MH *Mesembryanthemum crystallinum* cD... 66 2e-40
 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU *Lycopersicon* ... 110 4e-40
 35 emb|AF000965|AF000965 *Poa pratensis* chitinase (Chi3) pseudogene ... 91 4e-40
 emb|X95610|CSHITIB *C.sativa* mRNA for chitinase Ib. 88 9e-40
 gb|U48687|CSU48687 *Castanea sativa* endochitinase mRNA, complete ... 88 9e-40
 emb|AW676775|AW676775 DG1_14_C09.g1_A002 Dark Grown 1 (DG1) Sorg... 161 2e-39
 emb|Z78202|PACHI1 *Persea americana* mRNA for endochitinase. 96 2e-39
 40 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 163 2e-39
 emb|AW922596|AW922596 DG1_46_C01.b1_A002 Dark Grown 1 (DG1) Sorg... 94 2e-39
 gb|BE034616|BE034616 ML04B04 ML *Mesembryanthemum crystallinum* cD... 77 5e-39
 gb|L22032|ULMCHITIN *Ulmus americana* chitinase (pHS2) mRNA, compl... 106 6e-39
 emb|AW924229|AW924229 WS1_51_H04.b1_A002 Water-stressed 1 (WS1) ... 161 7e-39
 45 emb|AW560048|AW560048 EST315096 DSIR *Medicago truncatula* cDNA cl... 109 7e-39
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 emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root *Medicago* t... 78 3e-38
 gb|U02287|HVVU02287 *Hordeum vulgare* cultivar NK1558 chitinase gen... 96 4e-38
 emb|AI897657|AI897657 EST267100 tomato ovary, TAMU *Lycopersicon* ... 101 1e-37
 50 emb|AF098302|AF098302 *Brassica juncea* chitinase mRNA, complete cds. 106 1e-37
 emb|AW746429|AW746429 WS1_53_G09.b1_A002 Water-stressed 1 (WS1) ... 97 4e-37
 emb|X74919|PVGEC9 *P.vulgaris* gene for endochitinase. 149 6e-37

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60 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AJ238439 CAR238439 Cicer arietinum mRNA for a cytochrome P45...	328	e-136
	emb AB022732 AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy...	322	e-136
10	emb AB025016 AB025016 Lotus japonicus mRNA for cytochrome P450, ...	291	e-134
	emb AJ012581 CAR012581 Cicer arietinum mRNA for cytochrome P450.	324	e-134
	emb AJ000478 HTCYP81L Helianthus tuberosus mRNA for cytochrome P...	227	e-124
	emb AJ000477 HTCYP81C Helianthus tuberosus mRNA for cytochrome P...	227	e-124
	emb AJ239051 CAR239051 Cicer arietinum mRNA for cytochrome P450 ...	237	3e-82
15	emb AJ249800 CAR249800 Cicer arietinum partial mRNA for cytochro...	290	3e-79
	emb AW185361 AW185361 se90e02.y1 Gm-c1027 Glycine max cDNA clone...	280	3e-74
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20	emb AW307234 AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone...	258	1e-67
	emb AW733691 AW733691 sk83g07.y1 Gm-c1016 Glycine max cDNA clone...	253	3e-66
	emb AW171738 AW171738 N100632e rootphos(-) Medicago truncatula c...	251	1e-65
	emb AJ249801 CAR249801 Cicer arietinum partial mRNA for cytochro...	242	5e-63
	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber Gossypium...	180	4e-58
25	emb AW329224 AW329224 N200436e rootphos(-) Medicago truncatula c...	224	1e-57
	emb AI725744 AI725744 BNLGHi12803 Six-day Cotton fiber Gossypium...	180	4e-57
	emb AI495626 AI495626 sb11c08.y1 Gm-c1004 Glycine max cDNA clone...	222	6e-57
	emb AW100311 AW100311 sd22g12.y2 Gm-c1012 Glycine max cDNA clone...	206	5e-56
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30	emb AI774414 AI774414 EST255514 tomato resistant, Cornell Lycope...	144	5e-54
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40	dbj D83968 SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)...	104	1e-45
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	emb AW617814 AW617814 EST324213 L. hirsutum trichome, Cornell Un...	148	1e-41
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 30 emb|AW034115|AW034115 EST277610 tomato callus, TAMU Lycopersicon... 147 4e-40
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 (2805 letters)

55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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60 Score E
 Sequences producing significant alignments: (bits) Value

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5	emb AI759920 AI759920 sb66c06.y1 Gm-cl017 Glycine max cDNA clone...	84	4e-15
	gb BE022401 BE022401 sm85d03.y1 Gm-cl015 Glycine max cDNA clone ...	55	3e-13
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	emb AW622410 AW622410 EST313197 tomato root during/after fruit s...	40	3e-06
	emb AW160184 AW160184 EST290041 L. pennellii trichome, Cornell U...	40	4e-06
	emb AW933376 AW933376 EST359219 tomato fruit mature green, TAMU ...	52	2e-05
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45 Database: plantfungal

661,018 sequences; 426,114,510 total letters

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 60 emb|AI896054|AI896054 EST265497 tomato callus, TAMU Lycopersicon... 47 4e-04
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60	emb X87941 SCDNAGENS S.cerevisiae CRM1, YML9, PET54, SMI1, PHO81...	28	7.5
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5 emb|AW924917|AW924917 WS1_73_B03.b1_A002 Water-stressed 1 (WS1) ... 33 9.9
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emb|AW991081|AW991081 SsS0293 Suaeda salsa ZAP cDNA library Suae... 33 9.9
10 emb|AW399343|AW399343 EST309843 L. pennellii trichome, Cornell U... 33 9.9
emb|AA784746|AA784746 g2a12a1.fl Aspergillus nidulans 24hr asexu... 33 9.9
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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

30 emb|AI486803|AI486803 EST245125 tomato ovary, TAMU Lycopersicon ... 358 6e-98
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emb|AW459665|AW459665 sh90c10.y1 Gm-c1016 Glycine max cDNA clone... 285 5e-76
emb|AI898341|AI898341 EST267784 tomato ovary, TAMU Lycopersicon ... 282 3e-75
35 gb|L42466|PIAEFE Picea glauca ethylene-forming enzyme (EFE) mRNA... 156 4e-75
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emb|AI777799|AI777799 EST258678 tomato susceptible, Cornell Lyco... 267 1e-70
emb|AW574101|AW574101 EST316692 GVN Medicago truncatula cDNA clo... 198 2e-67
emb|AW268031|AW268031 EST306309 DSIR Medicago truncatula cDNA cl... 126 6e-65
40 emb|AW775553|AW775553 EST334618 DSIL Medicago truncatula cDNA cl... 210 3e-63
emb|AW509400|AW509400 si22f08.y1 Gm-c1029 Glycine max cDNA clone... 237 8e-62
emb|AB003779|AB003779 Perilla frutescens mRNA for leucoanthocyan... 115 5e-59
emb|AW349732|AW349732 GM210006A11F12R Gm-r1021 Glycine max cDNA ... 228 6e-59
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45 emb|AF082862|AF082862 Pisum sativum unknown mRNA, partial cds. 220 2e-56
emb|Z22543|PHFLASYNA P.hybrida flavonol synthase mRNA. 99 1e-55
emb|X83229|NTRNA1A1C N.tabacum mRNA for 1-aminocyclopropane-1-ca... 176 1e-54
emb|AF184273|AF184273 Daucus carota leucoanthocyanidin dioxygena... 110 9e-54
emb|AW030000|AW030000 EST273255 tomato callus, TAMU Lycopersicon... 186 1e-53
50 emb|AF026058|AF026058 Matthiola incana anthocyanidin synthase mR... 116 2e-53
emb|AF184274|AF184274 Daucus carota leucoanthocyanidin dioxygena... 110 2e-53
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- emb|AB023786|AB023786 Ipomoea batatas ans I mRNA for anthocyanid... 111 4e-50
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emb|X04792|LEETHYBR Tomato mRNA expressed during fruit ripening ... 159 1e-49
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5 emb|A35021|A35021 L.esculentum pTOM13. 159 1e-49
emb|AF053354|AF053354 Phaseolus vulgaris 1-aminocyclopropane-1-c... 159 2e-49
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10 gb|U68215|CPU68215 Carica papaya ACC oxidase mRNA, complete cds. 152 5e-49
emb|AF117270|AF117270 Malus domestica flavanone 3-hydroxylase (F... 100 5e-49
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gb|M97961|ACTACCOXI Actinidia deliciosa ACC oxidase homologue pr... 154 7e-49
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25 emb|AB023790|AB023790 Ipomoea batatas f3h III mRNA for flavanone... 96 2e-48
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30 emb|X87097|PCPCACO1G P.communis mRNA for 1-aminocyclopropane-1-c... 155 5e-48
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emb|X98493|NTACCO Nicotiana tabacum mRNA for ACC-oxidase (clone ... 154 9e-48
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gb|L35152|DINACCA Dianthus caryophyllus amino-cyclopropane carbo... 158 1e-47
40 emb|AW685110|AW685110 NF025C04NR1F1000 Nodulated root Medicago t... 158 1e-47
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45 emb|Y10034|PP1AMCSYN R.palustris mRNA for 1-aminocyclopropane-1-... 159 2e-47
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50 emb|AJ001646|MDACCOXI2 Malus domestica mRNA for ACC oxidase. 153 3e-47
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- emb|AB010992|AB010992 Lycopersicon esculentum Le3OH-2 mRNA for 3... 133 2e-46
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 15 <http://www.ncgr.org/cgi-bin/ff?al035527>
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- Database: plantfungal
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 emb|AF016713|AF016713 Lycopersicon esculentum oligopeptide trans... 138 3e-89
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 30 emb|X92852|LENIT2 L.esculentum exon 1 of NIT2 gene. 140 1e-80
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 emb|X92853|LEMIT1 L.esculentum exon 1 of NIT1 gene. 150 9e-74
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 35 emb|AW278758|AW278758 sf97b05.y1 Gm-c1019 Glycine max cDNA clone... 127 2e-47
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 40 emb|AW219289|AW219289 EST301771 tomato root during/after fruit s... 144 3e-34
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5 emb|AW201920|AW201920 sf08g07.y1 Gm-c1027 Glycine max cDNA clone... 105 4e-27
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15 emb|AI736700|AI736700 sb32d07.y1 Gm-c1012 Glycine max cDNA clone... 102 3e-25
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20 emb|AA739757|AA739757 522 PtIFG2 Pinus taeda cDNA clone 8840M 3'... 115 1e-24
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25 emb|AW256423|AW256423 EST304490 KV2 Medicago truncatula cDNA clo... 46 4e-23
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35 emb|AW563695|AW563695 LG1_248_G02.g1_A002 Light Grown 1 (LG1) So... 70 6e-21
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emb|AW257391|AW257391 EST305528 KV2 Medicago truncatula cDNA clo... 93 8e-18
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 http://www3.ncbi.nlm.nih.gov/htbin-
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 10 http://www.ncgr.org/cgi-bin/ff?ac006580
 (828 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Score E
 Sequences producing significant alignments: (bits) Value

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 emb|AW931430|AW931430 EST357273 tomato fruit mature green, TAMU ... 214 5e-55
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 30 emb|AI488758|AI488758 EST247097 tomato ovary, TAMU Lycopersicon ... 200 1e-50
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Score E

Sequences producing significant alignments: (bits) Value

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 (990 letters)

60 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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60	emb AQ946977	AQ946977	Sheared DNA-47C11.TF Sheared DNA Trypanoso...	92	8e-18
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55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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 (711 letters)

5 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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60 (168 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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30	emb AW979578 AW979578 EST341174 tomato root deficiency, Cornell ...	85	2e-17
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 35 emb|AW617954|AW617954 EST314028 L. pennellii trichome, Cornell U... 71 3e-13
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55 Database: plantfungal
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 35 emb|A46806|A46806 Sequence 3 from Patent EP0684312. 35 1.7
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 60 emb|AI213031|AI213031 y6f05a1.r1 *Aspergillus nidulans* 24hr asexu... 33 5.9
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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35	emb AW560934 AW560934 EST315982 DSIR Medicago truncatula cDNA cl...	49 6e-12
	emb AW781249 AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone...	49 6e-12
	gb U68763 GMU68763 Glycine max putative transcription factor SCO...	48 8e-12
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	gb BE059872 BE059872 sn38c04.y1 Gm-c1016 Glycine max cDNA clone ...	48 8e-12
40	dbj D26086 PETZFP4 Petunia zinc-finger protein gene.	50 1e-11
	emb AW219517 AW219517 EST301915 tomato root during/after fruit s...	52 1e-11
	gb U76554 BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR...	52 2e-11
	emb AW729218 AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ...	48 2e-11
	emb AW279005 AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone...	51 2e-11
45	emb AW164639 AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone...	51 2e-11
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50	gb BE123920 BE123920 EST394045 DSIL Medicago truncatula cDNA clo...	46 4e-11
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	emb AW706944 AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone...	47 4e-11
	emb AW219736 AW219736 EST302218 tomato root during/after fruit s...	52 4e-11
	dbj D26085 PETZFDB3 Petunia zinc-finger DNA binding protein gene.	46 5e-11
55	emb AW777036 AW777036 M111167e DSIR Medicago truncatula cDNA clo...	59 2e-10
	emb AW032112 AW032112 EST275566 tomato callus, TAMU Lycopersicon...	43 4e-10
	emb AT000773 AT000773 AT000773 Brassica rapa guard cell Brassica...	65 4e-10
	emb AW216968 AW216968 EST295682 tomato callus, TAMU Lycopersicon...	53 4e-09
	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA...	52 6e-09
60	gb BE058334 BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone ...	48 1e-08
	emb AI966679 AI966679 sc55a11.y1 Gm-c1015 Glycine max cDNA clone...	54 3e-08

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	emb AF119050 AF119050 Datisca glomerata zinc-finger protein 1 (z...	56	3e-07
	emb AW030314 AW030314 EST273569 tomato callus, TAMU Lycopersicon...	53	4e-07
5	emb X60700 PHEPF1 P.hybrida EPF1 gene for DNA-binding protein.	55	7e-07
	emb AW620780 AW620780 sj09e02.y1 Gm-cl032 Glycine max cDNA clone...	54	9e-07
	emb AI960244 AI960244 sc80g07.y1 Gm-cl018 Glycine max cDNA clone...	54	9e-07
	emb AB000452 AB000452 Petunia hybrida mRNA for PETHy;ZPT2-6, com...	54	9e-07
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	gb L46574 L46574 BNAF1975 Mustard flower buds Brassica rapa cDNA...	84	2e-29
	emb AB006600 AB006600 Petunia x hybrida mRNA for ZPT2-13, comple...	57	2e-25
25	emb AB006599 AB006599 Petunia x hybrida mRNA for ZPT2-12, comple...	57	5e-23
	emb AI485362 AI485362 EST243683 tomato ovary, TAMU Lycopersicon ...	64	4e-22
	emb AI898309 AI898309 EST267752 tomato ovary, TAMU Lycopersicon ...	63	8e-22
	emb AI483886 AI483886 EST249757 tomato ovary, TAMU Lycopersicon ...	64	2e-21
	emb AB006604 AB006604 Petunia x hybrida mRNA for ZPT2-9, complet...	102	2e-21
30	emb AW030869 AW030869 EST274159 tomato callus, TAMU Lycopersicon...	61	4e-21
	emb AI485555 AI485555 EST243876 tomato ovary, TAMU Lycopersicon ...	55	7e-21
	emb AB000451 AB000451 Petunia hybrida mRNA for PETHy;ZPT2-5, com...	62	2e-20
	emb AI486627 AI486627 EST244948 tomato ovary, TAMU Lycopersicon ...	55	2e-20
	emb AI486228 AI486228 EST244549 tomato ovary, TAMU Lycopersicon ...	55	2e-20
35	emb AI771123 AI771123 EST252223 tomato ovary, TAMU Lycopersicon ...	55	6e-20
	emb AB006601 AB006601 Petunia x hybrida mRNA for ZPT2-14, comple...	62	6e-20
	emb AI488341 AI488341 EST246663 tomato ovary, TAMU Lycopersicon ...	55	8e-20
	emb AI959966 AI959966 sc35g05.x1 Gm-cl014 Glycine max cDNA clone...	60	1e-19
	emb AI966235 AI966235 sc35g05.y1 Gm-cl014 Glycine max cDNA clone...	60	1e-19
40	emb AI897376 AI897376 EST266819 tomato ovary, TAMU Lycopersicon ...	64	2e-19
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	emb AI485123 AI485123 EST243427 tomato ovary, TAMU Lycopersicon ...	60	2e-18
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	emb AW216442 AW216442 EST295072 tomato callus, TAMU Lycopersicon...	57	1e-17
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	emb AW687462 AW687462 NF009H03RT1F1031 Developing root Medicago ...	57	8e-17
50	emb AV422177 AV422177 AV422177 Lotus japonicus young plants (two...	56	8e-17
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	emb AI487993 AI487993 EST246315 tomato ovary, TAMU Lycopersicon ...	53	2e-15
	emb AW034640 AW034640 EST278324 tomato callus, TAMU Lycopersicon...	53	2e-15
	emb AI896031 AI896031 EST265474 tomato callus, TAMU Lycopersicon...	53	3e-15
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60	emb AW033257 AW033257 EST276828 tomato callus, TAMU Lycopersicon...	53	3e-15
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- emb|AW032357|AW032357 EST275811 tomato callus, TAMU Lycopersicon... 53 3e-15
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 5 emb|AI488445|AI488445 EST246784 tomato ovary, TAMU Lycopersicon ... 55 2e-13
 emb|AB035133|AB035133 *Petunia x hybrida* gene for C2H2 zinc-finge... 53 2e-13
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 dbj|D16415|WHTWZF1A Wheat gene for WZF1, complete cds. 47 3e-13
 dbj|D16416|WHTWZF1B Wheat mRNA for WZF1, complete cds. 47 3e-13
 10 emb|AW924420|AW924420 WS1_69_C08.b1_A002 Water-stressed 1 (WS1) ... 48 5e-13
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 emb|AW037956|AW037956 EST279600 tomato mixed elicitor, BTI Lycop... 52 7e-13
 emb|AI485651|AI485651 EST243972 tomato ovary, TAMU Lycopersicon ... 52 9e-13
 emb|AI487287|AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... 52 1e-12
 15 emb|AW034622|AW034622 EST278306 tomato callus, TAMU Lycopersicon... 50 2e-12
 gb|U76555|BRU76555 *Brassica rapa* zinc-finger protein BcZFP1 (BcA... 52 2e-12
 emb|AW035987|AW035987 EST282846 tomato callus, TAMU Lycopersicon... 53 2e-12
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 emb|AW625323|AW625323 EST319146 tomato radicle, 5 d post-imbibit... 52 3e-12
 20 emb|AW924443|AW924443 WS1_69_C08.g1_A002 Water-stressed 1 (WS1) ... 57 3e-12
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 emb|AB035132|AB035132 *Petunia x hybrida* gene for C2H2 zinc-finge... 50 4e-12
 emb|AB006597|AB006597 *Petunia x hybrida* mRNA for ZPT2-10, comple... 50 4e-12
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 gb|U76554|BRU76554 *Brassica rapa* zinc-finger protein-1 (BR42) mR... 52 2e-11
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 60 emb|AI960244|AI960244 sc80g07.y1 *Gm-c1018* Glycine max cDNA clone... 54 9e-07
 emb|AB000452|AB000452 *Petunia hybrida* mRNA for PETHy;ZPT2-6, com... 54 9e-07

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Score E

Sequences producing significant alignments: (bits) Value

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emb|Y11607|MSMP2C M.sativa mRNA for protein phosphatase 2C. 164 7e-70

emb|AJ242803|SST242803 Sporobolus stapfianus partial mRNA for pu... 154 4e-61

emb|AI055336|AI055336 coau0003L08 Cotton Boll Abscission Zone cD... 163 7e-56

emb|AI488711|AI488711 EST247050 tomato ovary, TAMU Lycopersicon ... 158 5e-46

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emb|AI489841|AI489841 EST248180 tomato ovary, TAMU Lycopersicon ... 173 1e-42

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emb|AW423616|AW423616 sb69d07.y1 Gm-cl015 Glycine max cDNA clone... 110 3e-36

emb|AW278110|AW278110 sf39h03.y1 Gm-cl009 Glycine max cDNA clone... 119 2e-35

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emb|AW698103|AW698103 NXNV_066_C09_F Nsf Xylem Normal wood Verti... 120 2e-33

emb|AI489730|AI489730 EST248069 tomato ovary, TAMU Lycopersicon ... 62 3e-29

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emb|AF092431|AF092431 Lotus japonicus nodule-enhanced protein ph... 64 1e-18

emb|AF092432|AF092432 Lotus japonicus protein phosphatase type 2... 73 8e-18

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emb|AI731667|AI731667 BNLGHi10427 Six-day Cotton fiber Gossypium... 80 4e-16

emb|AW458317|AW458317 sh86c05.y1 Gm-cl016 Glycine max cDNA clone... 77 7e-16

emb|AW035781|AW035781 EST281935 tomato callus, TAMU Lycopersicon... 84 1e-15

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gb|H07534|H07534 cbn054 BNL2 Brassica napus cDNA 5'/3', mRNA seq... 82 5e-15

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emb|AW201723|AW201723 sf06e04.y1 Gm-cl027 Glycine max cDNA clone... 73 9e-15

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emb|AI812394|AI812394 IH12 Pine Lambda Zap Xylem library Pinus t... 75 1e-14

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emb|AA080599|AA080599 EST054 Sugarcane leaf roll Saccharum sp. c... 74 3e-14

emb|AW328993|AW328993 N200187e rootphos(-) Medicago truncatula c... 78 8e-14

emb|AW926387|AW926387 HVSMEg0007B08 Hordeum vulgare pre-anthesis... 78 8e-14

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emb|AW560026|AW560026 EST315074 DSIR Medicago truncatula cDNA cl... 77 1e-13

emb|AW981447|AW981447 EST392609 DSIL Medicago truncatula cDNA cl... 77 1e-13

emb|AW775291|AW775291 EST334356 DSIL Medicago truncatula cDNA cl... 77 1e-13

emb|AW223860|AW223860 EST300671 tomato fruit red ripe, TAMU Lyco... 69 1e-13

emb|AW930922|AW930922 EST356765 tomato fruit mature green, TAMU ... 69 1e-13

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emb|AW126261|AW126261 N100368e rootphos(-) Medicago truncatula c... 71 3e-13

emb|AW217002|AW217002 EST295716 tomato callus, TAMU Lycopersicon... 75 6e-13

emb|AW560025|AW560025 EST315073 DSIR Medicago truncatula cDNA cl... 74 8e-13

emb|AI855433|AI855433 sc16a02.y1 Gm-cl013 Glycine max cDNA clone... 73 1e-12

gb|BE057188|BE057188 sm97g04.y1 Gm-cl015 Glycine max cDNA clone ... 55 3e-12

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emb|AI898557|AI898557 EST268000 tomato ovary, TAMU Lycopersicon ... 66 6e-12

gb|BE055043|BE055043 GA_Ea0031H07f Gossypium arboreum 7-10 dpa ... 71 1e-11

- emb|AI895824|AI895824 EST265267 tomato callus, TAMU Lycopersicon... 66 1e-11
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 5 emb|AW309195|AW309195 sg05e02.y1 Gm-c1019 Glycine max cDNA clone... 62 2e-11
 emb|AW934653|AW934653 EST353545 tomato flower buds 0-3 mm, Corne... 69 3e-11
 emb|AW736469|AW736469 EST332483 KV3 Medicago truncatula cDNA clo... 69 3e-11
 emb|AI052979|AI052979 Mpc9 Ice plant seedlings, RT-PCR, pCRII M... 63 3e-11
 gb|BE049699|BE049699 NXNV_142_B11_F Nsf Xylem Normal wood Vertic... 63 3e-11
 10 emb|AW224147|AW224147 EST300958 tomato fruit red ripe, TAMU Lyco... 69 3e-11
 emb|AW623772|AW623772 EST321717 tomato flower buds 3-8 mm, Corne... 68 5e-11
 emb|AW929331|AW929331 EST338119 tomato flower buds 8 mm to pre-a... 68 5e-11
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 emb|AW648269|AW648269 EST326723 tomato germinating seedlings, TA... 68 5e-11
 emb|AW755847|AW755847 sl10a10.y1 Gm-c1036 Glycine max cDNA clone... 68 5e-11
 15 emb|AW290631|AW290631 NXNV044C04F Nsf Xylem Normal wood Vertical... 68 5e-11
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 emb|AI052978|AI052978 Mpc7 Ice plant seedlings, RT-PCR, pCRII M... 36 1e-10
 emb|AI900423|AI900423 sc05e10.y1 Gm-c1012 Glycine max cDNA clone... 44 2e-10
 emb|AW567769|AW567769 si54f05.y1 Gm-r1030 Glycine max cDNA clone... 44 2e-10
 20 emb|AI489404|AI489404 EST247743 tomato ovary, TAMU Lycopersicon ... 66 2e-10
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 emb|AW442288|AW442288 EST311684 tomato fruit red ripe, TAMU Lyco... 66 3e-10
 emb|AW039555|AW039555 EST281836 tomato mixed elicitor, BTI Lycop... 66 3e-10
 emb|AW094483|AW094483 EST287663 tomato mixed elicitor, BTI Lycop... 66 3e-10
 25 emb|AI167089|AI167089 xylem.est.857 Poplar xylem Lambda ZAPII li... 48 6e-10
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 emb|AW101459|AW101459 sd78e02.y1 Gm-c1009 Glycine max cDNA clone... 55 2e-09
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 35 emb|AW739238|AW739238 gb39a01.y1 Moss EST library PPN Physcomitr... 59 3e-08
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 gb|L33918|USMUAC1A Corn smut fungus uac1 gene, complete cds. 41 5e-07
 50 emb|AW278161|AW278161 sf40e04.y1 Gm-c1009 Glycine max cDNA clone... 55 7e-07
 emb|AI060326|AI060326 Mpc5 Ice plant seedlings, RT-PCR, pCRII M... 37 8e-07
 emb|AW616138|AW616138 EST296905 L. hirsutum trichome, Cornell Un... 54 9e-07
 emb|AW119467|AW119467 sd47d10.y1 Gm-c1016 Glycine max cDNA clone... 54 9e-07
 emb|Z48008|SC8119 S.cerevisiae chromosome IV cosmid 8119. 53 2e-06
 55
 Query= AC004138.105_at 16257_at /id_source genbank /description
 gb|aac32915.1| (ac004138) putative nucleoside triphosphatase
 [arabidopsis thaliana] /blast_score 0 /ec_number ec_3.6.1.42 /family
 diphosphatase /chip nova /gb_link
 60 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004138|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004138|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004138|/ncgi)

<http://www.ncgr.org/cgi-bin/ff?ac004138>
(1551 letters)

Database: plantfungal
5 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
10	Sequences producing significant alignments:	(bits)	Value
	gb U58597 STU58597 Solanum tuberosum ATP-diphosphohydrolase (RRO...	66	1e-31
	emb Z32743 PSNTPASE P.sativum (Alaska) NTPase mRNA for nucleosid...	64	1e-30
	emb AB022319 AB022319 Pisum sativum mRNA for apyrase, complete cds.	64	1e-30
15	emb AB027616 AB027616 Pisum sativum mRNA for apyrase, partial cd...	64	2e-29
	emb AW925295 AW925295 HVSMEg0001H23 Hordeum vulgare pre-anthesis...	69	2e-29
	emb AF156782 AF156782 Medicago sativa nod factor binding lectin-...	66	8e-29
	emb AW983120 AW983120 HVSMEg0008D22f Hordeum vulgare pre-anthesi...	70	2e-28
	emb AI771115 AI771115 EST252215 tomato ovary, TAMU Lycopersicon ...	71	4e-28
20	emb AW934554 AW934554 EST353446 tomato flower buds 0-3 mm, Corne...	71	8e-26
	emb AW621504 AW621504 EST312302 tomato root during/after fruit s....	62	7e-25
	emb AF156780 AF156780 Lotus japonicus nod factor binding lectin-...	60	2e-23
	emb AW618513 AW618513 EST320499 L. pennellii trichome, Cornell U...	67	5e-22
	emb AF139807 AF139807 Dolichos biflorus nod factor binding lecti...	65	6e-22
25	emb AW928903 AW928903 EST337691 tomato flower buds 8 mm to pre-a...	71	7e-22
	emb AB032754 AB032754 Solanum melongena EEF45 mRNA, partial cds.	65	2e-21
	emb AW428956 AW428956 EST306496 tomato flower buds 0-3 mm, Corne...	68	1e-19
	emb AW201606 AW201606 sf05b09.y1 Gm-c1027 Glycine max cDNA clone...	57	8e-18
	emb AV421159 AV421159 AV421159 Lotus japonicus young plants (two...	62	8e-18
30	emb AL121741 SPAC824 S.pombe chromosome I cosmid c824.	53	2e-17
	emb AL121783 SPCC11E10 S.pombe chromosome III cosmid c11E10.	52	1e-16
	emb AZ048365 AZ048365 LMAJFV1_lm77d11.x1 Leishmania major FV1 ra...	65	2e-16
	emb AI900961 AI900961 sc17g01.y1 Gm-c1013 Glycine max cDNA clone...	61	4e-16
	emb AW233919 AW233919 sf32a09.y1 Gm-c1028 Glycine max cDNA clone...	72	6e-16
35	emb AI729322 AI729322 BNLGH113103 Six-day Cotton fiber Gossypium...	56	4e-15
	gb U18779 SCE8199 Saccharomyces cerevisiae chromosome V cosmid 8...	47	9e-15
	gb L19560 YSCGUANDIP Saccharomyces cerevisiae guanosine diphosph...	47	1e-14
	emb AI855475 AI855475 sc16e11.y1 Gm-c1013 Glycine max cDNA clone...	56	6e-13
	emb AI488582 AI488582 EST246921 tomato ovary, TAMU Lycopersicon ...	60	8e-13
40	emb AJ388942 AJ388942 AJ388942 Medicago truncatula R108 Medicago...	63	1e-12
	emb AW620334 AW620334 sj03g08.y1 Gm-c1032 Glycine max cDNA clone...	61	2e-12
	emb AF156781 AF156781 Dolichos biflorus apyrase mRNA, complete cds.	62	7e-12
	emb AA660474 AA660474 00360 MtRHE Medicago truncatula cDNA 5' si...	65	7e-12
	emb AI441990 AI441990 sa82g03.y1 Gm-c1004 Glycine max cDNA clone...	60	2e-11
45	emb AW696828 AW696828 NF109D12ST1F1101 Developing stem Medicago ...	57	2e-11
	gb BE059022 BE059022 sn24b03.y1 Gm-c1016 Glycine max cDNA clone ...	53	4e-11
	emb AW306606 AW306606 se53a03.y1 Gm-c1017 Glycine max cDNA clone...	56	8e-11
	emb AI490444 AI490444 EST248770 tomato ovary, TAMU Lycopersicon ...	61	2e-10
	emb AW564791 AW564791 LG1_301_H10.b1_A002 Light Grown 1 (LG1) So...	51	2e-10
50	emb AI771846 AI771846 EST252946 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AI897295 AI897295 EST266654 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AI485852 AI485852 EST244173 tomato ovary, TAMU Lycopersicon...	61	3e-10
	emb AI899079 AI899079 EST268522 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AW922880 AW922880 DG1_47_F10.b1_A002 Dark Grown 1 (DG1) Sorg...	48	4e-10
55	emb AI490499 AI490499 EST249033 tomato ovary, TAMU Lycopersicon ...	61	5e-10
	emb AI488302 AI488302 EST246624 tomato ovary, TAMU Lycopersicon ...	60	1e-09
	emb AV418181 AV418181 AV418181 Lotus japonicus young plants (two...	57	2e-09
	emb AW924275 AW924275 WS1_52_E03.b1_A002 Water-stressed 1 (WS1) ...	64	3e-09
	emb AW257004 AW257004 EST305141 KV2 Medicago truncatula cDNA clo...	48	8e-09
60	emb AI771696 AI771696 EST252796 tomato ovary, TAMU Lycopersicon ...	61	3e-08
	emb AW623313 AW623313 EST321258 tomato flower buds 3-8 mm, Corne...	58	2e-07

- emb|AA231755|AA231755 CDO38.R cDNA from oat Avena sativa cDNA cl... 56 7e-07
 emb|AW736308|AW736308 EST332392 KV3 Medicago truncatula cDNA clo... 54 4e-06
 emb|AW563435|AW563435 LG1_214_E12.b1_A002 Light Grown 1 (LG1) So... 38 4e-05
 emb|AB010444|AB010444 Neospora caninum mRNA for NTPase, complete... 41 1e-04
 5 emb|AL160371|LMFLCHR15 Leishmania major Friedlin assembled chrom... 44 0.004
 emb|AF203695|AF203695 Saccharomyces cerevisiae golgi nucleoside ... 43 0.005
 gb|U18778|SCE9537 Saccharomyces cerevisiae chromosome V cosmids ... 43 0.005
 emb|AZ124337|AZ124337 T223080b Medicago truncatula BAC library M... 41 0.026
 emb|AW225681|AW225681 ST70C07 Pine TriplEx shoot tip library Pin... 41 0.026
 10 emb|AW774350|AW774350 EST333501 KV3 Medicago truncatula cDNA clo... 41 0.026
 emb|AI974272|AI974272 T110271e KV0 Medicago truncatula cDNA clon... 40 0.035
 emb|AL049184|PFMAL13P3 Plasmodium falciparum chromosome 13 strai... 39 0.13
 emb|AI728079|AI728079 BNLGHi9928 Six-day Cotton fiber Gossypium ... 29 0.23
 emb|X61608|BNLHCB3A B.napus gene for LHCI Type III chlorophyll ... 37 0.33
 15 emb|AW671082|AW671082 LG1_284_C02.b1_A002 Light Grown 1 (LG1) So... 37 0.33
 emb|AZ124338|AZ124338 T223081b Medicago truncatula BAC library M... 36 0.85
 emb|AF188744|AF188744 Brassica napus high-affinity ammonium tran... 35 1.2
 dbj|D37795|D37795 Ipomoea nil Tpn1 gene. 35 1.2
 dbj|E08493|E08493 gDNA encoding transposable element, Tpn1 which ... 35 1.2
 20 emb|AL356192|NCB24B19 Neurospora crassa DNA linkage group II BAC... 30 1.3
 emb|AF106939|AF106939 Phanerochaete chrysosporium 1,4-benzoquino... 29 1.4
 emb|AL163492|LMFL787 Leishmania major Friedlin chromosome 19 cos... 35 1.5
 emb|AW234282|AW234282 sf23d03.y1 Gm-c1028 Glycine max cDNA clone... 35 1.6
 emb|AL116534|CNS01D9A Botrytis cinerea strain T4 cDNA library un... 35 1.6
 25 emb|AW428880|AW428880 Ljirmp25-999-b7 Ljirnp Lambda HybriZap ... 35 1.6
 gb|N60092|N60092 TgESTzy11d09.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.2
 emb|AW056764|AW056764 ST55E11 Pine TriplEx shoot tip library Pin... 35 2.2
 gb|N81562|N81562 TgESTzy59h03.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.2
 emb|AW286610|AW286610 LG1_335_A07.g1_A002 Light Grown 1 (LG1) So... 35 2.2
 30 emb|AQ656308|AQ656308 Sheared DNA-27M14.TR Sheared DNA Trypanoso... 35 2.2
 emb|AL162692|SPBP4H10 S.pombe chromosome II P1 clone p4H10. 34 3.0
 emb|AQ652731|AQ652731 Sheared DNA-18C6.TR Sheared DNA Trypanosom... 34 3.0
 emb|AF016222|AF016222 Schizosaccharomyces pombe Rsvlp (rsv1) gen... 34 3.0
 emb|AW350237|AW350237 GM210008A10B2R Gm-r1021 Glycine max cDNA 3... 34 4.1
 35 emb|AQ943814|AQ943814 Sheared DNA-34A9.TF Sheared DNA Trypanosom... 34 4.1
 emb|AW666160|AW666160 sk32h08.y1 Gm-c1028 Glycine max cDNA clone... 34 4.1
 emb|AL109736|SPCC18B5 S.pombe chromosome III cosmid c18B5. 27 4.6
 emb|AW441608|AW441608 EST311004 tomato fruit red ripe, TAMU Lyco... 33 5.7
 emb|AL035476|PFMAL4P3 Plasmodium falciparum chromosome 4 strain ... 33 5.7
 40 emb|AW398001|AW398001 sg71a06.y1 Gm-c1007 Glycine max cDNA clone... 33 5.7
 emb|AW933585|AW933585 EST359428 tomato fruit mature green, TAMU ... 33 5.7
 emb|AI069343|AI069343 mgae0006cG03f Magnaporthe grisea Appressor... 33 5.7
 emb|X62697|NCACU3 N.crassa acu-3 gene for isocitrate lyase. 26 5.7
 emb|AI488866|AI488866 EST247205 tomato ovary, TAMU Lycopersicon ... 31 6.2
 45 emb|Z79690|ANPFA A.niger pfkA gene. 26 7.3
 emb|X13508|HVGHRDSP Barley gene for storage protein gamma-hordein. 28 7.8
 gb|M36378|BLYG1HORDA Barley gamma-1 hordein storage protein gene... 28 7.8
 emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 33 7.8
 emb|AI900865|AI900865 sb95d08.y1 Gm-c1012 Glycine max cDNA clone... 33 7.8
 50 emb|AZ124341|AZ124341 T223084b Medicago truncatula BAC library M... 33 7.8

Query= AL035679.144_at 17653_at /id_source genbank /description
 emb|cab38823.1| (al035679) putative protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 55 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al035679>
 (1455 letters)

- 60 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
5	Sequences producing significant alignments:	(bits)	Value
	emb AW091895 AW091895 EST285075 tomato mixed elicitor, BTI Lycop...	306	3e-82
	emb AW040183 AW040183 EST282682 tomato mixed elicitor, BTI Lycop...	306	3e-82
	emb AW776130 AW776130 EST335195 DSIL Medicago truncatula cDNA cl...	204	2e-51
10	emb AI897609 AI897609 EST267052 tomato ovary, TAMU Lycopersicon ...	182	4e-45
	emb AI055000 AI055000 coau0002L23 Cotton Boll Abscission Zone cD...	90	1e-42
	emb AI055639 AI055639 coau0004K19 Cotton Boll Abscission Zone cD...	107	2e-22
	emb AW693198 AW693198 NF061D12ST1F1000 Developing stem Medicago ...	66	6e-10
	emb AW684256 AW684256 NF014F09NR1F1000 Nodulated root Medicago t...	43	0.007
15	emb AW667681 AW667681 GA_Ea0010D15 Gossypium arboreum 7-10 dpa ...	43	0.007
	emb AW736130 AW736130 EST332126 KV3 Medicago truncatula cDNA clo...	39	0.12
	emb AW683515 AW683515 NF015C12LF1F1097 Developing leaf Medicago ...	36	0.21
	emb AI781902 AI781902 EST262781 tomato susceptible, Cornell Lyco...	36	0.57
	gb U12141 SCU12141 Saccharomyces cerevisiae chromosome XIV left ...	35	0.73
20	emb AW277626 AW277626 sf84e07.y1 Gm-cl019 Glycine max cDNA clone...	36	0.79
	emb Z71330 SCYNL054W S.cerevisiae chromosome XIV reading frame O...	35	0.80
	emb AW692595 AW692595 NF057C11ST1F1000 Developing stem Medicago ...	35	1.1
	emb X54145 ANPECT A.niger gene for pectinesterase.	35	1.5
	emb A35008 A35008 A.niger PE gene.	35	1.5
25	emb A34997 A34997 A.niger pectinesterase coding sequence.	35	1.5
	emb AQ162316 AQ162316 mgxb0012I08r CUGI Rice Blast BAC Library P...	34	2.8
	emb AF132029 AF132029 Hortonia floribunda chloroplast atpB-rbcL ...	34	2.8
	emb AW567917 AW567917 si67c02.y1 Gm-r1030 Glycine max cDNA clone...	34	2.8
	emb AQ951657 AQ951657 Sheared DNA-48F5.TR Sheared DNA Trypanosom...	34	2.8
30	gb U81520 CIU81520 Cichorium intybus sucrose: sucrose 1-fructosyl...	34	3.9
	emb AZ047925 AZ047925 LMAJFV1_lm68e11.x1 Leishmania major FV1 ra...	34	3.9
	emb AI730144 AI730144 BNLGHi6313 Six-day Cotton fiber Gossypium ...	34	3.9
	emb AQ942723 AQ942723 Sheared DNA-42J12.TR Sheared DNA Trypanoso...	34	3.9
	gb U05812 HMU05812 Herpetomonas muscarum ATCC 30261 kinetoplast ...	34	3.9
35	emb AW681095 AW681095 WS1_8_B09.g1_A002 Water-stressed 1 (WS1) S...	34	3.9
	emb AL049180 PFMAL13P1 Plasmodium falciparum chromosome 13 strai...	27	4.9
	emb AW832107 AW832107 sm30e05.y1 Gm-cl028 Glycine max cDNA clone...	33	5.3
	gb N82224 N82224 TgESTzy37d01.r1 TgRH Tachyzoite cDNA Toxoplasma...	33	5.3
	emb A94222 A94222 Sequence 5 from Patent EP0952222.	33	5.3
40	emb AA741851 AA741851 LmLv39p3/584B Leishmania major promastigot...	33	5.3
	emb AW728096 AW728096 GA_Ea0029O02 Gossypium arboreum 7-10 dpa ...	33	7.3
	emb AW278032 AW278032 sf89g07.y1 Gm-cl019 Glycine max cDNA clone...	33	7.3
	gb N82117 N82117 TgESTzy36b06.r1 TgRH Tachyzoite cDNA Toxoplasma...	33	7.3
	emb AL355930 NCB2O8 Neurospora crassa DNA linkage group II BAC c...	32	10.0
45	emb AW688738 AW688738 NF011A11ST1F1000 Developing stem Medicago ...	32	10.0
	emb AI781529 AI781529 EST262408 tomato susceptible, Cornell Lyco...	32	10.0
	emb AI397765 AI397765 NCC5A11T7 Conidial Neurospora crassa cDNA ...	32	10.0
	emb AF127239 AF127239 Nicotiana tabacum cultivar Burley 21 argin...	32	10.0
	emb AW180260 AW180260 MgA0351fMgA Library Mycosphaerella gramin...	32	10.0
50	emb AF127240 AF127240 Nicotiana tabacum cultivar Xanthi arginine...	32	10.0
	gb BE055666 BE055666 GA_Ea0009H20f Gossypium arboreum 7-10 dpa ...	32	10.0
	gb BE036548 BE036548 MP01C02 MP Mesembryanthemum crystallinum cD...	32	10.0
	emb AW038750 AW038750 EST280611 tomato mixed elicitor, BTI Lycop...	32	10.0
	emb AL133484 LMFL236 Leishmania major Friedlin chromosome 19 cos...	32	10.0
55	gb BE123936 BE123936 EST394061 DSIL Medicago truncatula cDNA clo...	32	10.0

Example 4

Immediate Early Transcriptional Responses Controlled by a Salicylic Acid Dependent Local Resistance Pathway

Salicylic Acid (SA) is an important mediator of local and systemic
5 defense responses. In *Arabidopsis*, accumulation of SA is essential for local
resistance against many pathogens including *Peronospora parasitica*
(*Peronospora*) isolates. Furthermore, numerous defense-related genes can be
activated by SA treatment. In addition to local resistance, SA-accumulation is
required for systemic acquired resistance (SAR). In the SAR pathway, SA has
10 been shown to act upstream of *NPRI*, which is also essential for SAR. Short
application of the SA analog BTH (e.g., 4 hours) to plant tissue appears to
simulate local defense responses to *Peronospora parasitica*, whereas sustained
SA treatment (e.g., 48 hours) elicits SAR-related plant responses (Maleck et al.,
2000).

15 A previous cDNA microarray study identified a cluster of roughly 30 co-
regulated genes that appear to be specifically involved in resistance of the
Arabidopsis ecotype WS against the *Peronospora* isolate Noco2 (Maleck et al.,
2000). These genes are strongly activated in response to infection with Noco2
(incompatible interaction) and 4 hours after BTH treatment. However, these
20 genes were not markedly activated during a compatible interaction with the
Peronospora isolate Emwal or an incompatible interaction with *Pseudomonas*
syringae (DC3000 avrRpt2) bacteria. BTH treatment for 48 hours (that
simulates SAR) even strongly repressed these genes. Thus, a rapid and transient
SA peak may control Noco2 triggered defense genes.

25 Resistance of the *Arabidopsis* ecotype Col-0 against the *Peronospora*
isolate Emoy2 appears to be regulated by a similar pathway that also is
dependent on accumulation of SA. Emoy2 resistance in Col-0 is controlled by
the resistance gene *RPP4*. To further explore early SA-dependent gene
regulatory events and to relate these to *Peronospora*-induced resistance
30 responses, immediate-early target genes of SA were identified using Affymetrix
chip experiments with the protein biosynthesis inhibitor cycloheximide (CHX).
Genes of this category likely are linked to transcriptional regulators acting
closely downstream of SA. Results from these "SA-chip" experiments were
combined with those from a set of chip experiments examining expression

profiles triggered in the *Arabidopsis* ecotype Col-0 by the *Peronospora* isolate Emoy2 to identify clusters of co-regulated *RPP4* controlled SA-dependent immediate early genes.

Results

5 To identify genes controlled by the *RPP4* pathway, interactions between the *Peronospora* isolate Emoy2 and Col-0 wild type plants, the defense mutants *ndr1*, *npr1* and *pad4* as well as transgenic NahG plants were examined by chip experiments. The interactions between Emoy2 and Col-0, *ndr1* or *npr1* are incompatible (plant is disease resistant), whereas the interactions involving *pad4* and NahG are compatible (plant is susceptible, i.e., disease develops). For each interaction three different time points were analyzed: 0, 12 and 48 hours post infection with 50,000 Emoy2 spores/ml. Genes that were at one or more time points more strongly expressed in Col-0, *ndr1* and *npr1* as compared to *pad4* and NahG were considered as controlled by the *RPP4* pathway. Genes represented by 271 probe sets showed at least one 2-fold expression difference in comparison between Col-0 and *pad4* or NahG and were selected for further analysis.

To identify immediate early target genes of SA, Col-0 wt seedlings were pretreated with CHX or mock treated 15 minutes before spraying with 2 mM SA or water and harvested 2 hours later (Table 28).

Table 28

<u>Plants</u>	<u>Treatment</u>
Col-0	untreated (mock)
25 Col-0	+ SA
Col-0	+ SA + CHX
Col-0	+ CHX

271 probe sets were found to be upregulated in a *RPP4* pathway-specific manner (SEQ ID NOs: 400-684). Emoy2-induced upregulation of these genes is compromised in *pad4* and NahG plants. These *RPP4* controlled genes were further analyzed concerning their responses to SA, CHX and SA + CHX. The 271 probe sets were subcategorized by K-means clustering over the SA/CHX data set. Nine K-means clusters comprised three subgraphs. For each of these subgraphs, the first data point represented the untreated control value, the second data point represented the response to combined SA/CHX treatment, the third

data point represented CHX treatment alone and the fourth data point represented SA treatment alone. K-means clustering defined two categories of RPP4 controlled CHX/SA-responsive genes: immediate early genes (SA-responsive, not CHX affected) and super-induced genes (additive effects of SA and CHX).

Two K-means clusters represent *RPP4*-controlled SA-induced immediate early genes (Table 29; SEQ ID NOs: 150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615 and 526). *RPP4*-controlled upregulation of these genes is SA dependent and SA induction is not compromised by CHX, which blocks or reduces protein biosynthesis. Thus, all essential regulators that mediate SA-responsiveness of these genes must be already preformed and, hence, are likely to act closely downstream of SA. This set of 15 genes includes seven potential regulator genes that may be involved in the control of secondary response genes (which require protein biosynthesis) or other late responses.

Table 29

12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase
14978_at	gb AAB64024.1 (AC002333) putative glucosyltransferase
15479_at	emb CAB39671.1 (AL049483) putative protein
15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1
16061_s_at	gb AAB97145.1 (AF000977) MEK1
16109_s_at	gb AAC05342.1 (AC002521) putative protein kinase
16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2
16603_s_at	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase
17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel
17930_s_at	emb CAA07352.1 (AJ006960) peroxidase
18966_at	gb AAC95196.1 (AC004561) putative glutathione S-transferase
20429_s_at	emb CAB10219.1 (Z97336) hypothetical protein - weak similarity to NF-kappa-B
20685_at	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein
13702_s_at	emb CAA19683.1 (AL024486) putative protein
14704_s_at	gb AAD15461.1 (AC006067) unknown protein

To further subcategorize these genes and to more precisely define a cluster of strictly co-regulated genes, the set of 15 genes was analyzed by K-means clustering over the *RPP4* data set (Emoy2 infections). This allows to use *RPP4* triggered expression timing as an additional criterion for subclustering. Normalized absolute expression levels at 0, 12 and 48 hpi in Emoy2 infected

Col-0 (w.t.), *ndr1*, *npr1*, *pad4* and *NahG* plants are displayed. Genes that share a pronounced almost linear and sustained expression increase were chosen for further analysis. These 5 genes (Table 30, which show a pronounced Emoy2-induced SA-dependent but *npr1*-independent linear expression increase and which encode potential regulators) are upregulated by the *RPP4* pathway, respond to Emoy2 recognition with a steep, sustained, almost linear expression increase. This pronounced "upregulation" is SA dependent and independent of *de novo* protein biosynthesis. Transcription factors that mediate this response must be present when SA is perceived and may act closely downstream of SA.

The mechanism that switches these genes on may involve posttranslational modifications of such preformed transcription factors.

Table 30

15	12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase
	15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1
	16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2
	17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel
20	20429_s_at	emb CAB10219.1 (Z97336) hypothetical protein - weak similarity to NF-kappa-B

To identify the potential binding sites of such key transcription factors, the promoters of these five genes were searched for conserved compact sequence motifs (Table 31; SEQ ID NOs: 757-764; SEQ ID NO:765 is a consensus sequence). Using the program "AlignACE", a strikingly conserved motif was found that is present in all five promoters. This motif resembles the described consensus binding site of WRKY transcription factors, W box. However, the W box core motif, TGAC, is followed by an "A". The permutation TGACA has never been associated with WRKY binding. In addition to this, four more positions are highly conserved. This motif may be the specific binding site of an unconventional WRKY transcription factor or a factor of a novel so far unknown type. Yeast one hybrid screens can reveal the identity of this factor.

Table 31

35	W box-like Motif		
	MAP Score: 4.4		
	ACAGTGACA 0 391 1	(12345)	SEQ ID NO:757
	ACAGTGACA 1 236 1	(16140)	SEQ ID NO:758

ACAGTGACA 1 317 1 (16140) SEQ ID NO:759
 ACAGTGACA 2 281 1 (15616) SEQ ID NO:760
 ACAGTAACA 3 84 1 (17498) SEQ ID NO:761
 AAAGTAACA 3 1557 0 (17498) SEQ ID NO:762
 5 AAAGTGACA 4 1840 0 (20429) SEQ ID NO:763
 AAAGTGACA 4 2131 0 (20429) SEQ ID NO:764

ACAGTGACA SEQ ID NO:765

A

10 Expt. Frequency: 0.02/1kb
 Obs. in SOMc7: 0.06/1kb
 Obs. in this cluster: 0.50/1kb

15 One K-means cluster of the 271 RPP4 controlled probe sets represents
RPP4-controlled SA/CHX super-induced genes (Table 32; SEQ ID NOs: 214,
 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551).
RPP4-controlled upregulation of these genes is SA-dependent; these genes are
 weakly inducible upon both SA and CHX treatment alone. The response to
 20 combined treatment with SA and CHX is stronger than the response to either
 single treatment. Induction of genes in response to CHX alone has been
 described before and has been attributed to hypothetical proteins that are rapidly
 turned over and either repress transcription of the respective gene or control
 degradation of the respective mRNA. Block of synthesis of such hypothetical
 25 proteins may lead to increased mRNA levels by either increased transcription or
 reduced mRNA degradation. Like the set of immediate early SA responsive
 genes shown before, genes of this set also appear not to require *de novo* protein
 biosynthesis for their response to SA. In contrast to the previous gene set,
 however, the observed CHX-induced up-regulation may point to a de-repression
 30 mechanism.

Table 32

	12505_s_at	gb AAC63643.1 (AC005309) putative CONSTANS-like B-box zinc finger protein
35	13656_at	gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function
	14116_at	gb AAC26243.1 (AF077407) contains similarity to sugar transporters
	14170_at	gb AAF29406.1 AC022354_5 (AC022354) unknown protein
40	14223_at	emb CAA19683.1 (AL024486) putative protein

14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to
	gb X97864 cytochrome P450
14608_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to
	gb AF038007 FIC1, member of the PF 00122 E1-E2 ATPase
5	family.
14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase
15646_s_at	gb AAC37474.1 (L42212) serine acetyltransferase
16054_s_at	emb CAA74639.1 (Y14251) glutathione S-transferase
16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4
10 16968_at	emb CAA17559.1 (AL021961) glucosyltransferase -like protein
18235_at	gb AAB61480.1 (AC000348) T7N9.4
18567_at	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase
18591_at	emb CAA52772.1 (X74756) ATAF2
19845_g_at	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2)
15 20017_at	gb AAC16079.1 (AC004521) unknown protein

To further subcategorize these genes based on *RPP4* triggered expression timing, the set of 17 SA/CHX super induced genes was K-means clustered over the *RPP4* (Emoy2) data set (Table 33; SEQ ID NOs: 214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551). A group of five

20 genes was identified that consistently respond quickly ("fast", within 12 hpi) and that have elevated expression ground states in the *npr1* mutant. The fast response is SA dependent (is abolished or attenuated in *pad4* and *NahG*). The elevated expression ground states in *npr1* together with the observed CHX inducibility may point to an *NPR1*-dependent repression mechanism. Since

25 *NPR1* has been shown previously to act closely at the level of transcriptional regulation, a *NPR1* dependent repressor may shut expression of these genes down. Upon CHX treatment this hypothetical repressor is not synthesized anymore and expression of these genes is elevated. This repressor may also participate in *RPP4* triggered activation of these genes and allow Emoy2-

30 induced de-repression.

Table 33

18591_at	emb CAA52772.1 (X74756) ATAF2
14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to
35	gb X97864 cytochrome P450
14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase
15646_s_at	gb AAC37474.1 (L42212) serine acetyltransferase
16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4

To identify binding sites of activating or repressing factors responsible for the co-regulation of this small cluster, the promoters of these genes were searched for conserved compact motifs with "AlignACE" (Table 34; SEQ ID NOs: 766-772, SEQ ID NO:773 is a consensus sequence). One strictly
5 conserved octameric motif was found, which, however, is absent in one of the promoters. Yeast one hybrid screens can identify factors binding to this motif.

Table 34

Motif 15			
10	MAP Score: 1.23758		
	AATCGAAT 0 40 0	(18591)	SEQ ID NO:766
	AATCGAAT 0 1741 1	(18591)	SEQ ID NO:767
	AATCGAAT 1 386 1	(PAD3, 14248)	SEQ ID NO:768
	AATCGAAT 2 334 1	(14614)	SEQ ID NO:769
15	AATCGAAT 2 660 1	(14614)	SEQ ID NO:770
	AATCGAAT 2 2105 1	(14614)	SEQ ID NO:771
	AATCGAAT 3 1570 1	(15646)	SEQ ID NO:772

	AATCGAAT		SEQ ID NO:773
20			
	expt.:	0.08/kb	
	obs.:	0.70/kb	
	SOMc7:	0.06/kb	
	Random20:	0.00/kb	
25	SOMc3:	0.10/kb	
	SOMc1:	0.10/kb	

As described hereinbelow, sets of genes specifically controlled by the *RPP7* and *RPP8* pathways were defined. Similarly a set of *RPP4* pathway
30 controlled genes was defined (see Figure 4). Figure 4 shows a "Venn diagram" including only the transcription factor genes of these *RPP4*, *RPP7* and *RPP8* controlled genes. Three transcription factor genes were found to be specifically upregulated by each of the three *Peronospora* defense pathways: AtERF1, HSF4, ATAF2. Furthermore, ERF transcription factors appear to play an
35 important role in controlling defense responses directed against *Peronospora* in general. Table 35 gives four potential target genes of ERF transcription factors. These genes contain ERF binding motifs in their promoters.

Table 35

40 Genes with potential ERF binding sites (GCCGCC or GCCGAC):

thioredoxin (13189) RPP7/RPP8 and (weakly) RPP4 controlled
 C2H2 zinc finger (15665) RPP7/RPP4 and (weakly) RPP8 controlled
 SigA binding protein (14148) RPP7/RPP4 controlled
 HSP70 (13284) RPP7/RPP8 controlled

5

These genes are specifically controlled by at least two different *Peronospora* defense pathways and show an almost linear increase of transcript levels during incompatible Hiks1 interactions (K-means clusters 3+5).

6 potential ERF binding sites in K-means cluster 3+5: 0.5 motifs /

10 1kbExpected: 0.1 motif / 1kb; Enrichment in K-means cluster 3+5: 5-fold

SEQ ID NO:789

MPTSATAVAPSTGSVQKKDQDWRAILSPEQFRVLREKGTENRGKGEYT
 KLFDDGIYSCAGCATPLYKSTTKFDSGCGWPSFFDAIPGAIKQTDMFGSN
 15 AADGSIVTSGLDYILISINEKLKAYT

SEQ ID NO:790

1 tgcattcttt tgaggggttt aattttctgc atagctttgt ctaatctctt agagctcaat
 61 aagagaagat ggatgttcca cggccagctt tcaaattgtt tgatgacgat ggccggctta
 20 121 aacgttcagg gacggttgg accgcgagtg cgcatacat aaccgccgtg attggatctg
 181 gtgttctatc gcttgcgtgg gctataggtc aactcggttg gatcgcaggt cctacagtga
 241 tgttgttgtt ctctttgtc acttactact ctccacgct tcttagcgac tgctacagaa
 301 ccggagatcc tgtctctggg aagagaaact atacttacat ggacgctgtc cgatcaatcc
 361 taggtggctt taggttcaag atttgtgggc tgattcagta ttgaatctg ttggtatca
 25 421 cggtcgggta cacaatcgca gcattataa gtatgatggc gatcaagagg tccaactgtt
 481 tccacgagag cggagggaaa aaccgcgtgc acatgtcgag caatccatac atgatcatgt
 541 ttggtgtgac cgagatcttg ctctctcaga tcaaagattt tgaccagatt tgggtggctct
 601 ccattgtcgc tgctatcatg tctttcacat actctgcaat cggtttagct ctcggaatca
 661 ttcaagtgcg ggcaaatgga gttgtcaagg gaagtctcac cggaattagc atcggcgcag
 30 721 tgactcagac ccaaaaaata tggagaacct ttcaagcact tggagacatt gcctttgctt
 781 attcactc tgttgttctt attgaaattc aggacactgt aagatctcca ccagcagaat
 841 caaaaacgat gaagatcgcc acaagaatca gcacgctgt tacaacgaca tttacatgc
 901 tatgtggttg tatgggctat gcggccttcg gagataaagc accgggaaac ctcttaaccg
 961 gttttggtt ctacaatccg ttttggctcc ttgacgtggc taacgctgcc atagttatcc
 35 1021 acctgtagg agcttatcaa gtctttgctc agcccatctt cgcctttatt gagaacaac
 1081 tggccgctag gttcccgcac agtgacttgg tgaccaagga atacgaaatc cgaatccctg
 1141 gttttaggtc accgtacaaa gtcaacgttt tcagagcagt ttaccgaagc gggtttgtgg
 1201 tttgaccac tgtgatatcc atgcttatgc cgttttcaa cgacgtcgta gggatttag
 1261 gtgcgttagg gtttggcct ttgacggtt actttccggt ggagatgtat ataagacaga
 40 1321 ggaagggtga gagatggagt atgaagtggg ttgtctgca gatgttgagc tgtggttgtt
 1381 tgatgatcac gttggtcgcc ggagttggct ccatcgccgg agtaatgcta gaccttaagg
 1441 ttacaagcc gttaagact acttactaaa caaacatga tgatagatga agaagaagaa
 1501 ggtgggtggag aaaaaaaca aaagatataa attttaatga tgattttcat tggggaaatg
 1561 tgaataatgt aaaagtctt cgtttcgtat aattttatc ttgcgtaatt tatatacat

45

SEQ ID NO:791

MVKNLKVDP LAKVTASTTSMVILSSLFITDDSYVLVSAKENKNQSEAE
 PSYYETLETYQGLPCPYGGYYGYYPGLDGSVGEAKDNGYYGYGTEVQ
 YPVMQGENGSVIYLMPGFQSYDASQTYMPINPVGVSSQALHSPMYAAQ
 GYYQNQFGYADVSSPTYLWDPVGDYVYGVASYTPPLKQNISSSSHNNH
 5 NNYYSKSKNSFTGHGMGDRPKTPRKASQNSYAPPPLLNQEKGR IAYPM
 DPVKKKSGALNRDETEKAKARTKENGTSMN DLANGQDHITNGECESCS
 LDAEGNERSNGVGSVIRRDQYNLPSFQTKYEEAIFVVIKSYSEDDIHKSIK
 YNVWSSTLNGNKKLDSAYQESQKKAADKSGKCPVFLFFSVNASGQFCG
 VAEMIGRVDYEKSMEFWQQDKWTGYFPVKWHI IKDVPNPQLRHIILEN
 10 NENKPVTNSRDTQEVRLPQGNEVLNIFKNYAAKTSILDDDFDYENREKV
 MVQKKLRFPPVLKKKEEDLVADFKT MEMSNTVEEGNTELTGTVS

SEQ ID NO:792

1 cgatcacgga tctggcttgg ttcatacaaa accgccgttg ccgcggcacg ggcctacgat
 15 61 accgctgtgt tttacttacg tggctcttcg gcgagactca atttcctga agaggtcttt
 121 aaggatggaa acggcggtga aggccttagga ggagatatgt ctccgacgtt gatacgggaag
 181 aaggcggtcg aggtgggagc tagagtcgac gcagagttgc ggttagagaa taggatggt
 241 gagaacttag acatgaataa gttgccggag gcatatggat tgtaattat agtttgtag
 301 ttataggtt ggagattgcc cggagacaga gtcaaacaga ggttctctga ctcatatgag
 20 361 gcataatata gtaatatag taattttgt ttgagcata gtaattatgt cataacc

SEQ ID NO:793

1 gggcaatgat tttcgttcg ccggaaccag aagtcaaat ttggtagat agggatecca
 61 taaaaacttc ttcgaggaa tgggctaac ccggtcattt ctcaagaaca atagctaagg
 25 121 gacctgatac taccacttgg atctggaacc tacatgctga tgctcacgat ttgatagtc
 181 ataccagtga ttggaggaa atctctcgaa aagtatttag tggccatttc ggccaactct
 241 ctatcatctt tctttggctg agtggcatgt attccatgg tgctcgttt tccaattatg
 301 aagcatggct gactgacct actcacattg gacctagtc tcaggtggtt tggccaatag
 361 tgggccaaga aatctgaat ggagtagtgg gcggaggctt ccgaggaata caaataacct
 30 421 caggctttt tcagatttg gcgacatccg gaataactag tgaattacaa ctttattgta
 481 ccgcaattgg cgcattggtc ttcgcagcct taatgcttt tgctggttgg ttcattatc
 541 acaaagcagc tcaaaattg gcttgggtcc aagatgtaga atctatgtg aatcaccatt
 601 tagcagggt actaggactt gggtccttt cttgggcagg acatcaagta catgtatctt
 661 atccgattaa ccaattcta aacgctggag tagatcctaa agaaataccg ctctctcatg
 35 721 aatttatctt gaatcgggat ctttggctc aactttatcc aagtttgct gaaggagcaa
 781 ctccctttt taccttaaat tggcaaat actcggaatt tcttacttt cgtggcggt
 841 tagatccagt gactgggggt ctatggttaa ccgatatagc acatcatcat ttacgtatcg
 901 caattcttt tctaatecgc ggtcatatgt ataggaccaa ctgggggtatt ggtcatggt
 961 taaaagatat ttagaggct cataaaggct catttacagg ccaaggccat aaaggcctat
 40 1021 atgaaattct aacaacatca ttgccc

SEQ ID NO:794

MEGSSSSSSSLISKSDAELEEM LDRMLTRLALCDDSKLESLVSNLLPLTISS
 LSSQSPVVRNKAMCVDFIFQVLEILSHVNKR VKHQHEIGLPLLALWKLY
 45 TDPAAPMVRNFAIVYVEMAFERAPAKVIGECHASKISDDVSAKYRSLIT
 SQDKDLFLDFCLHMLLYQPSSQGGGSSPGLSVFQVNRIIGKQALKGDTLT
 RRKLPSNTFLTKNYHFLKINQFLKQLGILNVIGNMDLPGESVYPLYIAAS
 VDRVGM DLLVKIHSSQEPVAKRGEELLKKIASGTNLD DPKLINRLFLFN
 GTTG TENVAPEHNVAPGNISLKMKLMSGFCRSIAAANSFPATLQCIFGC
 50 MYDILFLLNLTFREKTEMAVRLFDALKLETQSLRSTIQEAIVSLAAAYKD

SPENILRDLEVLLLANSLAEQNEARFCALRWATSLYNHHCPSLYICMLS
 AADPKLDIREIALEGLFLKEEGRSIVSNHDKYPKFIEMLEYILKQQPKLL
 DSSEMRSQKLLFPSQVYLVMIKFLVKCFELEMEESENTQAVGTEFLDSAQ
 KMCSLLEHSLAFEGSAELHACASKALVSVGSYLPENVELYFSRKIVWLR
 5 SLLSHTDLSTRESVSRLLGMASCALSDAESCSLLSELISSISQPQKLRFEAQ
 HGGLCAVGFVSAHCLHRIPTVSKAVTQNAV KYLVEVVNLETAPLASVA
 MEALGHIGICGALPFLVNDSSPGTQVLEILQERLSKLLSGDDIKSVQKIAL
 SLGHICSNETSSSHLKIALDLLFSLSRSKAEELFAAGEALSFLWGGVPVT
 ADMILKTNYSLSLSTDSNFLMKEVKSLSVDVKTDEEDSRTTTTRETITGKLF
 10 DTLLYSSRKEERCAGTVWMLSLTMYCGQQPSIQLMLPKIQEAFSHLLGD
 QNELTQELASQGMSTIYELGDASMKKSLVDALVNTLTGTSKRKRAIKLV
 EESEVFQEGTIGESPSGGKISTYKELCNLANEMGQPDLIYKFMDLANHQA
 SLNSKRGAAFGFSKIAKQAGDALRPHLRLLIPRLIRYQYDPDKNVQDAM
 AHIWKALIQDPKKA VDEHLNHIFDDL VQCGSRLWRSREASCLALADIQ
 15 GRKFDQVKEHLKKLWIAAFRAMDDIKETVRNAGDKLCRAVTSLTRICD
 VTLTELADAKQAMDIVLPFLSEGIMSKVNSVRKASIGVVMKLAKFYSK
 HEINQFELLASFGELNVLLGNIDPLSDFVLFVTVCRLLHAANIGIETEKLE
 NLRISISKGSPMWETLDCINIVDIESLEQLIPRLTQLVRGGVGLNTRVGV
 ASFISLLVQKVGSEIKPFTGMLLRLLFPVAKEEKSSAAKRAFSSACGIVLK
 20 YSSPSQAQSLIEETAALHSGDRSSQIACASLFKSFSSTAADIMSSHQSAIVP
 AIFISRFEDKQISSLFEEVWEDITSGERVTLQLFLQEI VNHICESITSSSRFK
 LSFSLGKDALLDALGALSVACHEAITKEDPTTPTTILSLICSACKKKLKKY
 RESAFSCLEKVIAFGDPKFFHAVFPMLYEMCNTASIKTNTQVQAASDAV
 KTESENGEDGHVPLEKIMECVKSCIQVATIDDILSAKADLIHVLIISLSPGF
 25 LWTVKMSGISCVGKLC SRFPSLWTD SMDDLSPSDATK FVHEL FHS LVPK
 LLECIHTVKIAQFHVAASQCLLELIELYSTISSLHPVEVDFKA EVVSLLELE
 KSEEAKSLLRKSRDALANLPSLN

SEQ ID NO:795

30 MDKETEILSRLAANHLHLAQFEPLKATLLALRVNPDAL TILQTIVSNA
 GRFDNVLWSRSCPSPLLSFLSTIELLRFENPTSPWGF DSETLSLRADFL
 MVQVLIDRVTERIKEDEESEDENSGLGNCRLRVLQGVLELGVERLKFVVD
 TSSSEGSNKIEEDAVVSLRSIVLDYSDVFDALCCNIQRQLAGCESYGTCL
 VEEVQGEEQRKEMNEATCIGSPELDNINVFALIQRN VQLAQLDAMKTKL
 35 DEGDERGAADRIRYLHLDYGVKENYHAVLKALLSRVMEKKDEYGDS
 WHMVRQNLLFMYKEALSSNCGDLVQMIQGIQDDMLLP HSQ LHLSLDNE
 QIPLPLECFRRYLVDLKTERNIEDKSSPMSRAINSCLRDMYHYARISGSHV
 LECVMCAALSSVKKEKLQEANDVLTLPRLRPLVASM GWDLLPGKTAT
 RRKLMRLLWTSDSQALRLEESSLYGNQTDELELASFAACVNSGKSWTP
 40 KASFLMHGNVSSAHDDAEVDPFVENLVLERLSAQSP LRVLFDVVP GIKF
 QDAISLISMQPIASTAEAWKRIEDIELMHMRYALEAIVLALGAMEEAMK
 DETDASHRVVFYHLKDLTNHLEAIKNVPRKIMMVNIVISLLHIDDIRLSST
 QSASSACFSEKSNTPGLDPGDLGTEGEKEIVISFTKQLLDVLRNLPSHPIE
 QECQLDGNYSTDGRQALEWRVSMARFIEDCEWRLSVMQHLLPLSERQ
 45 WGLKEVLSILRAAPEKLLNLCMQRAKYDIGEEAVNRFALSAEDKATLEL
 AEWVDNAFKGTLVEDVMSRTAEGAAAVQDLDFHSLGSQLSPLAMVLLF
 AQSQVMLSEIYPGGAPKVGFTYWDQVHEVAIISVLRRLKRLQEFLEQDD
 PQILQASFSGDTIISCTESHRRQGQKDRALAMLHQMIEDAHRGKRQFLSG
 KLHNLARALADEKPEVDVLKGDGSDMAVEKDGV LGLGLKYTKQSPGS
 50 ANRAVDGNPVSHETEDKGKKSFGPLSNKTSTYLSQFILYTAAIGDIVDGT

DTTHDFNFFSLVYEWPKDLLTRLVFDRSSTDAAAKVAEVMSADDFVHEVI
 SACVPPVYPPRSGHWACIPVIPTTPCSHSEGKVLSPSIEAKPNCYVRSSA
 TPGVPLYPLQLDVIRHLVKISPVRVLACVFGGSILYNGSDSISSSLNDEF
 PSSPDADRLFYEFSLDQSERYP TLNRWIQMOTNLHRVSEFVVTPKQKPD
 5 DTRIKPDERTGIKRLLEHDSDESDETEETFSKNNIQPALTDGSARDGGSFE
 NGVCRTDPTVFLSFDWENEVPYEKAVNRLIDEGKLMDALALSDFRLRN
 GASDWLLQLLIKSREENPSTSGRSQGYGGQSNWSWQYCLRLKDKQLAAT
 LALKCCIGDKLCRSTATYFRQMIAIAGKRLSFFLLFEIMFGSWYARCVTL
 KNLNGKQVEAECKEDPEGLALRLAGKGAVSAALEVAESAGLSIDLREL
 10 QGRQLVKLLTTDPLNGGGPAEASRFLSSLQDSADALPVVMGAMQLLPD
 LRSKQLLILKEFPALRDNNVIMAYAAKAISVTIIPPPREPRITVSASRLRQK
 SRAGPAVKASFTSSLSNFQREARRAFSWAPRNAENRTTSKDVYRKRKNS
 GLGASERAAWEAMTGIQEDQGSSYSADGQDRLPSVSIAEEWMLTGDKT
 KDEGVRASHKYESTPDILFKALLSLCSDELVSARSAMDLCISQMKNVLS
 15 SKQLSEGASVETIGRAYHATEAFVQGLSYAKSLLRKLLGTTESTNNNGE
 RSRDVDDISSDAGSSSVGSQSTDEPSDVLSLTEIWLGRAELLQSLLGSGIS
 TSLDDIADQLSSECLRDRLISDERYSMAVYMCKKCKIDVFPVWKA WGL
 ALLRMERYAQARVKFKQAFQLKGEDIPDVIQEIINTIEGGPPVDVSVIRS
 MYDHLAKSAPTILDDSLSADSYLNVLHMPSTFPRSERSRRSLESEKNSSV
 20 PGSDFEDGPRSNLDTTRYSECTNYLQEHARQNLLGFMFRHGHFKDACM
 LFFPQSGLPPLQTSSVGAVSTSSSPQRTDPLATEYGTIESLCEFCVGYGAI
 SSLEEVITERLES AKNQDQAINQYIAGALTRICAFFEINRHFNYLYKFLVL
 KKDYVTSGYCCIQLFMNSTTQEDAVRHLEHAKKYWSLTILGVQAHFEE
 ALTARHRGSDSKKLVTKGVRGKSAAEKLSEETLVKLSSRVKMQIDVVK
 25 SFSDSEGAPWKHSLFGNPNDSETSRRRCEIVETLVEKNFDLAYSVIYEFK
 LSAVDIYAGVATSLADRKKGSQLTELFKNIKGTIQDDDWDQVLNIADTG
 KARSVWLIFCEMLQVLGAAINIYANKHKERPDRIDLMLTSSHRKVLACV
 VCGRLKSAFQIASKSGSVADVQYVAHQALHANSHTVLD MCKQWLAKY
 M
 30

References

- Aarts et al., Proc Natl Acad Sci 95:10306 (1998).
 Allison et al., (1986).
 Altschul et al., J. Mol. Biol. 215:403 (1990).
 35 Altschul et al., Nucleic Acids Res. 25:3389 (1997).
 An et al., EMBO J. 4:277 (1985).
 Aoyama T. et al., N-H Plant Journal, 11:605 (1997).
 Bailey and Elkan In: Proceedings of the second international Conference on
 Intelligent Systems for Molecular Biology (Altman, R., ed), pp 28-36, AAAI
 40 press (1994).
 Ballas et al., Nucleic Acids Res. 17:7891 (1989).
 Bansal et al., Proc. Natl. Acad. Sci. USA, 89:3654 (1992).
 Batzer et al., Nucleic Acid Res., 19:5081 (1991).

- Beals et al., Plant Cell, 9:1527 (1997).
- Belanger et al., Genetics, 129:863 (1991).
- Bevan et al., Nature, 304:184 (1983).
- Blochinger & Diggelmann, Mol Cell Biol, 4:2929.
- 5 Bourouis et al., EMBO J., 2:1099 (1983).
- Boyes et al., Proc Natl Acad Sci USA, 95:15849 (1998).
- Byrne et al. Plant Cell Tissue and Organ Culture, 8:3 (1987).
- Campbell and Gowri, Plant Physiol., 92:1 (1990).
- Cao et al., Plant Cell, 6:1583 (1994).
- 10 Cao et al., Cell, 88:57 (1997).
- Century et al., Science, 278:1963 (1997).
- Chandler et al., Plant Cell, 1:1175 (1989).
- Christou et al., Biotechnology, 9:957 (1991).
- Christou et al., Plant Physiol., 87:671 (1988).
- 15 Cordero et al., Plant J., 6:141 (1994).
- Corpet et al., Nucleic Acids Res. 16:10881 (1988).
- Crameri et al., Nature Biotech., 15:436 (1997).
- Crameri et al., Nature, 391:288 (1998).
- Creelman et al., Annu Rev Plant Physiol Plant Mol Biol 48:355 (1997).
- 20 Crossway et al., BioTechniques, 4:320 (1986).
- Czako et al., Mol. Gen. Genet. 23 5 (1), 33-40 (1992).
- Datta et al., Bio/Technology, 8, 736 (1990).
- Dayhoff et al., Atlas of Protein Sequence and Structure, Natl. Biomed. Res. Found., Washington, C.D. (1978).
- 25 De Blaere et al., Meth. Enzymol. 143:277 (1987).
- de Framond, FEBS, 290:103 (1991).
- Delaney et al., Proc. Natl. Acad. Sci. USA 92:6602 (1995).
- Della-Cioppa et al., Plant Physiology, 84:965 (1987).
- Dennis et al., Nucleic Acids Res., 12:3983 (1984).
- 30 Dong et al., Curr Opin Plant Biol 1:316 (1998).
- Dzelkalns et al., Plant Cell, 5:855 (1993).
- Eisen et al., Proc. Natl. Acad. Sci. USA, 95:14863 (1996)
- Eisen et al., Trends in Plant Sci. 95:14863 (2000).
- Ellis and Jones, Curr Opin Plant Bio 1:288 (1998).

- Elroy-Stein et al., PNAS USA, 86:6126 (1989).
- English, et al., Plant Cell 8:179 (1996).
- Eulgem et al., Trends in Plant Sci. 5:199 (2000).
- Falk et al., Proc Natl Acad Sci USA 96:3292 (1999).
- 5 Feys et al., Plant Cell 6:751 (1994).
- Franken et al., EMBO J., 10:2605 (1991).
- Fromm et al., Bio/Technology 8:833 (1990).
- Gallie et al., Molecular Biology of RNA, 237 (1989).
- Gallie et al., Nucl. Acids Res., 15:8693 (1987).
- 10 Gan et al., Science (1995), 270 (5244), 1986-8).
- Gatz Current Opinion in Biotechnology, 7:168 (1996).
- Gatz, C., Annu. Rev. Plant Physiol. Plant Mol. Biol., 48:89 (1997).
- Gelfand, eds., PCR Strategies (Academic Press, New York (1995)).
- Glazebrook et al., Genetics 143:973 (1996).
- 15 Glazebrook et al., Proc. Natl. Acad. Sci. USA 91:8955 (1994).
- Gordon-Kamm et al., Plant Cell, 2, 603 (1990).
- Graham et al., Biochem. Biophys. Res. Comm., 101:1164 (1981).
- Graham et al., J. Biol. Chem., 260:6555 (1985).
- Graham et al., J. Biol. Chem., 260:6561 (1985).
- 20 Guerineau et al., Mol. Gen. Genet. 262:141 (1991).
- Hammond-Kosack and Jones, Ann. Rev. Plant Physiol. Plant Mol. Biol., 48:575 (1997).
- Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA, 89:10915 (1989).
- Hiei et al., Plant J. 6:271 (1994).
- 25 Higgins et al., Gene 73:237 (1988).
- Higgins et al., CABIOS 5:151 (1989).
- Hinchee et al., Biotechnology, 6:915 (1988).
- Hoekema, In: The Binary Plant Vector System. Offset-drukkerij Kanters B.V.
- 30 Huang et al., CABIOS 8:155 (1992).
- Hudspeth & Grula, Plant Molec. Biol., 12:579 (1989).
- Huffman et al., J. Cell. Biochem., 17B: Abstract.
- Hunt et al., Mol. Plant-Microbe Int. 9:261 (1997).
- Ingelbrecht et al., Plant Cell, 1:671 (1989).

- Innis et al., eds., PCR Protocols: A Guide to Methods and Applications
(Academic Press, New York (1995).
- Innis and Gelfand, eds., PCR Methods Manual (Academic Press, New York)
(1999).
- 5 Jobling et al., Nature, 325:622 (1987).
John et al., Proc. Natl. Acad. Sci. USA 89(13):5769 (1992).
Jones et al., Adv Bot Res 24:89 (1997).
Joshi et al., Nucleic Acid Res. 15:9627 (1987).
Joshi, NAR, 15:6643 (1987).
- 10 Karlin and Altschul, Proc. Natl. Acad. Sci. USA 87:2264 (1990).
Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90:5873 (1993).
Keller et al., Genes Dev., 3:1639 (1989).
Kirsh et al., Plant J. 26:217 (2001).
Klein et al., Bio/Technology, 6:559 (1988).
- 15 Klein et al., Nature (London) 327:70 (1987).
Klein et al., Plant Physiol., 91:440 (1988).
Klein et al., Proc. Natl. Acad. Sci. USA, 85:4305 (1988).
Kohler et al., Plant Mol. Biol., 29:1293 (1995).
Knauf, et al., Genetic Analysis of Host Range Expression by *Agrobacterium*
- 20 In: Molecular Genetics of the Bacteria-Plant Interaction, Puhler, A. ed.,
Springer-Verlag, New York, 245 (1983).
Koziel et al., Biotechnology, 11:194 (1993).
Kridl et al., Seed Science Research, 1:209 (1991).
Kriz et al., Mol. Gen. Genet., 207:90 (1987).
- 25 Kunkel, Proc. Natl. Acad. Sci. USA, 82:488 (1985).
Kunkel et al., Methods in Enzymol., 154:367 (1987).
Langridge et al., Cell, 34:1015 (1983).
Lindstrom et al., Dev. Genet., 11:160 (1990).
Lommel et al., Virology, 81:382 (1991).
- 30 Lorz et al. Mol. Gen. Genet. 199:178 (1985).
Macejak et al., Nature, 353:90 (1991).
Maleck et al., Nature Genetics, 26:403 (2000).
Mansson et al., Gen. Genet., 200:356 (1985).
Martin and Paz-Ares, Trends in Genetics 13:67 (1997).

- Martinez et al., J. Mol. Biol., 208:551 (1989).
- McBride et al., Proc. Natl. Acad. Sci. USA, 91:7301 (1994).
- McCabe et al., Bio/Technology, 6:923 (1988).
- McDowell et al., Plant J. 22:523 (2000).
- 5 McDowell et al., Plant Cell 10:1861 (1998).
- McNellis et al., Plant J. 1998, 14:247-257.
- Meinkoth and Wahl, Anal. Biochem., 138:267 (1984).
- Messing & Vierra, Gene, 19:259 (1982).
- Mogen et al., Plant Cell 2:1261 (1990).
- 10 Moore et al., J. Mol. Biol., 272:336 (1997).
- Munroe et al., Gene 91:151 (1990).
- Murray et al., Nucleic Acids Res., 17:477 (1989).
- Myers and Miller, CABIOS 4:11 (1988).
- Needleman and Wunsch, J. Mol. Biol. 48:443 (1970).
- 15 Odell et al., Nature, 313:810 (1985).
- Odell et al., Nature, 313:810 (1985).
- Ohtsuka et al., J. Biol. Chem., 260:2605 (1985).
- Okamuro et al., Biochemistry of Plants, 15:1 (1989).
- Paszkowski et al., EMBO J., 3:2717 (1984).
- 20 Pacciotti et al. Bio/Technology 3:241 (1985).
- Park et al., J. Plant Biol. 38(4):365 (1985).
- Pearson et al., Meth. Mol. Biol. 24:307 (1994).
- Pearson and Lipman, Proc. Natl. Acad. Sci. 85:2444 (1988).
- Penninck et al., Plant Cell 8:2309 (1996).
- 25 Perlak et al., Proc. Natl. Acad. Sci. USA, 88:3324 (1991).
- Pieterse et al., Plant Cell, 10:1571 (1996).
- Pieterse et al., Plant Cell, 8:1225 (1998).
- Potrykus Mol. Gen. Genet. 199:183 (1985).
- Proudfoot, Cell 64:671 (1991).
- 30 Quigley et al., J. Mol. Evol., 29:412 (1989).
- Ralston et al., Genetics, 119:185 (1988).
- Reina et al., Nucleic Acids Res., 18:6425 (1990).
- Reina et al., Nucleic Acids Res., 18:7449 (1990).
- Riggs et al., Proc. Natl. Acad. Sci. USA, 83:5602 (1986).

- Rochester et al., (1986).
- Ronald, Curr Opin Plant Biol 1:294 (1998).
- Rossolini et al., Mol. Cell. Probes, 8:91 (1994).
- Roth et al., Nature Biotechnology, 16:939 (1998).
- 5 Ruiz et al., Plant Cell 10:937 (1998).
- Ryals et al., Plant Cell 8:1809 (1996).
- Ryals et al., Plant Cell 9:425 (1997)
- Sambrook et al., Molecular Cloning: A Laboratory Manual (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York) (1989).
- 10 Sanfacon et al., Genes Dev. 5:141 (1991).
- Sanford et al., Particulate Science and Technology, 5:27 (1987).
- Schernthaner et al., EMBO J., 7:1249 (1988).
- Schindler et al., Plant Cell 4:1309 (1992).
- Schwob et al., Plant J., 4:423 (1993).
- 15 Shah et al., Mol. Plant-Microbe Interact. 10:69 (1997).
- Shimamoto et al., Nature, 338:274 (1989).
- Shirasu et al., Plant Cell 9:261 (1997).
- Shulaev et al., Plant Cell 7:1691 (1995).
- Simpson, Plant Mol. Biol., 19:699 (1985).
- 20 Skuzeski et al., Plant Molec. Biol., 15:65 (1990).
- Slater et al., Plant Mol. Biol., 5:137 (1985).
- Smith et al., Adv. Appl. Math. 2:482 (1981).
- Smith et al., Planta 168:94 (1986).
- Spencer et al., Theor Appl Genet, 79:625 (1990).
- 25 Staswick et al., Proc. Natl. Acad. Sci. USA 89:6837 (1992).
- Staub et al., EMBO J., 12:601 (1993).
- Staub et al., Plant Cell, 4:39 (1992).
- Stemmer, Nature, 370:389 (1994).
- Stemmer, Proc. Natl. Acad. Sci. USA, 91:10747 (1994).
- 30 Sukhapinda et al. Plant Mol. Biol. 8:209 (1987).
- Sullivan et al., Mol. Gen. Genet., 215:431 (1989).
- Svab et al., Proc. Natl. Acad. Sci. USA, 87:8526 (1990).
- Svab et al., Proc. Natl. Acad. Sci. USA, 90:913 (1993).

Tijssen, Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes, part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays" Elsevier, New York (1993).

- 5 Turner et al., Molecular Biotechnology, 3:225 (1995).
VanTunen et al., EMBO J., 7:1257 (1988).
Vasil et al., Biotechnology, 11:1553 (1993).
Vernooij et al., Plant Cell 6:959 (1994).
Vodkin, Prog. Clin. Biol. Res., 138:87 (1983).
- 10 Vogel et al., EMBO J., 11:157 (1992).
Walker and Gastra, eds., Techniques in Molecular Biology, MacMillan Publishing Company, New York (1983).
Wandelt et al., Nucleic Acids Res., 17:2354 (1989).
Waterman, M.S. Introduction to Computational Biology: Maps, sequences
15 and genomes. Chapman & Hall. London (1995).
Weeks et al., Plant Physiol., 102:1077 (1993).
Weissinger et al., Annual Rev. Genet., 22:421 (1988).
Wenzler et al., Plant Mol. Biol., 13:347 (1989).
Weymann et al., Plant Cell 7:2013 (1995).
- 20 White et al., Nucl Acids Res, 18:1062 (1990).
Willitset al., Mol Plant-Microbe Interact 11:795 (1998).
Xie et al., Science 280:1091 (1998).
Yamamoto et al., Nucleic Acids Res., 18:7449 (1990).
Yang & Klessig, PNAS 93:14972 (2000).
- 25 Yu et al., Proc Natl Acad Sci USA 95:7819 (1998).
Zhang et al., Proc. Natl. Acad. Sci. USA, 94:4504 (1997).
Zhou et al., Plant Cell 10:1021 (1998).
Zhou et al., Plant Cell 8:2235 (1996).

- 30 All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the

details described herein may be varied considerably without departing from the basic principles of the invention.

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 or the complement of the open reading frame, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
2. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which is substantially similar to an *Arabidopsis* nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
3. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
4. The isolated polynucleotide of claim 1, 2, or 3 which is DNA.
5. The isolated polynucleotide of claim 1, 2, or 3 which is RNA.
6. The isolated polynucleotide of claim 1 wherein the nucleotide sequence encodes a polypeptide having at least 90% amino acid sequence identity to the *Arabidopsis* polypeptide encoded by the open reading frame.
7. The isolated polynucleotide of claim 1 wherein the nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.

8. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a dicot.
9. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a monocot.
10. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a cereal plant.
11. An isolated polypeptide encoded by the polynucleotide of claim 1, 2, or 3.
12. An expression cassette comprising the polynucleotide of claim 1, 2, or 3 operably linked to suitable regulatory sequences.
13. The expression cassette of claim 12 wherein the polynucleotide is linked to a promoter for expression in a plant.
14. A recombinant vector comprising the polynucleotide of claim 1, 2, or 3.
15. A host cell comprising the expression cassette of claim 12.
16. A host cell comprising the polynucleotide of claim 1, 2, or 3.
17. The host cell of claim 15 or 16 which is selected from the group consisting of yeast, bacteria and plant.
18. A transformed plant, the genome of which is augmented with the polynucleotide of claim 1, 2, or 3 or a polynucleotide which comprises one of SEQ ID NOs: 1-684 and 789-795 which is expressed in an amount which confers resistance or tolerance to the plant to pathogen infection.

19. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene corresponding to the polynucleotide of claim 1, 2, or 3 or a gene corresponding to one of SEQ ID NOs: 1-684 and 789-795.
20. The plant of claim 19 which is altered by T-DNA insertion, transposon insertion, or targeted DNA insertion.
21. The plant of claim 19 in which expression is inhibited by transcription or post-transcriptional mechanisms.
22. The plant of claim 18 or 19 which is a monocot.
23. The plant of claim 18 or 19 which is a dicot.
24. The plant of claim 18 or 19 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
25. A method of expressing a polynucleotide in a cell, comprising:
introducing the polynucleotide of claim 1, 2, or 3 into a cell so as to express the open reading frame.
26. The method of claim 25 wherein the cell is a plant cell.
27. The method of claim 25 wherein the cell is a monocot cell.
28. The method of claim 25 wherein the cell is a dicot cell.
29. A composition comprising the polynucleotide of claim 1, 2, or 3 or comprising the polypeptide of claim 11.

30. A method to identify an open reading frame in the genome of a plant cell, the expression of which is altered by oomycete infection of the cell, comprising:
- a) contacting a plurality of isolated nucleic acid samples on a solid substrate with a probe comprising plant nucleic acid corresponding to RNA isolated from plant cells infected with an oomycete, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
 - b) comparing complex formation in a) to complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising plant nucleic acid corresponding to RNA from uninfected plant cells or from mutant plant cells which have a response to pathogen infection that is different than the plant cells in a), so as to identify which samples corresponding to genes having an open reading frame, the expression of which is altered in response to oomycete infection, wherein the genes comprise orthologs of *Arabidopsis* genes comprising one of SEQ ID NOs: 1-684 and 789-795.
31. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is induced in response to infection.
32. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is decreased in response to infection.
33. The method of claim 30 wherein the probe comprises nucleic acid from a dicot.
34. The method of claim 30 wherein the probe comprises nucleic acid from a monocot.

35. An isolated polynucleotide comprising an open reading frame of a gene identified by the method of claim 30.
36. A method to confer resistance or tolerance to a plant to a pathogen, comprising:
 - a) contacting plant cells with an expression cassette comprising a polynucleotide encoding a polypeptide that is substantially similar to a polypeptide encoded by a nucleic acid sequence comprising an open reading frame comprising one of SEQ ID NOs: 1-684 and 789-795 so as to yield transformed plant cells; and
 - b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the polynucleotide in the cells of the plant in an amount effective to confer resistance or tolerance to the plant to the pathogen relative to a corresponding plant which does not comprise the expression cassette.
37. The method of claim 36 wherein the polynucleotide hybridizes under moderate hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
38. The method of claim 36 wherein the polynucleotide hybridizes under stringent hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
39. A transformed plant prepared by the method of claim 36.
40. A seed of the plant of claim 39.
41. A progeny plant of the plant of claim 39.
42. A method for identifying a plant cell infected with a pathogen, comprising:

- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence substantially similar to one or more of SEQ ID NOs:1-184, 301-494 or 500-803, or a portion thereof so as to yield an amplified product; and
 - b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the product is indicative of pathogen infection.
43. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence is from a gene encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising at least one of SEQ ID NOs: 685-788.
44. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, which nucleotide sequence hybridizes under high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788 or which nucleotide sequence hybridizes under very high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788.
45. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, wherein the plant nucleotide sequence comprises SEQ ID NO: 710, SEQ ID NO: 711, SEQ ID NO: 714, SEQ ID NO: 715, SEQ ID NO: 764 or SEQ ID NO: 773.
46. The isolated polynucleotide of claim 43, 44, 45 or 46 wherein the nucleotide sequence which directs transcription is 25 to 2000 nucleotides in length.

47. A recombinant vector comprising the polynucleotide of claim 43, 44, 45 or 46.
48. The vector of claim 47 which is a plasmid.
49. An expression cassette comprising the polynucleotide of claim 43, 44, 45 or 46 operatively linked to an open reading frame.
50. The expression cassette of claim 49 operably linked to other suitable regulatory sequences.
51. A host cell comprising the expression cassette of claim 49.
52. A transformed plant, the genome of which is augmented with the expression cassette of claim 49.
53. A plant cell containing the expression cassette of claim 49.
54. A transformed plant comprising transformed plant cells, the transformed plant cells containing the expression cassette of claim 49.
55. The transformed plant of claim 54 wherein the plant is a dicot.
56. The cell of claim 53 which is a dicot cell.
57. The transformed plant of claim 54 wherein the plant is a monocot.
58. The cell of claim 53 which is a monocot cell.
59. The transformed plant of claim 54 which is a cereal plant.
60. A method of augmenting a plant genome, comprising:
 - a) contacting plant cells with the expression cassette of claim 49 so as to yield transformed plant cells; and

- b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.

61. A transformed plant prepared by the method of claim 60.
62. A seed of the plant of claim 61.
63. A progeny plant of the plant of claim 61.
64. A method of using a plant promoter, comprising: introducing the expression cassette of claim 49 to a plant cell and detecting the expression of the product of the open reading frame.
65. A recombinant vector comprising the expression cassette of claim 49.
66. A plant cell comprising the vector of claim 65.
67. A transformed plant, the cells of which comprise the vector of claim 65.
68. The plant of claim 52, 54, 61 or 67 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
69. The expression cassette of claim 49 wherein the open reading frame is in an antisense orientation.
70. The expression cassette of claim 49 wherein the open reading frame is in a sense orientation.
71. A transformed plant, the genome of which is augmented with a polynucleotide which is substantially similar to any one of SEQ ID NOs:

1-684 and 789-795 and which is expressed in an amount which inhibits or prevents pathogen infection.

72. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene comprising a polynucleotide substantially similar to any one of SEQ ID NOs: 1-684 and 789-795.
73. The plant of claim 71 or 72 wherein the polynucleotide is substantially similar to SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 32, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 792, SEQ ID NO: 57, SEQ ID NO: 68, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 102, SEQ ID NO: 111, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 682, SEQ ID NO: 129, SEQ ID NO: 137, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 157, SEQ ID NO: 161, SEQ ID NO: 165, SEQ ID NO: 170, SEQ ID NO: 174, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 184, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 197, SEQ ID NO: 208 or SEQ ID NO: 211.
74. The method of claim 36 wherein the polynucleotide is substantially similar to SEQ ID NO: 308, SEQ ID NO: 300, SEQ ID NO: 272, SEQ ID NO: 362, SEQ ID NO: 265, SEQ ID NO: 241, SEQ ID NO: 261, SEQ ID NO: 380, SEQ ID NO: 228, SEQ ID NO: 658, SEQ ID NO: 243, SEQ ID NO: 254, SEQ ID NO: 216, SEQ ID NO: 225, or one of SEQ ID NOs: 400-684.
75. The expression cassette of claim 12 wherein the polynucleotide is in antisense orientation.
76. The expression cassette of claim 12 wherein the polynucleotide is in sense orientation.

77. A method for identifying a plant cell infected with a pathogen, comprising:
- a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by an open reading comprising sequences selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 so as to form a complex; and
 - b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.
78. A method for identifying a plant cell infected with a pathogen, comprising:
- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with a probe comprising at least a portion of a polynucleotide that is substantially similar to any one of SEQ ID NOs: 1-684 and 789-795 under conditions effective to form a specific complex between the probe and the nucleic acid; and
 - b) detecting and determining the presence or amount of complex formation wherein the presence or amount of complex formation is indicative of pathogen infection.
79. A computer-readable medium having stored thereon a data structure comprising:
- a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a nucleotide molecule selected from the group consisting of SEQ ID NOs: 1-791 or the complement thereof; and
 - b) a module receiving the nucleic acid molecule which compares the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

80. The computer readable medium of claim 79 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
81. A computer-readable medium having stored thereon computer executable instructions for performing a method comprising:
- a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-791 or the complement thereof; and
 - b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.
82. The computer readable medium of claim 81 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
83. The method of claim 42, 60, 77 or 78 wherein the cells are dicot cells.
84. The method of claim 42, 60, 77 or 78 wherein the cells are monocot cells.
85. The method of claim 42, 60, 77 or 78 wherein the cells are maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat cells.

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RPP-DEPENDENT DEFENSE PATHWAYS

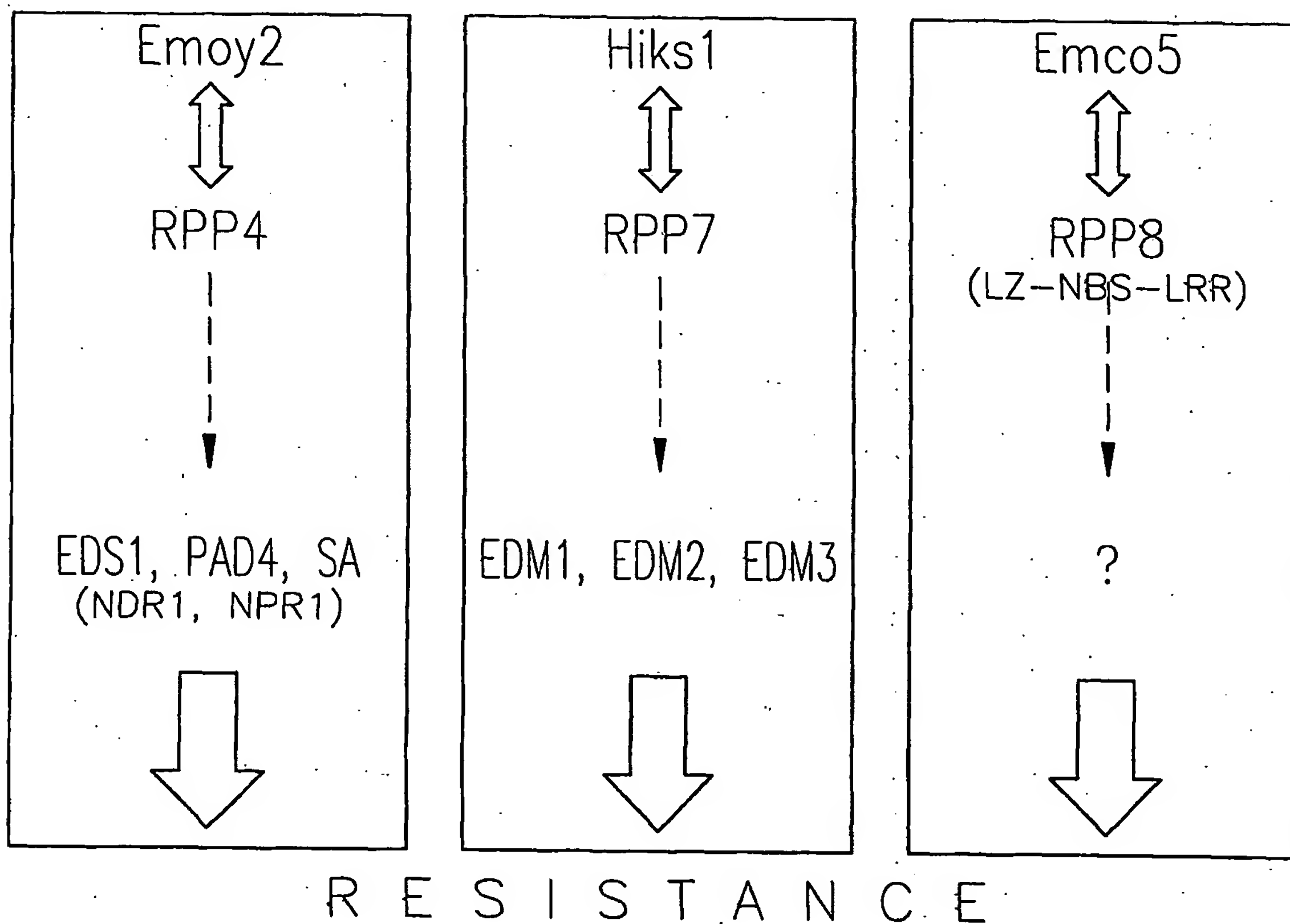


FIG. 1

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motifs:

Motif 1/ MAP Score: 6.87857

CAACAATGAC

TT TT

Motif 2 MAP Score: 2.22382

GATGGGNCNAA

TT A

C

Known stress-responsive cis-elements:

ttgacc, ttgact, ggtcaa and agtcaa W box

ttgaca and tgtcaa W box-like

tgacg and cgtca TGA-bZIP binding site

acgt bZIP binding site core

cacgtg G Box

gccgcc and ggccgc GCC box

| Subcluster A
17014 ribonuclease RNS1SEQ ID NO:
774

tagaattgaaaaagggtaatgtgaaaaggggtattctcaacaattattcaagataaaaaat
 tgtataggtgttaaataataatgtgtaaaagagaagacgatgtgaagtattaaaagaaa
 aaaaaaatggatgttgtatatataagtaaccattgtagatagtttaagcaagaaaaattga
 tgttgcattggaaattaaaaaatttcaataaaattagaaaagcaactctaaatcattac
 ttattttattattttcaagaagttataaagtattaaacaattcgTTGACAaataagttt
 gatcgacattgtgtgacaaattttaaacacatcattaataacaacgaggacaaatacag
 ttcagatatcgtctactattaaaacacttcttctataggagcaaagaaaaattgtcggc
 aacgaactggggaccaataatattccgagtttgagttcaaactgagtaattttattttg
 agaaaatttgccaagttaacttataattctggtttACGTgtagtaattttattaagttgt
 tataggaaaatgagaaaataactaagacacatccaagaaagtttcacacgaaatttactt
 aaaaaagattgtttatttaataacttccgtatatagatatataaatatttaacacatta
 attataaagttcaagataattgattatctatctttttttgtcatctgaaattattatcg
 ctcaaacgaagtaattctgaggaaagttgtttacaaactagttattttcattattgtcta
 cttatataatagaattaaaaaaaattattgcttaatgcaatttagtttttagataaaatc

FIG. 2A

SUBSTITUTE SHEET (RULE 26)

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attaaacttaatagattatataagttagatatcaataattgggcttgcttaaaaacata
aatataaaatattattgggccgttACGTgcatacaaaaacgaaccttctaacaacaagt
gtgaACGTtacgacttcaaaaattaaaaaaacacaacaactatgtccacACGTaatct
catatgattcagattccaaggagaacaaaattaaaaacaaatctcgtaaacatacatat
acttcacataaaaacaaaagggtacagtatataaccataaatctccgagattcttttgatgt
atctgtccatttcattattacacaaactaggaaactgatatctctctattcacattcct
ctgattctatttctctttatatatatattcaccatttaaccatctcaatcttataaccctc
aaaatcacaaatcttctcttacaaaaaactttgaaagatg

14609 putative cytochrome P450

SEQ ID NO:
775

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acatatatgtatgatagtatgtatgtatgtatatattatgagtacatatacattagaaa
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gaaagcGTTGGGtgcttttaagttttttctttcgcctaaatattttaaggtcttttgtc
aggaatagaaatatgataaagtctattgagtttgtaagacctatgtatattgggtccgg
atgcaatgcttttttactcatgcgcattcaatagaagaatttgttatcagtgaacgagt
acaatTGTCAAtatatttaacaaattatttaaaaccttttaaatatgtgcatagttttt
ttcgtactcggatagaaattaataaatacaaaaattactgatttgataaaaatgaatttc
gctttgtaataaattatatataattcaaaatcctcatcgtcgaaaacaatttttaaaat
aaaacaaccaagataattttccacaaattaaattaatttttagttttgaattcagatata
taacaaacaatgatataaagaatatttcattaaataaaaagatattcttaactgaat
ttatttattaatttggaatatacttattaccgaaataaaggattgtttatttcttacaac
tcgtcttattagtggtgcatagcataacaagggtgaaagagaaaacatg

16649 putative S-adenosyl-L-methionine:trans-caffeoyl-
Coenzyme A 3-O-methyltransferase (function:disease resistance) (promoter up to next ORF) SEQ ID NO:
776

catgtctcttgagtctcgtgggtgtgtgcaaattgttcgttggtataaacgagagatgt
atgtcaatatatatattggccttctgggtcaaactaattgagctactaataagacccaaat
taaggactaacacaccaattgatcttatccatgacttttcaaccatgggactagaaaat
caattatctagacagtacttgatgcgaatatattaacgtttatgtttcttaaggatttt

FIG. 2B

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ttttctctcttaagggttgcatacaaatgttgaaatatgcaagcaggcgaacagtttgca
atgtagtttttattgactaatataaatttggtatgtgagattttaaataatgcaaaaaaagta
tatagtatagaattatttaaagaatatatcaaattgaagggtactaaaaaaacggatttg
aattcgaatgctaacaataacgaataaccagcataaatctccaaagatgattcaaattttg
cagtttcaatccctcaatccgcttcaacggatgaaacaataataattcaacatgttc
taacaatttttcaagtatgcatgaagaaatcacttaaaaaattccaagatatgtattta
aagtttagtgaatcatcaaagcgcaaaaattcacaactaagtaagaagggtgtcgataa
aaagcaaaaaacaaaagttacagaatgtcttgaggagaggattcctcaaacctcctaaga
aaagatcttttgggtttttgtaatctgtcattgtaagttaagcaaagtttggtgaataa
gtgttccagagatatgataagttgaccttttggattgtctaactctggaatcttttagtt
tatggtgaactctcaccccaagctcaatgtgatgtccatgtaactaatcttaggcaaca
tgatgtggcataggagattgggcatcctcatcatcaagatccctaaatgacgaaatgat
tttaaataataattcctaagatttcacatccttaaaccttattaagtcctaaccattc
gaaaatacacacattcatttgatttaatttaaatttttatattaacttctctattttc
attaaaaattgtaaaataattttttttattgtcgtaaaatgttttacttttctatttccat
taaagttgtaaatatgttttattaacgtcgtaaaatgttatttttttaataaaaaatat
ctgttggggccaaaga

17653 (similarity to DNA damage inducible)
(promoter up to next ORF)

SEQ ID NO:
777

acaataatttccataattcaaatagttttcagaaaggatttctcaatacagggttaaaaat
atcaatctaattctttgcaaactcattaaactaatttagttactttccttaactttaaga
aaacaaatctcaaattttgtggctataaccaccattttcattgaaactaactactcaatt
aacggtctgaaagaggacaaaaagattttcacaagtgtacaccaataaaaagaaaatcgt
ttttttcccttataaaaatgacaaaaattaccaagaaattaaatggaacataacttacga
cgaaatttacctgacgattttttttccttactgaaaattaccaagaaatcgcggtggaag
tcggaaatgttacataactttttctttgttaactacactgcgaaagcaaaaaaaaaaacat
aaagtcaaccttttgggaaaattgtcgtctttgacatcagaagagattcaaactaaaat
gaatgagtacgttacttgcggttatgggtgggttttcttttttaatttttagaaacttttc
ttacttatattttgaatcaacagttgataacacaagtataaattattattttcgccatc
acactggagtcagagctcgagagagacttgtttcttaatttaattcataaacttgtttcg
acagtgaatatatacatcttcgaagaaataacaccattgacttaaaaccaaataaata
acaatagtctttataattttatattttcacacttaaaattacaatacaagtcttttcaa
agtcttttaatttatataaacaatagaagtctttttcattgtctctttttgactaattaa
taaagaccatgaaaagacttgattgttaagttttgagtgtaaatgttaataaattacta
tggttttggttggttttatattttctgccatctaaataattacatttatatgataaaataat
taccctagcgacaaatgacagctagaaatgtaataagaacaccaactaaataattatgc
aggttaataatggagcaagtgatgttctttctatatactgtacatttttcttttttaaaaa
attatgtaatttcgcagaaagagaaaagaaaaacacgtgggtgattagagagtagtataaa
gatagttgggtgggttctgtttttttctgtatctcgaggcgccaaaaacaacaaaa
aaaacttcagagcggtgatcagattcaccgattttttctcaaaatg

FIG. 2C

SUBSTITUTE SHEET (RULE 26)

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17008 putative tyrosine aminotransferase

SEQ ID NO:
778

cataggactactacaatcagTTGAGAgagacgacgatctggttaatggcatggccactg
agtttgatagcttccttggagatggcatgacgatcatagaaaccttttagtcTGTCAAa
tatttcttgtaccactgattcgtcggttcctatcgatatcctcacccaattctctgccc
ctagagccactcctaaaaatttcaacacaaaataaataaataaagtaaataaaaaaag
attgatcataattaacgatgcaaatttataaattaaaatcatatgtaagaagattgacta
tgggagccccaagtctttaagatggtgtatattgttaaagagatcaatacctggtataa
ggataagactctcctcactaactagcttcgTGACGaaatcaaaatcatttttgatatta
ttcaacattgatgTGTCAAgcttcaactgtaaaataaatacgtttaagctaatacatttat
tattataagcaaaatatggagcatccaatagcaaaaaaaaatctagaaaaccaagaatc
caagaaaaagaattaaagtacccataaataagaacaagattcggggtttcttgggacaaa
agagacaaggaatatccttgagcctctcacatgaaagctcgACGTtgcgtctcatggct
ttgatcttcttctcgaagaactctttaggtgttttctccaatatatcaggaagtgttc
ctatcaaaatccataataatctcacattatttagagaaccaaaacttatagcttacgat
gatagtgagagattacaaacctggagaataaatagaaggctgtggagttaaatacaagaaa
atcctctatttgcttgaactacctgttggtgaacgaaaggcccatatattagttagaatc
ttcttaattggtgcggtaatcttatttttaagtaaaaactatagtgtttagaagTGACTg
accctgtagatacaaagataccattaggatcgttcatggcgatccagccaactctcca
gcctgggTGACCcatcctttggatatggatccgagcgtgatcacccggagctattgatg
caaacttccccatgggaataaaaggcttgtctccatatacaacatgatcatatacttcg
tcggatattatcattataccgagttttctagccatctccgcgacctaaagattagtcga
tatattaccaaaaaACGTtagttgttttacacttcaaaaaaacttatattacattaat

15042 cinnamyl alcohol dehydrogenase-like
protein (promoter up to BAC end)SEQ ID NO:
779

cattttttgatgattctttcttctttcttatcttgatctgctgctttcacgcttttgct
gtttatgtgtgtgtattactatatatatatatagagaaagttggaaacgtaacgtatgc
gtatgtgtgatgaaataattggtgtttctgcatagcacacatttgatggctataattga
gtgtaaatgtgttatattattgacaaaatttagtcaaaagcttaaaatcttttttagtc
gttgaaagatccttctagaaaaagacatttttttcttcttctttcatacgtggctc
atggctgtgtagttttattagaatttttaggtgaaaaaaatattagaagccaacaaaactt
aaatgaaatttatttgcattcataattcattttaccagtttataacaacaacgtaatcc
aaaaagtaaaatgagaaagaatggaatttgtgtactttgaaaggaagaaaaaccactat
tgacgtggacacgtcggctaaaggagggtccacgggggttggtgaacaaacaatgtggg
gtctaatacgtgtgtttgctttggtttaaaatcatgggtggccacgtgttgattcttgac
ctctctctgacatgaaactgtagcattgacggcccagatcagctgcgagaatacttccc
acaacatggaaattttacggcccagatcaacaaagaatcgatttgctctttactattt
cgaagaacaaagagtgcagttatgaataatagaaaagaaggacaaagagtgtgtgaat
ggcttcacattaaaacaaaagcccattatgaatgaccattcacatttcacaccagtt
tgaaaaatcgaccgtccaattaagtaacattcaaaaacccaaaagataaacctctaatt
cacgaatcacaacagcagcatgagccgtttcatcacgacgttatctcagagtttcttgg
aaataatttgttgtagcggacttgtggctgtaaatggggcccaatgcttaaatttacttg
tctcgtctcttctacacgtcttctcttccgaccacacccttcattcaattcaacgtctc

FIG. 2D

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12778 Lipase/Acylhydrolase with GDSL-motif family SEQ ID NO:
(promoter up to next ORF) 780

catcatttagagagagggagaaacagaactgtgaaaagagaagaagattgcttttgtgc
cttagctcgtagaccgattcggttatatttatattgcaagtactacaatttggcaatgaa
aataatagttcattttactatacaataataacgtgtagcgcgagggttcattttactat
acacctatttaacgcactagcaaacgattatcgatcaattatattatagttcgctta
atcacgtctgacgcattactgggtttctcttctactttatttttaattctcaacaaaata
tctattgttactacgagtaccaagaaagatcgtgcttttttttttttgggttcaacaaca
acttacaattacacaagagtctgaatacacataagctttaacccaatccggcaatatag
aatacaatttgggatcataattcagaaaagaaagagattccctagcaattctatctgcc
acacaattcccttctcatcgggtaaaagtcactttaacctcttcgaagtgtgaaaaga
tcgtgcatttagaggcaagaagtagaattaaacatacaaatcaccggaaatatagggt
gtaaatggtaaacactaaaccagattcagtaatttctgcagtaaccatttgcataaaaact
aaattttgctgactagccaaattcaacaaaaaaatttcaacaccaacatatagtagat
atgtttatttctgctaaaacttttggataatttacgagtacacaactcgaattaaaata
tttttaatatcaaaaatacatatcaaatagatatttttaataagtcagattatactgat
acgatatatgaataatatagatacataaaaatatcactaccagaatagacaagagacgaa
tatgttcggataattatagataatttggataataattttaataacgttttagataactta
aatcaattattaaaattttgcaaaaacaactcatacctatgctaagatatctttaaaa
gataaattatagtaatttccttaatcatcctcatcatattattgattaaattacttgaa
aacaattaaaaaaaacaattaacaatctatattttatcatcatgttaatttttgaaatt
attttcttaatagtgttttgacaaagattttcgtttaatttttacatatttttaatagt
tcaaatttaataaagaagaataactcaattttgcgttgacacaatcttaatagtatag

|| Subcluster B

20245 glutathione-conjugate transporter
AtMRP4

SEQ ID NO:
781

atttttctaataagacttttcttattctcatagactcttcttattcatctttcttaatc
aattcgaccaactcagtggaagacaaatctcacacgaccctttccactttttggtaact
ttattattaattttattagtagtggtgtagttcctttctttcttctgctgatctTGTCAAc
aaaataactaaatttttccctaagcggctgtttatatattattaacaaagggtttccgcgtg
tctcttgtttaactagtagactaaaaacaaatcgtaaaactcgattttctcaaccaaatt
tagaagatactacggcatgtaattagctaatagataaaagattcgaattttcgttccaat
ggatttgtcttttcttttgcccaaaaaccaagaatttgtcttctcttggcagtagtttagc
tagacaacgcataatagctatatattttgtgtacactGGTCAAggtcgtggatACGTCAc
taataatattatttccaataagtcctattaaaacattaaacaactttgagttttaaaac
aaacttagtgtaaagaaaataaaaatagcagacagtttacgggtaagactagatgacca
tatatgattgagtgcataaaacatctttttctttcttttttgaaaaagcgaaactaa
aagattattagttgttggaaatcagcttagcgtaatcttcgagaaaaatgactctaattgc
taaaatactgatttaataatcaattttctaattggTTGACCCAACagactttttttttttt
ctatcctctaataatatataatcatatagtagtaattatttagtagataatatgattaa
cACGTgaatagcaaagtttctatcatttttattcaaaaaaagattcataagtaataaaa
tgatAGTCAActtttctttttctttttgtgtttggccttttgtTGACGCGTCAAttgttg

FIG. 2E

SUBSTITUTE SHEET (RULE 26)

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tacaccaccagtcacactattgtgggatgtgataatcggtaccttttaatgtcaggagc
ttctttcttacattttccacttcaaacaaccgataattcagaggaattttctcttctcct
ctctctctctcttttttatattttttcactgggaaaaatg

17051 CTF2B involved in hydroxylation
and oxidation of an aromatic ring

SEQ ID NO:
782

catagccgcgttccaagaggaGGTCAAgtggattcacttttctataatcaatattaaat
tgtagtcacaaaattcaagaaacttatatagaccttatttttatttttgaacatcaatag
ttgtcgttgaaaagtatcttggggatatttagatttagcatatgAGTCAATGTTGgggtc
cttaagagttgaggctacaaattataactcagaaaaagtgtatatgccctttaatttt
tggcctattgggtcttttatggCGTCAactccaatttcagtttgaaaagaaaTGTCATA
actaacaatggttcttTTGACTttgaaatcttagaagtttegacttacceatttctac
aagtgttaaatagcactgttattcaaaatcttatatttggttaattgtgcttaatatatt
ttaaaatttaataacttcattaaaatccaatgttattcaaaactaaattacttttgaaa
tatgtgtatatgaagtcatttgaaatgaaatctcataaagtttcataagtaaattatta
gaataaaaacccaaggtaattgtatagatttttgaaatccacacaataatatcgaattgt
aaaatctagagaattcaatttcaattcatgaaggagtgttaataatcatcatggattttta
agttagttgattgaatataaaagtaggaaagatgtgggattcatgtgggtgggtttggccc
atctccatgatctctagtgaatttcagctTGACGcaactttcgttaagatcttacttca
ttgtgtgttggtgttgagcctcactggattgggtgtgtcggcttttttagttcactcagag
ttaagagtccttcgagtaagactctatcactatttaataaattaatgtaattgagttatg
ataattcaaattggatctccttcattccatagttgcatTTGACAtttttatataaaactt
gctgattatctaagtcacaatttgagtccttggtaatattcagtttcaatcatcaggag
atgtctaatagattaaaaaattaaagatagaaatgtctaattggattgaaatatataaagt
gactcagccaaaaacatgttaactgaaaatcttgataaaaatggagattctctgataac

19640 putative glutathione S-transferase

SEQ ID NO:
783

aatgtagttttttctgggttttgtggagttaatcactaccttttagcttggatttatagc
cttatgggtgttgatgggtcttgtgataaaacgacgacgaactttgccgttttatatgggc
ggcagtgatgtaaatgcaagagtcctagaaggaaacagatgTTGACTttacaacata
tttataACGTtccctttataatttttttttatctcttttttagtaagtggagatgtgtc
ctaattcctaaccttgccttatccctggagcatgtgtaccTTGACTtgatccattcatt
ttctgaagacaaccccatgcttCGTCAagaatttcttctgcttcccccaattatacccat
cactttatcgtgggtcttcataattgatccattttgtctgtgtatgaaacatcaacagc
tttaaaaccatttgcattctcgtttgttatattgacgcccccaagaaaacaaacaactct
atagtctgagctataaaaaaagaattagtactaatctgttatttgatgttccttttggc
atatattaaaaatgttgttgttataataggcgttgggtttttccggtttctccatctacga
acttgtttgctgaattttccttccaacaatgttataaagtatcgggtgaattttctatgg
ttacaagactcaccacctcacgataactaaaaatataactaaagaaatttggttatattgtg
ccgcaacaatatagaccacatgtccgttgtactttcctctgtttacacaacttcttACG
TgtcgaaatacatgttcacatttaatacatagttgtgggttttattaagaaggatgggtTTG

FIG. 2F

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ACTaaattatagctttttatctactttttctttcatatgaaaactccagggtttatgaacca
atcttcttatgatttgtaagaaattgaatactactacattttaaagtgtttataataatta
aTTGACAttagaatttagtaaaaaacactaattgttcatacaaatgtttcattttattggt
catacaaaactattataacaagattacacaaacatatagttaacatctactgatcgaaga
gtatcattggtgtctcttaggctgatttgattctttctacaactttcttcatatg

14248 PAD3_at member of the PF|00067
Cytochrome P450 family

SEQ ID NO:
784

gttctggtcgaaggatttgtcccgaatgccaatggcgattgctagtgtggaactagca
ttgatgaatttgctttattattttgattggagtatgcctgatgggactaaagggtgaaga
cattgatatggaagaagctggtaatatctctatTGTCAGaaaatacctcttcaacttg
tgctgttcaACGTtattgatgagcaataataagctcgataacatggaaagtgtatg
aagcaaaaaacataagattcttttagattttgttgtgttatataagaaagaaatgttcca
ataataaatcaagaaagaataacttttgttcatttacttaaaaactagatcataatcaa
cacggattaagatctttttcattcaacaaaattctaaattttgtttttttaagtaaaaa
atgttatagcataaatgttcagatttttatgtcgtatttatattgaattaaatataggac
aaagaaaaataagatacagaacaaagagaaattttgatccaaaaaaaaaagaaagaga
aataagatctagaacaaaaacgatacattcagattgattattgaaatcaaataatcgaa
tttataattgaatttgatggaatttataatgtattttttgtcatggaaataataaagtt
tgttaatatagtaggcacgatcgaatctggagcttcaattttttttaactaattgtta
tggaagatgctggaatgatctctttttacaagaaagctcctctcattcttgttccggtt
aaacaccattaatgacatcggcacacaaaaattcaaacaccggttgaagattgtttgcta
tactttatttttatcaataataagttgcggtacttggttaactgtatACGTacttctat
ttcttatagttgtgcgataattaccacaagtccaaaaaagtaaaatatgaatttgataa
agcagtgtaaacctgagattttcaagatttgggcctaaaccattagagaatgctACGT
agagaaccattgggcccataaaacttattttattcccgcgaaagcctgagtggaattcgaac
cactaccacaaaaagtaagagtttgggttattttgatttttaattcattcatttgaattat
tatagacaccggacagtgaacttatgataaagagatttttaacctttaaaactaaaacac
taaaatacataatccaaagaagacggaacaaaaaacaaaaacagagccaggaataatg

17500 athcallga_s_at calmodulin-like protein
(promoter up to next ORF)

SEQ ID NO:
785

catcaaaactaattttgggttattcttgagattaggaatgtgtgttcacctaaaagctagta
attgattactaaaatgtaatgcatgcaacaagaagagtcaatcgaatttttatagagata
agtcataataaaatgattaattatcgctagaggaagctgcgatgaaattttcttacagctt
ttgtctttttacccatctaatacatttaattctctgagcctacgccatcacacatatctaaa
agcaccttcttcgaaattcccttggaggacaaaacatggacctctttttgttccattg
gattttctcggaataatgacttgcattgtcttcttactatattttatgtatcccttcattc
tatactttttcgaaattctaatttaactctacataataatcccactcccaccagctaaag
tttagacatgacaagtattttatcaaagtctccttcaattcaaactactgaatattgtt
tggaataagtactttttggagacgtaagctatattttccaatccgaaatgaatgaaccaa
atgtccatagttctgttttttttctcctaaagtgaatatattaagagacactaaatt
ctagaaaatatgtttaaaataataataatcagtaattgtccaaaaaatgtgaataactta

FIG. 2G

SUBSTITUTE SHEET (RULE 26)

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aatcaaaatcaggatacgattgtcacaagaaacaaactttcctagataatgtatatatttt
atattattatcatattatgtatgcacttaagacatctccatccatgagaaacctacaaa
gtttttcaaacaaaaaaaatattaatattatattataatttgattattttttattaaaaa
agtatttttgttaaaaaattaaaccaatagtaagatgagaattgtcatgatgggttgta
caaagtatctcagagtatctcagagtttctcacttgagaaactttctacactctctctc
cttcattttttattattttttatttttttaattgtgagaaattcttatgagatacccacaa
tagagatgggtcttataaaatttatcaacatgggtgaatctctcatgttatatatagagggtg
atttaaaggctaaatagaataacacactacagcatataaactcaatgatatg

18928 putative endochitinase (promoter up to next repeat region) SEQ ID NO: 786

catttttgtgtatggagggtgttgtgtgaagaaatgaagaagggtgtgttgatgtatttat
agtgtaaatttggtctattcaaattgaaatattgatcagtggttagacatctttcacgat
tattgattggctttttctgagtc aaagtc aatgccactttgtaccacttaacaaaagtc
aatgacacagttttttctcttgtcgttatgagaaattccatgtcgggtcatagatcagat
caaaaacgaatatgtaatcaaaaattttaaagagccaagttacttggatgaaaatcattc
tcataaaaaacttgattgagataatcaagtttagattagttcaaacgtttgagatttttc
tattgaatagttccaagtttttggttaattagctcaaacgatattgttagctaataatagc
attttttttgggtcaactaatatagcatttagaacgttcttttaaagtcttactttgatt
tttaacaaaaattgtatggaattgtgagaaaaatgactagtgaagccaaaatgtttcta
tttataaatcaaaatcaacaaaattagaaaaatccaactcaattattgcaatttccaa
atagtcatgcgtcaaaaattaaaccagcatatcaataaaaagcggtttagtcttaccac
cctgggtctagagactctagaaccatcggagctcaagtgaaaaacgacgccgttaagctg
catctttcaagatagataaaaaacttttgtcgatcgcttcatctctcacagagtttcggc
tcctccgttgtgtttcaggacgacgcaaaggggaaaaaaaattgaattctttctctcca
agcgaaactagggtttcgaaagtctctgtctcatcaaagcttcgaaaaggtagatttat
ggtttcttactctcctttctctatgatattccaatttcttgcgagcttgctcagtggtc
ttaccttatatttaccgaaccagtgcccttatattctatcacattcgaagttattgggt
tctgggttacttatattgcttattgttctatgactacgatataattatcccaaagatttg
ttctttttctccgaatttggttagaaatggatataactcaaattctgaacatgcccagaa
gaatcct

14614 putative glucosyltransferase (promoter up to next repeat region) SEQ ID NO: 787

ttaatttatccacacctcaacgaaaatttccggttggtgcgctaacgaattcaggctgtg
aagttaaaagaaaataaacaaaattatagcttcacataagcgatcgatcttcaaactct
acacatgacagaagcaaataactaaattaaatagcgtaaatTTTGTaataatactagaa
aacctaaaaaccaaattgtaaaaaaccttatgggaaaaaatgtgataaagcacctaaacc
atagaataacttaaaaatttcaatttcccaatcaagggtatgatataaaaacccatggaaaa
caaattctcagccatatttctatctgaccgagtcctttttcaaaataatatatagacgggt
agagtccttatatagtaaaaaacatttttttaaaactaatttatcttctcatatgaaaatg
aatgcaaataaaaatgaccatatatgctgtaatgatattcaaggaagagatatcacaac
aagggtcgaagaaatatacaatatctgaaagtcgactatatgggtccactttccaaattag

FIG. 2H

SUBSTITUTE SHEET (RULE 26)

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agatggaaagaagaacgattatgcagcaaaccattgatcggacgaagaagaataaa
tatggaggccattactatagtatttggccttgaaatattttgggtccgagaaataataa
ataaacagttatggcttttcggatttgggttgctttcaattttctcaaagtgttgacaa
gtgttattacactcacctaaaacaggatcattccaatttcttgggctcagagtctgtac
tttcttcttctttaaaccaaggtcttataagtattctctaaaccaagtcactaaacaat
aattgggtcttgggtctgggtcaaacttggatcaatgttgccacatagccattagccaca
caaaacaaaaattgtcttgcctttatatggaatgaagaaaaatcgaattttgtaaccat
ttttgactttaagtcacactcgccgtatacggcacaccaaatagacaaaaacatttga
ccaccaactttgctttaatgttaaaaactttttttttgcatcccactactctcttctca
cctcctcaagtcacagtgaccaaatacacacacttcacaagaacaacctatg

||| Additional genes showing early and transient RPP-triggered
expression

13176 Contains Myb DNA-binding domain
repeat signatures

SEQ ID NO:
788

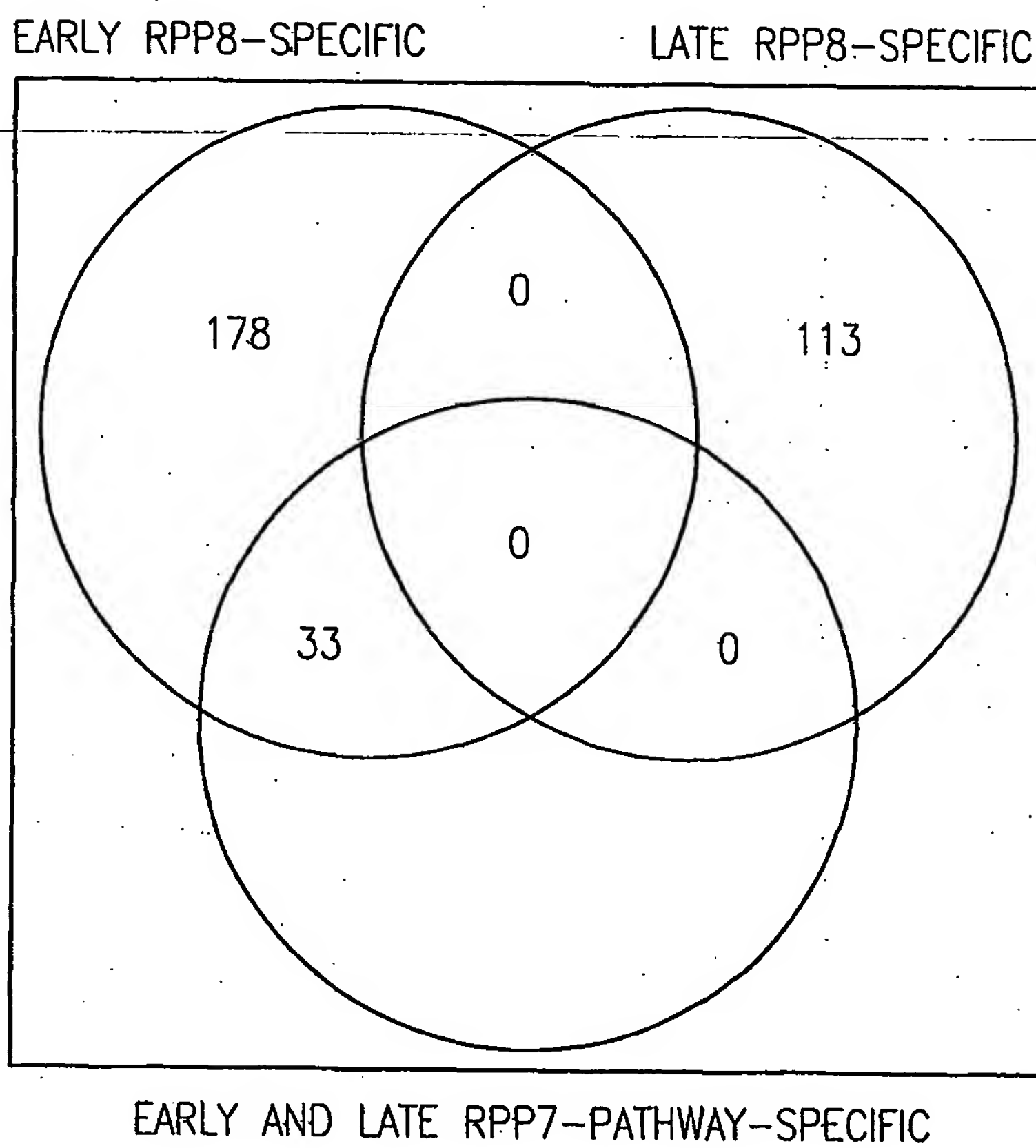
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FIG. 21

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26 *Peronospora* (Hiks1 and Emco5) induced
RPP7, EDM1,2,3 and RPP8-Dependent genes

**FIG. 3**

RPP4-pathway, RPP7-pathway and
RPP8-up-regulated transcription factor genes

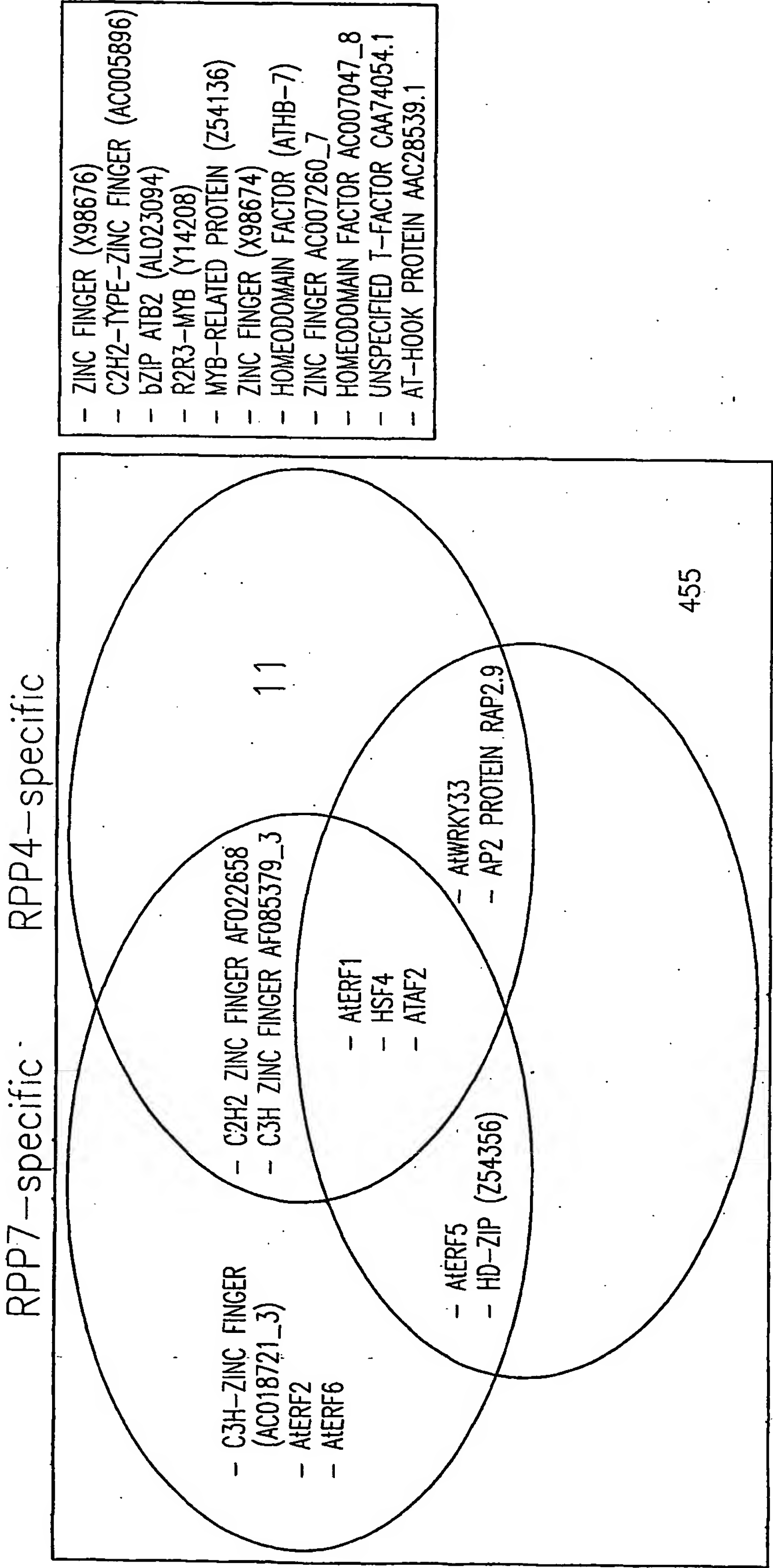


FIG. 4

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